Program & Abstracts

Foreword

"Most of the fundamental ideas of science are essentially simple, and may, as a rule, be expressed in a language comprehensible to everyone." Albert Einstein.

With that thought in mind, the local arrangements committee warmly welcomes the delegates to Plant Canada 2007 in Saskatoon from June 10–14, 2007. As an organization, Plant Canada promotes the interaction of six Canadian plant science societies, each with differing perspectives on science. By meeting once every few years, this meeting provides us with the opportunity to walk across multidisciplinary bridges and communicate the nuances and the passions of our particular sciences.

"When planning for a year, plant corn; when planning for a decade, plant trees, and when planning for life, train and educate people." Chinese Proverb.

We hope you will find the program both entertaining and enlightening. We offer two plenary sessions with seven international keynote speakers, and follow up with several special society sessions, education and industry symposia, student competitions, as well as *hands-on* workshops. With 162 posters and 179 oral presentations, there is a diversity to choose from and lots to learn. The trade show area has something for everyone. Don't forget to stop by the University of Saskatchewan Bookstore booth, specially set up with educational and recreational titles related to the plant sciences. Also, Riverbend Plantation has a table with Saskatchewan food delights that you can take home.

I also would like to acknowledge the efforts of Richard Gugel and Ginette Séguin-Swartz in preparing this program book and the final book of abstracts, which will be posted on www.plantcanada.ca.

Karen Bailey,
Chairperson, Organizing Committee

Plant Canada 2007

Program & Abstracts

Saskatoon, Saskatchewan
10–14 June 2007

Compiled by R.K. Gugel and G. Séguin-Swartz

Plant Canada (the Federation)

Plant Canada 2007 is organized under the direction of Plant Canada, a federation of Canadian plant science societies. The following information about Plant Canada is also available at the federation's website: **http://www.plantcanada.ca/**.

Purposes

- To organize and sponsor regular, effective scientific meetings and workshops under a national umbrella for plant science and related disciplines in Canada
- To operate and maintain a strong communication network among Member Societies and their individual members
- To be a strong and effective force for public education and advocacy in plant and related sciences

A Brief History

Prior to the formation of Plant Canada, the discipline of Plant Science or Plant Biology in Canada was fragmented into many small societies, each of which often met separately. In 1997, the Presidents of the CSPP and the CBA began discussing the possibility of merging the two societies. A committee to explore this idea was struck and was headed by Dr. Iain Taylor (UBC); this committee met several times during the next three years. It was soon established that a federation of existing societies was more agreeable than a merger and, at the 2000 joint meeting of the CBA and the CSPP, the Constitution and By-laws for the new federation were ratified in the business meetings of both societies. Since that time, we have been pleased to welcome four other societies as continuing members.

Board of Directors (as of 01 April 2007)

Made up of the president, secretary, and two individuals from each of the member societies:

- Hargurdeep Saini, President (CSPP)
- Gavin Humphreys, Secretary (CSA)
- Carol Peterson,Treasurer and Past President (CSPP)
- Robert Guy (CSPP)
- Peter Pauls (CSPP)
- Christian Lacroix (CBA)
- Rodger Evans (CBA)
- Bruce Gossen (CPS)
- Jim Menzies (CPS)
- Anne Légère (CWSS)
- Len Juras (CWSS)
- Tom Bruulsema (CSA)
- Shahrokh Khanizadeh (CSHS)
- David Percival (CSHS)

Please direct suggestions or comments about Plant Canada 2007 to the Plant Canada board members. Contact information is available at http://www.plantcanada.ca/.

Participating Societies and Organizing Committees

Plant Canada 2007 is a joint meeting of the following six scientific societies

- CPS (Canadian Phytopathological Society) http://cps-scp.ca/
- CBA (Canadian Botanical Association) http://www.cba-abc.ca/
- CSA (Canadian Society of Agronomy) http://agronomycanada.com/
- CSHS (Canadian Society for Horticultural Science) http://www.cshs.ca/
- CSPP (Canadian Society of Plant Physiologists) http://cspp-scpv.ca/
- CWSS (Canadian Weed Science Society) http://cwss-scm.ca/

National Organizing Committee

- CPS – Karen Bailey (Chair), Bruce Gossen
- CBA – Art Davis
- CSA – Bruce Coulman
- CSHS – Karen Tanino, Bob Bors
- CSPP – Gordon Gray
- CWSS – Tom Wolf, Anne Légère

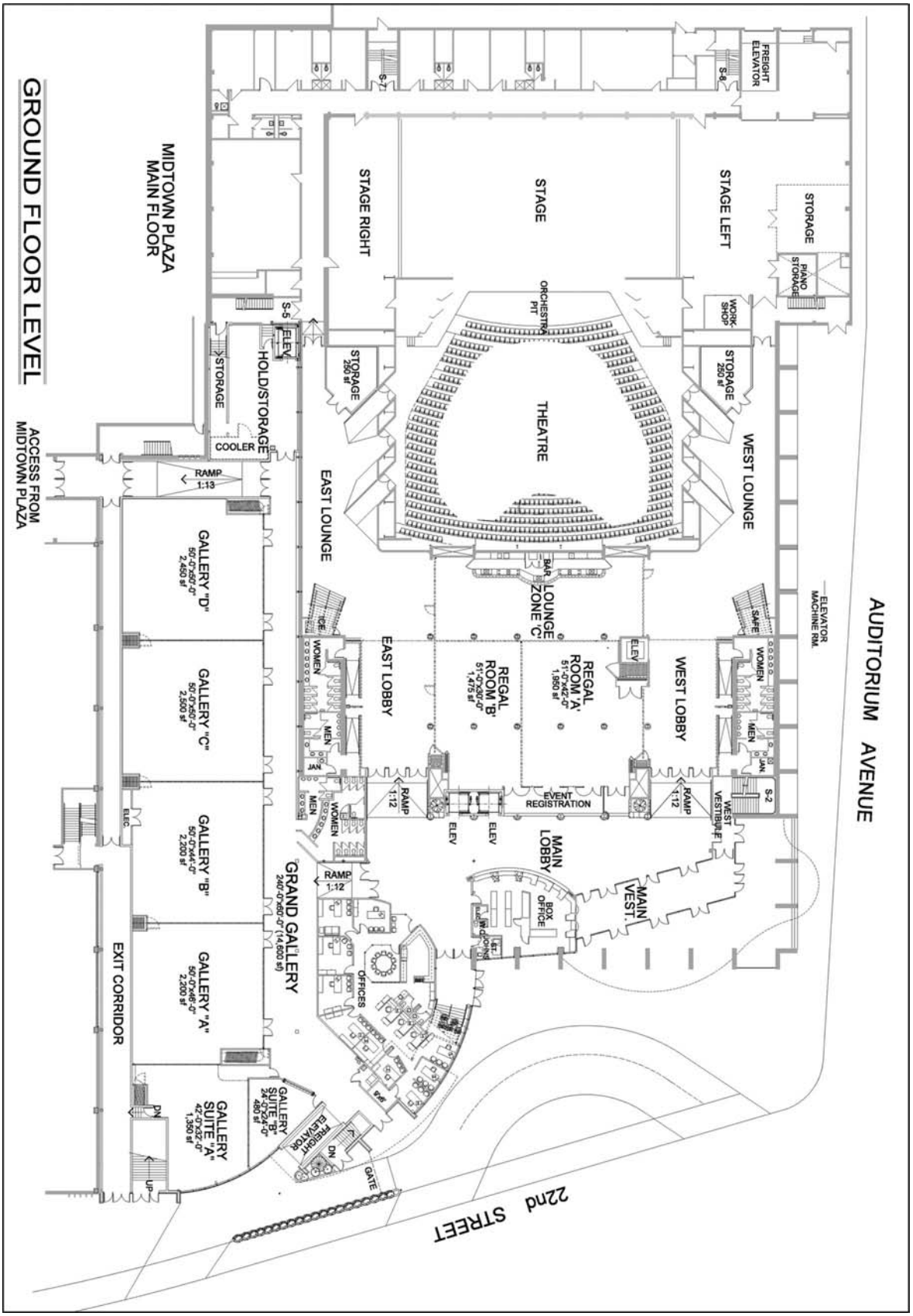
Local Arrangements Committee

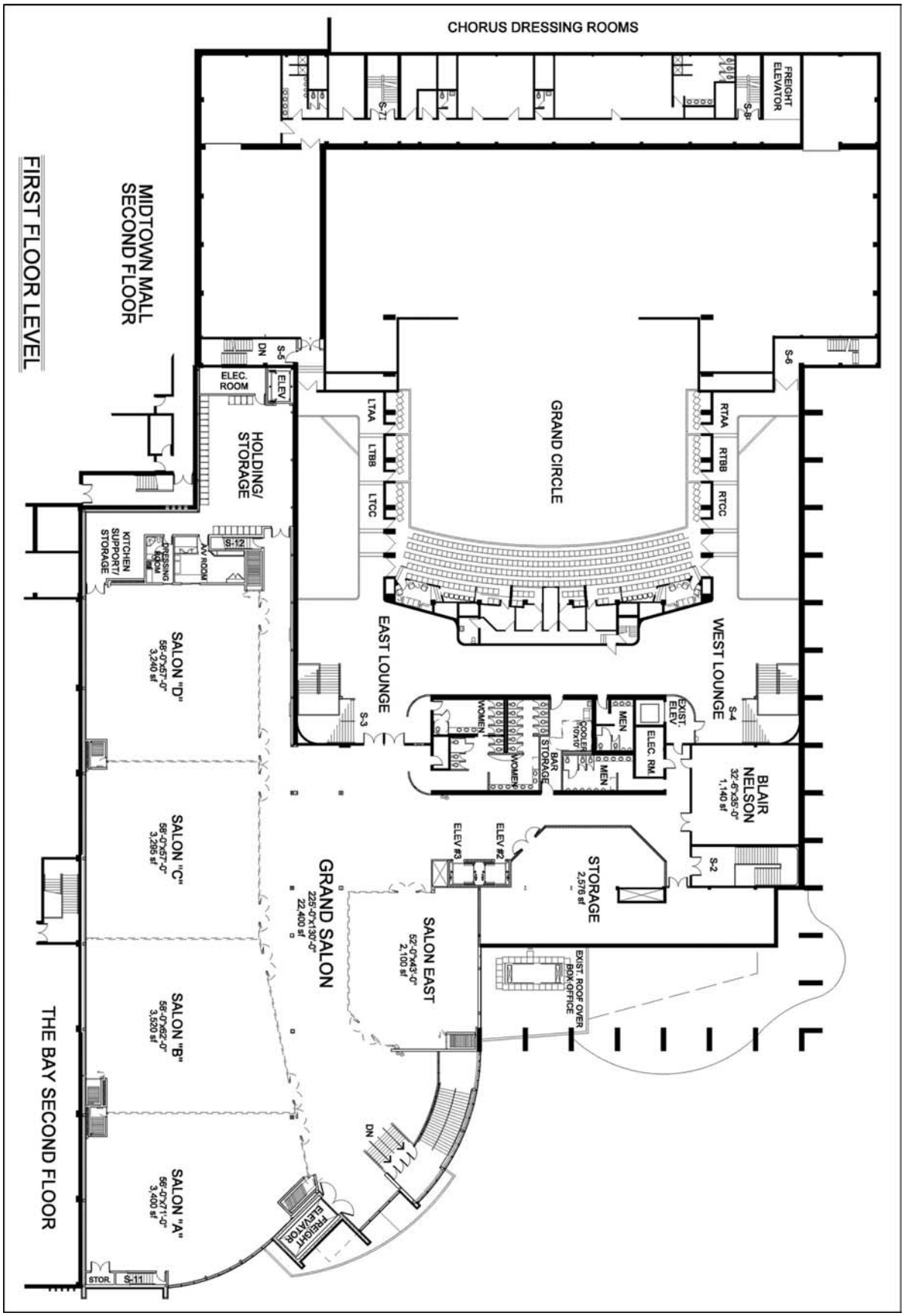
- Sabine Banniza
- Sue Boyetchko
- Bill Brooks
- Godfrey Chongo
- Coreen Franke
- David Greenshields
- Richard Gugel
- Regan Kennedy
- Mark Kuchuran
- Randy Kutcher
- Mary Leggett
- Robin Morrall
- Chrystel Olivier
- Penny Pearse
- Soledade Pedras
- Gary Peng
- Derek Potts
- Ginette Séguin-Swartz
- Jill Thomson
- Janice Tranberg
- Grant Wood

Conference Management Services

- Debbie Apfeld, McPhersonClarke (Calgary, AB)

Maps of Main Venue: TCU Place




CHORUS DRESSING ROOMS
FREIGHT ELEVATOR
S-7
S-8
FIRST FLOOR LEVEL
MIDTOWN MALL
SECOND FLOOR
DN
S-5
ELEC. ROOM
ELEV
HOLDING/ STORAGE
KITCHEN SUPPORT/ STORAGE
DRESSING ROOM
AV ROOM
S-12
SALON "D"
58'-0"x57'-0"
3,240 sf
SALON "C"
58'-0"x57'-0"
3,286 sf
SALON "B"
58'-0"x62'-0"
3,520 sf
SALON "A"
56'-0"x71'-0"
3,400 sf
THE BAY SECOND FLOOR
STOR.
S-11
FREIGHT ELEVATOR
DN
GRAND SALON
225'-0"x130'-0"
22,400 sf
SALON EAST
52'-0"x43'-0"
2,100 sf
ELEV #3
ELEV #2
STORAGE
2,576 sf
EXIST. ROOF OVER BOX OFFICE
GRAND CIRCLE
LTAA
LTBB
LTCC
RTAA
RTBB
RTCC
S-6
EAST LOUNGE
S-3
WEST LOUNGE
S-4
WOMEN
WOMEN
BAR STORAGE
COOLER 10'0"x10'
MEN
MEN
ELEC. RM.
EXIST. ELEV.
BLAIR NELSON
32'-6"x35'-0"
1,140 sf
S-2

Poster and Trade Show Exhibit Hours

Posters and trade show exhibits are to be set up at TCU Place, Salon A and Salon East, from 12:00–19:00 Sunday 10 June, and 07:30–10:00 Monday 11 June.

Poster presentations are organized by the following headings:

- Pest Management
- Plant Development and Improvement
- Plant Responses to the Environment

Poster sessions are from 17:00–18:30 on Monday 11 June and Tuesday 12 June. Authors with even numbered posters should be present Monday 11 June, and those with odd numbered posters should be present Tuesday 12 June. Posters entered in the student poster competition will be judged Monday 11 June. A cash bar and snacks will be provided at the poster sessions.

Salon A and Salon East will be open for viewing posters and the trade show throughout the conference, including coffee and lunch breaks.

Posters and trade show exhibits must be taken down by 10:30 Thursday 14 June.

Oral Presentations

Please come to the session room at least 15 minutes before the session start time to load your presentation onto the projector computer. Your presentation must be in WindowsXP-compatible PowerPoint format, on a CD-ROM or a USB memory stick. You will not be able to connect your personal computer to the projector.

Sessions with Invited Speakers

All sessions with invited speakers are at TCU Place.

Plenary Sessions

- Plenary 1: Natural Products: Biology, chemistry, and application.
  08:30–12:00 Monday 11 June, Salon B,C,D.
- Plenary 2: Plant health networks: The international experience.
  08:30–12:00 Wednesday 13 June, Salon B,C,D.

Society Sessions

CSHS

- Natural products from horticultural crops.
  08:30–10:00 Tuesday 12 June, Gallery D.
- Organic horticulture: Separating fact from fantasy.
  08:30–10:00 Thursday 14 June, Gallery A.

CBA

- Ontogeny of the flower: The next generation.
  08:30–10:00 Tuesday 12 June, Gallery C.
- Floristics for the future.
  10:30–12:00 Thursday 14 June, Gallery A.

CSPP

- Natural products.
  15:30–17:00 Tuesday 12 June, Blair Nelson Room.
- Phloem and long distance signalling.
  08:30–10:00 Thursday 14 June, Gallery B.

CPS

- Emerging plant disease epidemics.
  10:30–12:00 Tuesday 12 June, Gallery D.
- Linking plant pathology with industry.
  10:30–12:00 Thursday 14 June, Gallery B.

CSA

- Progress in organic cropping systems.
  10:30–12:00 Tuesday 12 June, Gallery C.
- Emerging barriers to marketing crops.
  13:30–15:00 Tuesday 12 June, Blair Nelson Room.

CBA/CSPP

- Education in action.
  08:30–10:00 Tuesday 12 June, Blair Nelson Room.

CWSS/CBA

- Plant ecology and invasive species.
  15:00–17:00 Wednesday 13 June, Gallery D.

Luella K. Weresub Mycology Lecture (CBA)

- 20:00–21:00 Tuesday 12 June, Gallery B.

Designing a New Agri-Food Industry

- 13:30–17:00 Tuesday 12 June, Gallery D.
  Sponsored by Saskatchewan Wheat Pool.

Communicating Plant Science

- 10:30–12:00 Tuesday 12 June, Blair Nelson Room.

CSHS Natural Products Special Seminar

- 18:00–18:30 Tuesday 12 June, Blair Nelson Room.

CSHS Organic Horticulture Forum

- 17:00–18:30 Wednesday 13 June, Gallery B.

AAFC/CSA Gaps Symposium

- 08:00–12:00 Thursday 14 June, Gallery D.

Other Sessions and Meetings

All the following conference sessions and meetings are at TCU Place.

Student Oral Presentation Competition Sessions

- 13:30–17:00 Monday 11 June.

Concurrent sessions are organized by Society. Room assignments are as follows:

- CPS – Salon B
- CBA – Salon C
- CSA – Salon C
- CSPP – Salon D

Contributed Oral Presentation Sessions

Contributed oral presentations are organized by the following headings:

- Pest Management
- Plant Development and Improvement
- Plant Responses to the Environment

There are several sessions for each of the headings. Consult the detailed program for times and locations.

Campbell Scientific Datalogger Demonstration

- 09:00–10:00 Tuesday 12 June, Gallery Suite A (1).

A demonstration of some new Campbell Scientific datalogger equipment.

Zeiss Microscopy Demonstration

- 10:30–11:30 Tuesday 12 June, Gallery Suite A (1).

A demonstration of Zeiss microscopes for different applications, including some newly introduced technologies.

CBA Section Meetings

Meeting times and room assignments for the CBA Section meetings are as follows:

- 12:00–13:00 Monday 11 June.
  Development – Gallery B
  Conservation – Gallery C
- 12:00–13:00 Tuesday 12 June.
  Mycology – Gallery A
  Teaching – Gallery B
  Systematics and Phytogeography – Gallery D
- 17:00–18:00 Wednesday 13 June.
  Ecology – Gallery D

Canadian Plant Hormone Profiling Centre Proposal

- 12:00–13:00 Monday 11 June, Gallery A.

The Canadian Plant Hormone Profiling Centre is looking for support from researchers and funding agencies to make hormone profiling available at a non-restrictive cost to all Canadian and international plant researchers. An update on the progress and future plans will be presented.

Other Events

Pre-Conference Field Trips

- 13:00–17:00 Sunday 10 June.

Two tours are scheduled for Sunday afternoon. Pre-registration is required.

1. Western Development Museum.
2. Wanuskewin Heritage Park.

Meet at the buses on the west side of TCU Place at 12:45. Walking shoes, a light jacket and a hat are recommended for those going on the Wanuskewin Heritage Park tour.

Post-Conference Field Trips

- 08:00–12:00 and 12:00–16:00 Thursday 14 June.

Three tours of various parts of the University of Saskatchewan campus are scheduled for Thursday morning and afternoon. Pre-registration is required.

1. University of Saskatchewan Agriculture Building and AAFC-Plant Gene Resources of Canada.
2. Canadian Light Source Synchrotron and Plant Science Greenhouse.
3. University of Saskatchewan Horticulture field plots and Patterson Garden.

Meet at the buses on the west side of TCU Place at 07:45 for the morning tour, and at 11:45 for the afternoon tour. Walking shoes, a light jacket and a hat are recommended for those going on the U of S Horticulture and Patterson Garden tour. Those going on two tours will have time for lunch at the Agriculture Building between tours (no need to go back to TCU Place between tours).

- 13:00–16:30 Thursday 14 June.

The CSA has organized a field trip to the U of S Kernen Crop Research Farm and the AAFC-Saskatoon Research Centre Research Farm on Thursday afternoon. Pre-registration is required. Meet at the bus on the west side of TCU Place at 12:45. Walking shoes, a light jacket and a hat are recommended.

Workshop on Scientific Publication

- 13:00–16:00 Sunday 10 June, Gallery Suite A (1).

Organized by Iain Taylor, NRC Press and Larry Peterson, Canadian Journal of Botany, this workshop will provide guidance and instruction for those learning to write scientific papers. Pre-registration is required.

Opening Reception

- 19:30–22:00 Sunday 10 June, Hilton Garden Inn (Commonwealth Ballroom).

Included with delegate and guest registration. A cash bar and light food will be provided, along with musical entertainment by the jazz trio POP'N the CLUTCH.

Lunches for Registered Delegates and Guests

Lunches on Monday 11 June, Tuesday 12 June, and Wednesday 13 June are included with registration. On Monday and Tuesday, lunch is from 12:00–13:30 at TCU Place (Grand Salon and Salon B,C,D). On Wednesday, each Society will have its own luncheon, annual general meeting and awards. Consult the detailed schedule or the "Society General and Executive Meetings" section of this program for Society luncheon room assignments.

Graduate Student Social

- 19:00–23:30 Monday 11 June, Winston's English Pub & Grill, 243 – 21st Street East.

All conference graduate students are invited to celebrate the end of the student presentations at a local pub, which is within easy walking distance of TCU Place. Drinks, pizza and finger food will be provided. The event is free to Society Student Members who pre-register for the event (free drinks start at 19:45). Students will meet at 18:30 in Salon B after the Poster Session on Monday to pick up their tickets. Transportation will be provided for those students who require it.

Wine Education

- 19:00–21:00 Monday 11 June, Hilton Garden Inn (Prince Albert East and West Rooms).

Members of the International Sommelier Guild will be present to guide you through the tasting of five wines and teach you what makes each one special through the different viticultural and vinification techniques used to produce them. Hors d'oeuvres selected to complement the wines will be served to demonstrate the influence of food-wine pairing. Pre-registration is required.

Society Awards

- 12:00–14:30 Wednesday 13 June, TCU Place.

Society awards will be presented at separate Society luncheons (included with registration). Consult the detailed schedule or the "Society General and Executive Meetings" section of this program for Society luncheon room assignments.

Conference Banquet

- 18:00–23:30 Wednesday 13 June, TCU Place (Salon B,C,D)

Conference banquet tickets must be purchased in advance. Cocktails (cash bar) begin at 18:00, and the banquet gets underway at 19:00. Piano entertainment by Martin Janovsky will accompany dessert, and live band entertainment by Solar Rio will commence after dinner. The band features Brazilian artists K.K. Nogueira on guitar and vocals, and Eduardo Valle on cavaquinho and percussion, along with accomplished local players Sheldon Corbett on saxophone, keyboards and flute, Lloyd Tomczak on bass, and Paul Benjamin on drums.

Society General and Executive Meetings

CPS

- Financial Advisory Committee meeting: 18:00–22:00 Saturday 09 June, Hilton Garden Inn (Kindersley Suite). Includes dinner.
- Board meeting: 09:00–15:30 Sunday 10 June, Hilton Garden Inn (Prince Albert East Room). Includes lunch.
- Luncheon, annual general meeting, awards: 12:00–14:30 Wednesday 13 June, TCU Place (Gallery A).
- Board meeting: 12:30–14:30 Thursday 14 June, Hilton Garden Inn (Prince Albert East and West Rooms).

CSPP

- Board meeting: 19:00–22:00 Monday 11 June, Hilton Garden Inn (Vice Regal Hospitality Room).
- Luncheon, annual general meeting, awards: 12:00–14:30 Wednesday 13 June, TCU Place (Gallery B).
- Board meeting: 12:30–14:30 Thursday 14 June, TCU Place (Gallery B).

CBA

- Board meeting: 17:30–19:00 Sunday 10 June, Hilton Garden Inn (Prince Albert East Room).
- Luncheon, annual general meeting, awards: 12:00–14:30 Wednesday 13 June, TCU Place (Gallery C).
- Board meeting: 14:00–15:30 Thursday 14 June, TCU Place (Gallery Suite A (1)).

CSA

- Board meeting: 09:00–15:00 Sunday 10 June, Hilton Garden Inn (Regina Room). Includes lunch.
- General discussion of members: 17:00–19:00 Tuesday 12 June, TCU Place (Gallery Suite A (1)).
- Luncheon, annual general meeting, awards: 12:00–14:30 Wednesday 13 June, TCU Place (Gallery D).
- Board meeting: 16:00–17:00 Wednesday 13 June, TCU Place (Gallery Suite A (1)).

CSHS

- Board meeting: 09:00–12:00 Sunday 10 June, Hilton Garden Inn (Prince Albert West Room).
- Luncheon, annual general meeting, awards, election: 12:00–15:00 Wednesday 13 June, TCU Place (Gallery Suite A (1)).

Plant Canada

- Board meeting: 15:30–17:30 Sunday 10 June, Hilton Garden Inn (Prince Albert West Room).
- Board meeting: 15:30–17:30 Thursday 14 June, Hilton Garden Inn (Prince Albert East and West Rooms).

BASF

The Chemical Company

BASF Canada Agricultural Products is committed to playing a key role in the success and sustainability of agriculture in Canada. Our diversified resources and investment in research, development and manufacturing allow us to bring global knowledge and technology to our customers.

At BASF, our vision is to be the world's leading agricultural innovator by optimizing crop production, improving nutrition and enhancing the quality of life. Our mission is to enhance value by delivering products and services that satisfy customers' needs and contribute to the sustainability of agriculture.

In Canada, BASF is a leading supplier of crop production products, including herbicides, fungicides, seed treatments and insecticides for cereal, oilseed, pulse, corn, soybean and specialty crops.

BASF has a comprehensive product portfolio which includes products such as ABSOLUTE®, ADRENALIN®, ALTITUDE FX™, CHARTER®, DYVEL®, DYVEL® DSp, EQUINOX™, FLAXMAX®, GEMINI™, HEADLINE®, LANCE®, ODYSSEY®, POAST® ULTRA, PURSUIT®, RONILAN®, and SOLO™.

The CLEARFIELD® Production System is another example of BASF innovation that combines advanced genetics developed using enhanced plant breeding methods with state-of-the-art herbicides.

BASF Canada Agricultural Products is a part of BASF, the world's leading chemical company: The Chemical Company. Its portfolio ranges from chemicals, plastics, performance products, agricultural products and fine chemicals to crude oil and natural gas. As a reliable partner to virtually all industries, BASF's intelligent system solutions and high-value products help its customers to be more successful. BASF develops new technologies and uses them to open up additional market opportunities. It combines economic success with environmental protection and social responsibility, thus contributing to a better future.

More information on BASF Canada Agricultural Products is available at www.agsolutions.ca.

Always read and follow label directions.

ABSOLUTE, ADRENALIN, CHARTER, DYVEL, FLAXMAX, HEADLINE, LANCE, ODYSSEY, POAST, PURSUIT, RONILAN and CLEARFIELD are registered trademarks and ALTITUDE FX, EQUINOX, GEMINI, and SOLO are trademarks of BASF.

Canadian Food Inspection Agency | Agence canadienne d'inspection des aliments

The Canadian Food Inspection Agency (CFIA) is pleased to support the guest speakers of Plenary Session II at Plant Canada 2007.

The CFIA is dedicated to safeguarding food, animals and plants through science-based regulation to enhance the health and well-being of Canada's people, environment and economy and to support Canada's competitive domestic and international markets.

While the safety of Canada's food supply is central to everything the CFIA does, the Agency also protects the plants upon which safe and high-quality food depends.

CFIA agrologists, biologists and inspectors visit commercial nurseries, grain storage facilities, farms, public parks and other locations to carry out inspections and conduct surveys for pests. CFIA scientists provide risk assessment, lab testing and scientific advice to support surveillance and identification of plant pests and new invasive species and their associated risks. If a new pest is found, the Agency imposes quarantine and other control measures to restrict the spread of, or eradicate, the pest. The CFIA also inspects imports of plants, plant products and soil to prevent the entry of pests that could affect Canada's plant resource base and market access.

The CFIA is an integral part to the government's capacity to respond rapidly and effectively in the event of a threat to agricultural or forest biosecurity. Agency surveillance and inspection programs are designed to detect the presence of hazards in plants and their products, and provide an early warning for problems whether they are accidental or intentional.

For more information about the CFIA, visit www.inspection.gc.ca.

Saskatchewan Agriculture and Food

Saskatchewan Agriculture and Food (SAF) promotes the growth of a commercially viable and sustainable agriculture and food sector. The department offers programs, technical support and specialist services to encourage expansion of the livestock sector, the diversification to higher value crops and additional processing of both livestock and crops. SAF's Development Division includes the Crop Development, Agriculture Research, Agri-Business Development, Market Development and Food, and Irrigation Development branches.

The Crop Development Branch provides services in crop production, industry development and production technology, including crop protection and soil management.

The Agriculture Research Branch, through its Agri-Value Program, provides funding to entrepreneurs and businesses wishing to explore value-added opportunities. The department also funds research and development in areas such as new crop varieties, dryland farming techniques and equipment, improved livestock genetics, disease control in both crops and livestock, and agricultural biotechnology.

The Agri-Business Development Branch provides specialized agriculture-based business expertise and technical support for a vibrant agricultural industry. The Agriculture Knowledge Centre in Moose Jaw conveys emerging trends in information and technology transfer to farmers. The specialists located in regional offices throughout the province provide agri-business management and development expertise to clients and community groups.

The Market Development and Food Branch supports the development of Saskatchewan's agri-food industry through the provision of food safety, quality, policy, regulatory, market and business development programs and services. They are involved in international market development initiatives to increase Saskatchewan company's presence in international markets.

The Irrigation Development Branch provides strategic, technical, economic and environmental support, including irrigation development, technical assistance, regulatory oversight, operation and maintenance for irrigation development in the province.

Saskatchewan Agriculture and Food
3085 Albert Street
Regina, Saskatchewan S4S 0B1
Telephone: (306) 787-4660
Fax: (306) 787-0428
Contact: Penny Pearse, Provincial Specialist, Plant Disease
E-mail: ppearse@agr.gov.sk.ca
Website: http://www.agr.gov.sk.ca/

Becker Underwood, founded in 1982, is an international developer of bio-agronomic and specialty products. In addition to being the leading manufacturer of seed coatings and colorants, the company is also the leading global producer of inoculants, beneficial nematodes, and a wide range of agricultural and horticultural products for a broad range of applications.

Becker Underwood's innovative seed enhancement technologies are compatible with most seed treatment products and provide seedsmen with technically advanced methods of coloring, coating and inoculating seed. Becker Underwood seed enhancement technologies add value to the seed and increase the yield for the farmers.

Becker Underwood is privately held, has more than 300 employees internationally and is headquartered in Ames, Iowa, United States. Becker Underwood Production plants, Research and Development facilities and Sales and Marketing offices are located in Ames, Iowa, USA; Saskatoon, Canada; Littlehampton, United Kingdom; St. Joseph, Missouri, USA; Caldwell, Idaho, USA; Pinhais, Brazil; Somersby, Australia; Nelson, New Zealand; Toulouse, France; and Buenos Aires, Argentina.

As a commitment to the control and production of quality products and services, many of Becker Underwood locations are ISO 9001:2000 registered. Becker Underwood operates in the following markets:

Seed Enhancements

- Rhizobium Inoculants to promote growth and value in legume crops
- Colorants & coatings to enhance seed value and performance
- Seed coating to increase value of seeds

Landscape Colorants & Coatings

- Colorants for mulch to increase value
- Machines to apply color to landscape materials
- Colorants and coatings for rock, sand and other

Horticulture and Specialties

- Turf ornamental specialties
- Biological pest control
- Industrial vegetation management colorants
- Repellents for natural control of damaging wildlife

To learn more about Becker Underwood and its products, please visit the company's web site at www.beckerunderwood.com.

Philom Bios is an industry leader in developing products that deliver greater fertility efficiency on the farm. We manufacture biological products that make farmers more money. We also market stabilized nitrogen products that increase the efficiency of nitrogen fertilizer.

Through continued investments in research and development, Philom Bios continues to lead the way in new products and services, to help farmers get the most from their crops. To date, our investments in agriculture:

- led to the introduction of the first pre-sterilized, self-sticking peat-based inoculant in the Canadian marketplace.
- pioneered the use of phosphate inoculants that drive better phosphate use efficiency.
- introduced the first MultiAction inoculant with our TagTeam line of inoculants, which have proved to be the most profitable on the market.

Besides providing top-quality products we pride ourselves in providing unparalleled service and support to our customers with more people from the lab to the field.

Our mission continues to be simple: 'To serve the needs of individual customers by developing and delivering high-value fertility efficiency tools.' One key word in our company's culture stands out in the fulfillment of our mission: respect — respect for our customers, our stakeholders and our people.

We work hard at not only delivering superior products, but also the agronomic knowledge to get the most out of them. We test new formulations, strains, agronomic practices (like our new line of stabilized nitrogen products), and the compatibility of our inoculants with leading seed treatments. Through educational tours, training camps, tradeshows and one-on-one meetings, we work with retailers and farmers to ensure our products deliver the highest value in the field. This support is part of our commitment to provide incremental value and better net returns on the farm.

Philom Bios Inc.
Corporate Office
3935 Thatcher Avenue
Saskatoon, Saskatchewan S7R 1A3
Telephone: 1-888-744-5662
Fax: (306) 668-4232
Website: www.philombios.com

Headquartered in Monheim, Germany, our 19,400 employees work in more than 120 countries. Bayer CropScience benefits significantly from its position within the global Bayer Group as one of the groups three core businesses, along with Bayer Healthcare and Bayer MaterialScience, all of which are focused on innovation and growth.

In Canada, Bayer CropScience Inc. is a leader in crop production in this agriculturally rich and diverse country. The company employs over 250 people with headquarters in Calgary, Alberta. Other locations include a formulation plant in Regina, a seed-breeding facility in Saskatoon, an eastern Canada operations centre in Guelph and a regulatory office in Ottawa. The company is currently building a new seed processing facility in Lethbridge for our leading InVigor hybrid Canola seed.

An Integrated product portfolio of crop protection products, seed treatment technologies and plant biotechnology offers Canadian farmers a wide choice of solutions.

Performance Plants Inc. is a leading plant biotechnology company, focused on gene discovery and the development of agronomically important traits in food and biofuel crops. Performance Plants' traits create value by improving yields and reducing the detrimental effects of environmental stress.

The Company's head office and Gene and Trait Discovery Centre are located in Kingston, Ontario, while its Crop Development Centre is in Saskatoon, Saskatchewan.

Performance Plants has global licenses with strategic partners in the corn, soybean, turf and ornamentals markets. Further business partnerships are being pursued to expand the introduction of its traits into additional food and biofuels crops.

Saskatchewan Wheat Pool Inc. is a Canadian publicly traded agri-business and is a leading service provider in Saskatchewan, Alberta and Manitoba. The Pool's business model optimizes its key position in the agri-food pipeline, connecting Prairie producers to destination customers here and around the world. From farm gate to end-use markets, the Pool offers quality programs and services to maximize value at each stage of its integrated pipeline.

The Pool's primary businesses are grain handling and marketing - supported by one of Western Canada's largest agri-products retail marketing operations. The Pool is involved in agri-food processing and through these businesses, together with its joint venture and strategic alliances has created an integrated agri-business from field to table.

The company has the most efficient and sophisticated grain handling, processing and marketing network in Western Canada. In addition to supplying Canadian Wheat Board commodities, the Pool is one of the largest exporters of Canadian canola, pulses and special crops, including oats, peas, canary seed and mustard.

Together with export capabilities, superior logistics expertise and a talented team of employees, the Pool's focus on quality has attracted a host of primary and end-use customers who demand excellent product quality, competitive prices and just in time delivery. The Pool's philosophy for more than 80 years has been built upon a foundation of customer satisfaction, quality products and dependable service. For more information, visit the Pool's website at www.swp.com.

The Canadian Wheat Board (CWB) is a farmer-controlled marketing organization that sells wheat, durum and barley for about 85,000 producers in western Canada. Its purpose is to market this grain within Canada and around the world and achieve the best possible returns for farmers. All sales revenue, less marketing costs, is returned to farmers.

The CWB is one of the largest grain marketers in the world, with annual sales revenue of more than $4 billion. Its status as the only seller of western Canadian wheat and barley positions the CWB to earn premium prices for farmers on annual sales of over 20 million tonnes of grain to more than 70 countries. The CWB has a proud reputation for high-quality products, reliable supply and delivery and unparalleled customer support.

The CWB is governed by a 15-member board of directors, 10 elected by farmers and five appointed by the federal government. Most of its staff of 430 is based in Winnipeg. The CWB also has offices in Tokyo, Beijing and Vancouver, as well as in Saskatoon and Airdrie, Alberta.

Since 2001, the CWB has offered farmers increased flexibility in grain pricing and payment through its Producer Payment Options. These programs are attracting a growing number of producers who wish to shoulder more market risk themselves. Other farmers choose to be paid though the CWB pool accounts, which return them the average price received from all markets across the entire crop year. For more information, visit the CWB website at www.cwb.ca.

The City of Saskatoon Corporate Business Plan is consistent with the mandate of the corporation, as well as its vision, mission, and values.

Our Vision:

Our vision for Saskatoon, building on our history, includes:

- an enhanced quality of life;
- a vibrant economy;
- responsible, progressive environmental management;
- continued river valley stewardship;
- recognizing the diversity of neighbourhoods while promoting a united community;
- planned growth; and,
- regional and global opportunities.

Our Mission:

Our Corporation, the City of Saskatoon, exists to provide excellent local government through leadership, teamwork, partnership, and dedication to the community. We will facilitate effective and efficient delivery of public services and nurture the economic, environmental, social, and cultural well-being of the community, now and in the future.

Our Values:

In order to achieve our vision, we commit ourselves to:

- quality service;
- fiscal responsibility;
- high performance;
- respect for others;
- providing open and accountable government;
- supportive work environment; and,
- cooperative spirit.

Ag-West Bio is a membership based organization at the forefront of Saskatchewan's bio-economy. We work as a catalyst for partnerships and industry growth through investments, aiding strategic alliances, providing regulatory advice and communications. Our membership has grown to include over 100 corporations, associations and individuals representing natural health products and functional foods, bio-products and bio-processes and agricultural biotechnology sectors.

Visit www.agwest.sk.ca to learn more about our organization and how we can help you become more competitive in the bio-based economy!

Contact information:
Dr. Ashley O'Sullivan, President & CEO
Ag-West Bio Inc.
101-111 Research Drive
Saskatoon, SK S7N 3R2
Telephone: 306-975-1939
E-mail: agwest@agwest.sk.ca
Website: www.agwest.sk.ca

NRC-PBI is a major research centre for plant biosciences in Canada, with expertise in genomics, metabolic pathways, gene expression, genetic transformation, structured biology, and natural product chemistry. Supporting technologies include DNA sequencing, gene synthesis, mass spectrometry, biological NMR and bioinformatics. NRC-PBI performs, assists, and promotes strategic discovery research and innovation in plant biotechnology with partnership with key stakeholders, to improve and diversify Canadian industry and strengthen Canada's competitive position in the global knowledge-based economy.

PBI contact information is as follows:
Dr. Kutty Kartha
Director General
National Research Council of Canada
Plant Biotechnology Institute
110 Gymnasium Place
Saskatoon, SK S7N 0W9, Canada
Telephone: (306) 975-5575
E-mail: Lisa.Jategaonkar@nrc-cnrc.gc.ca
Kutty.Kartha@nrc-cnrc.gc.ca
Website: www.pbi-ibp.nrc-cnrc.gc.ca

The Saskatchewan Canola Development Commission (SCDC) was established in 1991 to represent Saskatchewan's canola producers. Its mandate is to enhance canola producers' competitiveness and profitability through research, market development and communications (extension). These activities are funded through a check-off and administered by a producer elected Board of Directors.

An objective of the research component is to improve producers' net returns by increasing price and/or yield and providing recommendations for cost-effective use of inputs. Areas of focus include agronomic research, plant breeding for insect and disease resistance, seed costs, and evaluating oilseed crops with potential to become viable and economical. Another objective is to develop new products and uses from canola oil and meal, such as biodiesel and fuel additives, aquafeeds, bioplastics, potential nutraceutical and functional food products, and yellow seeded canola, for the food and non-food markets.

Market Development focuses on increasing the demand, price and quality of canola and canola products nationally and internationally.

Communication activities provide management information to producers and funding for consumer education programs. For more information, visit the SCDC website at www.saskcanola.com.

The Saskatchewan Research Council (SRC) has been providing smart science solutions in Saskatchewan for 60 years. We are Saskatchewan's leading provider of applied R&D and technology commercialization. We take the leading-edge knowledge developed in Saskatchewan and sell it to the world and, at the same time, bring the best knowledge the work has to offer and apply it to the unique Saskatchewan situations.

SRC was established in 1947 to advance the development of the province in the physical sciences. Today, the company is market driven, selling services and products to companies in Saskatchewan and around the world. The organization has more than 340 employees and annual revenues are over $32 million and growing.

SRC serves clients across most of Saskatchewan's strategic sectors including: Agriculture, Biotechnology and Food; Alternative Energy and Manufacturing, Energy; Environment and Forestry; and Mining and Minerals.

To learn more about how we can help you and your business visit our website at www.src.sk.ca.

UNIVERSITY OF SASKATCHEWAN

The Department of Biology is staffed and equipped to provide a broad, fundamental education in the field of Biology and to offer advanced or graduate training. Students wishing to enter the Biology program should have a strong high school background in Biology and Chemistry. The major in Biology consists of a core of basic courses which includes general biology, surveys of animals and plants, genetics, cell structure and function, ecology and population biology. Beyond these core courses, students may specialize in a wide variety of areas. Opportunities exist for interdisciplinary programs such as Agricultural Biology, Land Use and Environmental Studies, and Paleobiology.

The university location provides ready access to several habitat types. The Department is equipped with greenhouses, growth chambers, aquaria, animal rooms, isotope laboratory, electron microscopes and modern computer facilities.

The Biology department offers graduate programs towards M.Sc. and Ph.D. degrees. Faculty represent a variety of specializations within the two major disciplines of Botany and Zoology. Our faculty members are known internationally for their research work. The department has particular strengths in vertebrate ecology and behaviour, plant biotechnology and developmental biology. Biology faculty collaborate with scientists from a variety of provincial and federal laboratories.

Our graduates have found employment in teaching, technical work in laboratory or field research, environmental consulting, technical marketing, administration, and scientific writing in government, university, industrial and private sectors.

For more information, contact: Head, Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, telephone (306) 966-4399, or visit our website at www.usask.ca./biology.

A College of Agriculture was one of two Colleges established at the U of S in 1909. Since then, agricultural teaching and research have been consistent areas of strength at the University, and practical transfer of College research to producers has played a significant role in the development of the agriculture and food industries in Saskatchewan. Over this time the College has developed excellent relationships with agricultural/rural communities and with alumni.

In 2006 the College adopted the name Agriculture and Bioresources to reflect its expanding commitment in teaching, research and outreach beyond production agriculture into all aspects of the bioeconomy from renewable resources through the whole value chain to bioproducts. As such, the College's core competencies are in:

- **Sustainable production**
- **Food and bio-products**
- **Environment and ecology**
- **Rural economy and communities**

The College contributes to innovation and discovery through original research at both the basic and applied levels in the natural, life and social sciences. It educates individuals for careers in science and business and contributes to the economic and social development of Saskatchewan and beyond through its outreach. The student experience is greatly enhanced when teaching and scholarship are offered in a research-rich environment. Our research intensiveness is our competitive advantage. Certificate, diploma, undergraduate and postgraduate degree training is available in a wide range of specializations.

The work of the college is enabled by excellent facilities: a state-of-the art Agriculture Building, extensive animal facilities on and off-campus, greenhouses, land for animal, crop and horticulture research, and associated field laboratories.

For more information, contact: Dean, College of Agriculture and Bioresources, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, telephone (306) 966-4050, or visit our website at www.ag.usask.ca.

The Canadian Seed Growers' Association (CSGA), which represents 4,500 seed growers, provides leadership as the Canadian organization designated in federal *Seeds Act and Regulations* to certify pedigreed seed crops for all agricultural crops in Canada except potatoes.

Canadian seed production is respected around the globe because it ensures germination and mechanical purity, while providing an audit trail that assures varietal identity and genetic purity. It is a system that supports Canada's worldwide reputation as a supplier of quality agricultural products.

The Canadian Seed Growers' Association (CSGA) provides a field-to-table value chain based on identify preservation and quality assurance.

CSGA's Mission Statement is to:
Represent members by:

- Advancing a grower perspective on issues related to seed;
- Providing leadership to members and engaging in activities designed to give members a voice on seed related matters; and
- Supporting members in gaining and maintaining knowledge of seed crop certification.

Advance the seed industry by:

- Promoting the benefits of pedigreed seed throughout the seed industry and to end-users;
- Advocating the use of the seed certification system as an integral part of identity preserved and quality assurance programs;
- Cooperating with researchers, growers and processors to expand the use of pedigreed seed; and
- Facilitating transfer of end-use specific traits from research to commercial use through pedigreed seed.

Provide seed crop certification by:

- Developing varietal purity standards and regulations for pedigreed seed crop production;
- Maintaining a verifiable seed certification system; and
- Certifying the varietal purity of pedigreed seed crops.

The Canadian Journal of Botany is one of 16 journals published by the National Research Council Research Press, and is available in paper and electronic form. It is an international journal publishing articles, notes, mini-reviews, reviews and commentaries in several disciplines within Botany. All contributions are subject to normal reviewing processes. Manuscripts in both English and French are accepted for review. There are no page charges for publication in the journal. The journal is co-edited by Dr. R. Larry Peterson and Dr. Barry J. Shelp with the assistance of an Editorial Board of Associate Editors. The journal is based at the University of Guelph and is managed by Christopher Peterson, Assistant to the Editors, and Wendy Gibbs, Editorial Assistant.

Avensys Solutions

Products/Services:
As a leading Canadian distributor of instrumentation and systems for the environmental industry, Avensys offers equipment for the water, wastewater, groundwater, air quality, atmospheric emission, gas detection, hydrology and meteorology applications. Our team of highly knowledgeable professionals is committed to providing cost-effective, customer-driven solutions, high quality products from single instrument to fully integrated and customized systems.

Principals/Trade Names represented:

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Air sector:

- Crowcon, Gasmet, Casella, Photovac, Eastech, ADC, VIG Industries, Wilks Enterprise

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Éditeur de publications scientifiques évaluées par des pairs

NRC Research Press is Canada's foremost publisher of scientific journals and monographs. Visit our booth to learn about the *Canadian Journal of Botany* and our extensive list of plant books. *Canadian Journal of Botany* is always looking for comprehensive research articles and notes in all segments of plant sciences, including cell and molecular biology, ecology, genetics, mycology and plant-microbe interactions, paleobotany, phycology, physiology and biochemistry, structure and development, and systematics. The monographs program has recently published the second edition of *Culinary Herbs*, as well as *Flower Guide for Holiday Weekends*. Monographs include *Mycorrhizas: Anatomy and Cell Biology* as well as books on the flora of Canada's unique northern environment.

Fisher Scientific

Thermo Fisher Scientific is the world leader in serving science. We enable our customers to make the world healthier, cleaner and safer by providing analytical instruments, equipment, reagents and consumables, software and services for research, analysis, discovery and diagnostics. With annual sales of more than $9 billion, Thermo Fisher Scientific has 30,000 employees and serves more than 350,000 customers in pharmaceutical and biotech companies, hospitals and clinical diagnostic labs, universities, research institutions and government agencies as well as environmental, industrial quality and process control settings.

We deliver the industry's broadest selection of analytical instruments, equipment, consumables and laboratory supplies. Our growing portfolio of products includes innovative technologies for mass spectrometry, elemental analysis, molecular spectroscopy, sample preparation, informatics, fine and high-purity chemistry production, cell culture, RNA interference analysis, immunodiagnostic testing, as well as air and water quality monitoring and process control. We also give our customers the most convenient purchasing choices, including a direct sales force of 7,500 professionals, catalogs, e-commerce and distribution partners.

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Controlled Environments Limited
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Conviron has been a leading supplier of controlled environment products for over 40 years and is the only plant growth chamber manufacturer certified as an ISO 9001 company. All standard products are provided with product certification to both UL and CSA Standards by CSA International, or an equivalent Nationally Recognized Testing Laboratory (NRTL), for use in both the United States and Canada. Conviron products also carry CE marks. Our extensive product line includes reach-in and walk-in plant growth chambers, the Aurora Research Greenhouse, tissue culture chambers, multi-tier plant production rooms, seed germinators, incubators, dew rooms and related products for the agricultural research market. Systems provide precise control of temperature, relative humidity, CO_2 and light intensity. Host computer systems allow remote programming and monitoring of all environmental control parameters. A factory representative is available to answer your questions and assist you in determining which product would be most suitable for your research application.

LI-COR®

Biosciences

Visit LI-COR at Plant Canada 2007 to see the latest instrumentation for environmental research, including portable photosynthesis systems, radiation sensors, leaf area measurement equipment, and gas analyzers.

LI-COR Biosciences has been a leading manufacturer of instrumentation for the biological and environmental sciences since 1971. LI-COR Environmental has three major product lines: light measurement instrumentation, including light meters and sensors; gas exchange measurement instrumentation, including gas analyzers, portable photosynthesis systems, and soil CO_2 flux measurement systems; and leaf area measurement instrumentation.

Light sensors are available for photosynthetically active radiation, solar energy, and illuminance. Instantaneous, averaged or integrated measurements are provided when sensors are used with LI-COR light meters or dataloggers.

LI-COR also manufactures a complete line of infrared CO_2 and H_2O gas analyzers. Known world-wide for innovative engineering design, LI-COR analyzers feature solid state sources and detectors to provide low signal noise levels, high accuracy, fast response times, and excellent long-term stability.

The LI-6400 Portable Photosynthesis System has set the standard for photosynthesis, fluorescence and soil CO_2 flux measurements. When used with the Leaf Chamber Fluorometer, gas exchange and fluorescence are measured simultaneously.

LI-COR Area Meters offer you choices for fast, non-destructive leaf area measurements, rapid measurements of large amounts of detached leaves, or labor saving, direct measurements of Leaf Area Index.

The LI-8100 Automated Soil CO_2 Flux System is an automated system designed for measurements of soil CO_2 flux. The LI-8100 makes both short-term survey and long-term unattended measurements of soil CO_2 flux with interchangeable chambers. The LI-8100 also features a Multiplexer for connection of up to 16 long-term chambers.

LI-COR is based in Lincoln, Nebraska, with subsidiaries in Germany and the United Kingdom. LI-COR systems are used in over 100 countries and are supported by a global network of distributors. For more information visit www.licor.com.

UNIVERSITY OF SASKATCHEWAN

Bookstore

The University of Saskatchewan Bookstore stocks approximately 20,000 of the world's best reference and general interest titles in addition to texts required for classes. In the store, we offer everything from bestsellers to highly specialized technical and academic titles. We now have a website available where you can search our inventory.

The Bookstore also has a very active Special Order department. If we don't have a particular book in stock, we will gladly special order it for you. Orders may be placed in person, by phone, fax, or email. Our Mail Order department can mail or courier your books to you if you are unable to pick them up at the store.

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The Organic Agriculture Centre of Canada (OACC) was founded in 2001, and as the only institution of its kind in Canada, plays a leading role in organic research and education. Our vision is to "strengthen the science and practice of organic agriculture in Canada" and our mission is to "facilitate research and education for organic producers and consumers to build sustainable communities". The team at OACC has a high degree of enthusiasm for our mission and a strong commitment to academic rigour. With our associated colleagues in each province we link organic knowledge across Canada.

OACC is dedicated to farm profitability and enhancing the environmental and social integrity of agriculture. This will be achieved through scientific analyses of methods to improve the sustainability of farming. The results of this research are available to farmers and the public through our website (www.oacc.info), bulletins, news articles and web-based courses.

OACC is funded primarily by the ACAAF program of AAFC and NSERC. Additional funding is provided by the Canadian Wheat Board, Home Hardware, the EJLB Foundation and the provinces of British Columbia, Alberta, Saskatchewan, Manitoba, Ontario, New Brunswick, Nova Scotia, and Prince Edward Island with significant in-kind contributions from our home base, the Nova Scotia Agricultural College (NSAC). In-kind contributions are also provided by the Universities of Saskatchewan, Manitoba, Alberta, and Guelph.

The OACC website provides research summaries, files of all OACC newspaper articles, links to Canadian organic organizations, virtual farm tours, and many other resources. Traffic on our website has grown to above 4 million hits per year.

Hoskin Scientific Limited has been supplying testing and monitoring instruments since 1946. We operate out of three offices within Canada: Vancouver, Burlington and Montreal.

Hoskin specialises in instruments for environmental science, in particular: agronomy, plant physiology, eco-physiology, data logging, meteorology, soil moisture, solar energy studies and environmental monitoring. We are the sole Canadian distributors for companies such as Delta-T Devices, Soilmoisture Equipment Corporation, Onset (HOBO) Computer Corporation, Eijkelkamp, among others.

Corey Lunman
Environmental Sales Representative
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4210 Morris Drive
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Fax: (905) 333-4976
E-mail: clunman@hoskin.ca
Website: www.hoskin.ca

Please refer to the "Organizational and Financial Contributors – Platinum" section of the program book for the Saskatchewan Agriculture and Food company profile.

Nikon

The Eyes of Science

The Instrument Division of Nikon Canada Inc. represents optical microscope equipment and associated accessories for both the material and life sciences. Our product line ranges from stereomicroscopes and polarized light systems (transmitted and reflected light) through to confocal laser microscopes with spectral capabilities.

Nikon has knowledgeable, dedicated representatives and specialists located throughout Canada, as well as a dedicated support team at the head office in Mississauga, Ontario. We maintain the highest levels of quality control, product maintenance and customer service.

For a complete product listing or to contact a representative in your area please visit our website at www.nikon.ca or explore the world of microscopy at www.microscopyU.com.

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Founded as a workshop for precision mechanics and optics in the German city of Jena in 1846, Carl Zeiss is today a global leader in the optical and opto-electronic industries. We have offices in over 30 countries and are represented in more than 100 countries, with production centers in Europe, North America, Central America and Asia.

Our most important task, as we see it, is to enable science and technology to go beyond what man can see. "We make it visible" – our corporate slogan, and our promise to our customers to open doors that were previously sealed.

We are market leaders in the majority of our fields. We offer an extraordinary spectrum of leading-edge solutions and products for the life scientist ranging from simple high quality stereo microscopes to the most sophisticated laser scanning confocal microscopes. No matter what your observation or digital imaging need Carl Zeiss wants to help you to: "We make it visible".

BioChambers INCORPORATED
A Subsidiary of Enconair Technologies Inc.

BioChambers Incorporated, a subsidiary of Enconair Technologies Inc. has more than thirty years experience in the design and manufacture of quality Plant Growth Chambers, Plant Growth Rooms, Tissue Culture Chambers and Rooms and similar equipment.

In addition to a wide range of standard products, BioChambers produces many special and customized products to meet the exact needs of researchers in Canada, the United States, and overseas. For example, the 'Cold Hardiness' research chamber Model GC20BDAF "Cold Temperature" has the most advanced specification of its type in the world.

Visit our display to pick up literature on our latest models including our very popular "Bigfoot" chambers, our 'Research Saver' monitor and our new VNet Viewer, and learn about our other latest features.

Campbell Scientific (Canada) Corp. is a provider of rugged, reliable data acquisition systems. Our dataloggers feature wide operating ranges, durable construction and dependable stand-alone operation. In addition, they have low power consumption from a variety of sources, many telecommunications options, and have the flexibility to support a variety of measurement and control applications.

The University Health Network Microarray Centre (UHNMAC, www.microarrays.ca) is committed to providing our customers with reliable and affordable genomics services, quality array products, and unparalleled support.

We offer expression profiling, chromatin immuno-precipitation (ChIP)-on-chip, differential methylation, and array comparative genomic hybridisation (aCGH) on several platforms including Affymetrix, Agilent, and cDNA microarrays printed at the UHNMAC. We have several collaborations with academic researchers and commercial partnerships that apply our microarray expertise to genomics research. Our bioinformatics group offers a variety of data analysis solutions and maintains our searchable gene expression and CpG island databases that are available online (http://data.microarrays.ca). In addition, custom microarray printing and clone production services are also available.

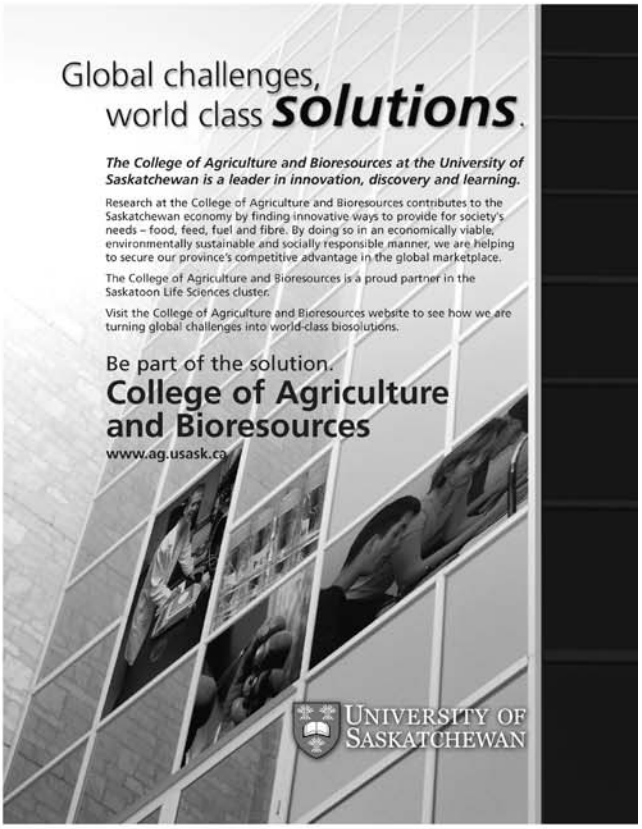
Plant researchers may be particularly interested in the Affymetrix platform, a platform fully supported by the UHNMAC. The Affymetrix platform offers GeneChips® (oligonucleotide microarrays) for many plant species including *Arabidopsis*, barley, citrus, cotton, grape, maize, *Medicago*, poplar, rice, soybean, sugar cane, tomato, and wheat. In addition, the Agilent platform offers arrays specific for *Arabidopsis* and rice studies. In addition to catalogue arrays, scientists can also design and customize arrays using the Agilent's SurePrint *in situ* synthesis for specific applications.

Since 2000, the UHNMAC has provided arrays, training and support to over 700 labs in 27 countries and over 100,000 arrays have been distributed. UHNMAC offers human, mouse, and yeast cDNA microarrays, human and mouse CpG island microarrays, and, due to the recent collaboration with Samuel Lunenfeld Research Institute Microarray Facility, now prints mouse, zebrafish, *C. elegans*, and focused human and yeast oligonucleotide microarrays. The UHNMAC also provides useful resources online including technical notes, platform comparisons, Frequently Asked Questions, and our technical support specialist is available during business hours.

The UHNMAC is also committed to developing new technologies and refining the existing technologies so that our customers have access to leading edge tools. Through our in-house R&D programme, we are currently developing protein, microRNA, and cell array technologies to further diversify our product line.

Other Exhibitors:

- Bio-Rad Canada
- Canada-Saskatchewan Irrigation Diversification Centre, Agriculture and Agri-Food Canada



Saturday, 09 June

18:00 – 22:00	CPS Financial Advisory Committee meeting	Hilton Garden Inn (Kindersley Suite)

Sunday, 10 June

09:00 – 12:00	CSHS Board meeting	Hilton Garden Inn (Prince Albert West Room)
09:00 – 15:00	CSA Board meeting	Hilton Garden Inn (Regina Room)
09:00 – 15:30	CPS Board meeting	Hilton Garden Inn (Prince Albert East Room)
12:00 – 19:00	**Poster and trade show set-up**	**Salon A and Salon East**
13:00 – 16:00	**Workshop on scientific publication**	**Gallery Suite A (1)**
13:00 – 17:00	**Pre-conference field trips**	**Buses will be on the west side of TCU Place**
	Field trip 1: Western Development Museum	
	Field trip 2: Wanuskewin Heritage Park	
15:30 – 17:30	Plant Canada Board meeting	Hilton Garden Inn (Prince Albert West Room)
16:00 – 19:00	**Conference registration**	**Gallery Suite B (2)**
17:30 – 19:00	CBA Board meeting	Hilton Garden Inn (Prince Albert East Room)
19:30 – 22:00	**Conference opening reception**	**Hilton Garden Inn (Commonwealth Ballroom)**

07:30 – 10:00	Registration	Gallery Suite B (2)
07:30 – 10:00	Poster and trade show set-up	Salon A and Salon East
08:00 – 08:30	**Conference opening ceremony**	**Salon B,C,D**
08:30 – 09:30	**Plenary 1:** Natural products: Biology, chemistry, and application	**Salon B,C,D**
09:30 – 10:00	Coffee break, posters and trade show	Salon A and Salon East
10:00 – 12:00	**Plenary 1** (continued)	**Salon B,C,D**
12:00 – 13:00	Canadian Plant Hormone Profiling Centre proposal	Gallery A (Bring your lunch)
12:00 – 13:00	CBA – Development Section	Gallery B (Bring your lunch)
12:00 – 13:00	CBA – Conservation Section	Gallery C (Bring your lunch)
12:00 – 13:30	Lunch	Grand Salon and Salon B,C,D
12:00 – 13:30	Posters and trade show	Salon A and Salon East
13:30 – 15:00	**Society student sessions A**	
	A1. CPS student session 1	Salon B
	A2. CBA/CSA student session 1	Salon C
	A3. CSPP student session 1	Salon D
15:00 – 15:30	Coffee break, posters and trade show	Salon A and Salon East
15:30 – 17:00	**Society student sessions B**	
	B1. CPS student session 2	Salon B
	B2. CBA/CSA student session 2	Salon C
	B3. CSPP student session 2	Salon D
17:00 – 18:30	**Poster session with authors present** (even #s) **Student poster judging**	**Salon A and Salon East**
18:30 – 19:00	**Graduate student meeting**	**Salon B**
18:30	Dinner (on your own) and free evening	
19:00 – 21:00	**Wine Education**	**Hilton Garden Inn** **(Prince Albert East and West Rooms)**
19:00 – 22:00	CSPP Board meeting	Hilton Garden Inn (Vice Regal Hospitality Room)
19:00 – 23:30	**Graduate student social**	**Winston's English Pub & Grill** **243 – 21st Street East**

07:30 – 10:00 Registration (Gallery Suite B (2))

07:30 – 10:00 Poster and trade show set-up (Salon A and Salon East)

08:00 – 08:30 Conference opening ceremony

Opening ceremony **Room: Salon B,C,D**
Moderator: Karen Bailey

08:00	His Worship, Saskatoon Mayor Don Atchison
08:10	Dr. Deep Saini, President, Plant Canada

08:30 – 09:30 Plenary 1

PL1. Natural products: Biology, chemistry, and application **Room: Salon B,C,D**
Moderators: Deep Saini, Gordon Gray

08:30	PL1-1	**Natural product-based insecticide development: Spinosad, Spinetoram and the future.** P. Lewer, P.R. Graupner, D.R. Hahn, D.O. Duebelbeis, J.R. Gilbert, L.L. Karr, G.D. Crouse, and T.C. Sparks. *Dow AgroSciences, Indianapolis, IN, USA.*

09:30 – 10:00 Coffee break, posters and trade show (Salon A and Salon East)

10:00 – 12:00 Plenary 1 (continued)

PL1. Natural products: Biology, chemistry, and application **Room: Salon B,C,D**
Moderators: Deep Saini, Gordon Gray

10:00	PL1-2	**Folate synthesis, storage, and salvage in relation to biofortification.** A.D. Hanson and J.F. Gregory III. *(A.D.H.) Horticultural Sciences and (J.F.G.) Food Science and Human Nutrition Departments, University of Florida, Gainesville, FL 32611, USA.*
11:00	PL1-3	**Associating gene discovery to biochemical function in the discovery of natural product pathways.** V. De Luca, J. Murata, M. Magnotta, D. Levac, and J. Roepke. *Department of Biological Sciences, Brock University, St. Catharines, ON, Canada.*

12:00 – 13:00 Canadian Plant Hormone Profiling Centre proposal (Gallery A); Bring your lunch

12:00 – 13:00 CBA – Development Section (Gallery B); Bring your lunch

12:00 – 13:00 CBA – Conservation Section (Gallery C); Bring your lunch

12:00 – 13:30 Lunch (Grand Salon and Salon B,C,D)

12:00 – 13:30 Posters and trade show (Salon A and Salon East)

13:30 – 15:00 Society student sessions A

A1. CPS student session 1 **Room: Salon B**

Moderator: Robin Morrall

13:30	A1-1	**Evaluation of new sources of resistance to anthracnose in lentil.** S. Vail and A. Vandenberg. *Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada.*
13:45	A1-2	**Incidence, virulence and symptoms of *Botryodiplodia* and *Fusarium* in root rot diseases of cassava.** S. Aigbe, S.U. Remison, and R. Bandyopadhyay. *Department of Crop Science, Ambrose Alli University, Ekpoma, Nigeria; and (R.B.) International Institute of Tropical Agriculture, Ibadan, Nigeria.*
14:00	A1-3	**The plant signalling components EDS1 and SGT1 enhance the disease caused by the necrotrophic pathogen *Botrytis cinerea*.** M. El Oirdi and K. Bouarab. *Centre de Recherche en Amélioration Végétale, Département de Biologie, Université de Sherbrooke, Sherbrooke, QC, Canada.*
14:15	A1-4	**Silencing mediates plant immunity induced by an elicitor.** V. Dufour, M. Langlois, F. Daayf, S. Kauffmann, O. Voinnet, and K. Bouarab. *Centre de Recherche en Amélioration Végétale, Département de Biologie, Université de Sherbrooke, Sherbrooke, QC, Canada; (F.D. & S.K.) Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada; and (O.V.) Institut de Biologie Moléculaire des Plantes CNRS UPR 2357, Strasbourg, France.*
14:30	A1-5	**Evaluation of promoter activity and over-expression of a rice peroxidase gene in transgenic carrot (*Daucus carota* L.).** O. Wally, J. Jayaraj, and Z.K. Punja. *Department of Biological Sciences, Simon Fraser University, Burnaby, BC, Canada.*
14:45	A1-6	**Detection of antibiotic-related genes of *Bacillus* species using polymerase chain reaction.** S.N.P. Athukorala, W.G.D. Fernando, K.Y. Rashid, and T. de Kievit. *Department of Plant Science and (T. de K.) Department of Microbiology, University of Manitoba, Winnipeg, MB, Canada; and (K.Y.R.) Agriculture and Agri-Food Canada, Morden Research Centre, Morden, MB, Canada.*

A2. CBA/CSA student session 1 **Room: Salon C**

Moderator: Rosalind Bueckert

13:30	A2-1	**Developmental morphology of several vine members of the Cucurbitaceae.** T. Zitnak and U. Posluszny. *Department of Integrative Biology, University of Guelph, Guelph, ON, Canada.*
13:45	A2-2	**Leaflet separation in *Chamaedorea seifrizii*.** J. Nowak, N.G. Dengler, and U. Posluszny. *Department of Molecular and Cellular Biology, University of Guelph, Guelph, ON, Canada; and (N.G.D.) Department of Botany, University of Toronto, Toronto, ON, Canada.*
14:00	A2-3	**Soil fertility and mycorrhizal association influences on lodgepole pine and interior hybrid spruce seedling growth.** C. Wagg, B. Husband, H.B. Massicotte, and R.L. Peterson. *Department of Integrative Biology, University of Guelph, Guelph, ON, Canada; (H.B.M.) Ecosystem Science and Management Program, University of Northern British Columbia, Prince George, BC, Canada; and (R.L.P.) Department of Molecular and Cellular Biology, University of Guelph, Guelph, ON, Canada.*
14:15	A2-4	**Screening for flax (*Linum usitatissimum* L.) dual purpose traits (seed oil and stem fibre) under western Canadian growing conditions.** S. Mitra and G.G. Rowland. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada.*
14:30	A2-5	**Hybrid origin of *Symphyotrichum anticostense* (Asteraceae: Astereae) based on three nuclear markers.** J. Vaezi and L. Brouillet. *Institut de recherche en biologie végétale, Université de Montréal, Montréal, QC, Canada.*
14:45	A2-6	**Evaluating regrowth traits of three bromegrass (*Bromus*) species in the field.** Biligetu and B.E. Coulman. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada.*

A3. CSPP student session 1 **Room: Salon D**

Moderator: Ken Wilson

13:30	A3-1	**Disruption of adenosine metabolism leads to altered cytokinin profiles.** S.C. Farrow, S. Schoor, K. Engel, R.J.N. Emery, and B.A. Moffatt. *Department of Biology, Trent University, Peterborough, ON, Canada; and (S.S., K.E. & B.A.M.) Department of Biology, University of Waterloo, Waterloo, ON, Canada.*
13:45	A3-2	**A redox-regulated transactivation domain in NPR1 controls *PR-1* activation when recruited to a TGA2-NPR1 complex.** A. Rochon, P. Boyle, T. Wignes, P.R. Fobert, and C. Despres. *Department of Biological Sciences, Brock University, St. Catharines, ON, Canada; and (T.W. & P.R.F.) National Research Council of Canada, Plant Biotechnology Institute, Saskatoon, SK, Canada.*
14:00	A3-3	**Towards the identification of common bacterial blight resistance genes in *Phaseolus vulgaris*.** G. Perry, Y. Reinprecht, J. Chan, and K.P. Pauls. *Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada.*
14:15	A3-4	**Characterization of DNA elements involved in carotenoid biosynthesis in *Arabidopsis thaliana.*** K. Narayanan, G. Khachatourians, B. Yu, S. Wei, D. Hegedus, and A. Hannoufa. *(K.N., G.K. & B.Y.) Department of Applied Microbiology and Food Science, University of Saskatchewan, Saskatoon, SK, Canada; and (K.N., B.Y., S.W., D.H. & A.H.) Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada.*
14:30	A3-5	**Identification and differential regulation of phloem proteins in *Populus*.** N.J. Dafoe and C.P. Constabel. *Department of Biology, University of Victoria, Victoria, BC, Canada.*
14:45	A3-6	**Characterization of a MRP transporter linked to cadmium accumulation in durum wheat grain.** D.M. Silver, N.S. Harris, and G.J. Taylor. *Department of Biological Sciences, University of Alberta, Edmonton, AB, Canada*.

15:00 – 15:30 Coffee break, posters and trade show (Salon A and Salon East)

15:30 – 17:00 Society student sessions B

B1. CPS student session 2 **Room: Salon B**

Moderator: Gary Peng

15:30	B1-1	**Differences in the infection process on lentil tissue between races Ct0 and Ct1 of *Colletotrichum truncatum*.** J. Wang and S. Banniza. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada.*
15:45	B1-2	**Karyotyping of *Pyrenophora tritici-repentis* reveals extensive chromosomal length polymorphism and independent locations of *ToxA* and *ToxB* genes.** R. Aboukhaddour, S. Cloutier, G.M. Ballance, G. Hausner, and L. Lamari. *Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada; (S.C.) Agriculture and Agri-Food Canada, Cereal Research Centre, Winnipeg, MB, Canada; and (G.H.) Department of Microbiology, University of Manitoba, Winnipeg, MB, Canada.*
16:00	B1-3	**Retargeting of autophagosomes in *Arabidopsis* in response to powdery mildew infection.** R.M. Kennedy and Y. Wei. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada.*
16:15	B1-4	**Fungal associates of the bronze birch borer on urban birch.** S.P.K. Andersen. *Faculty of Forestry and the Forest Environment, Lakehead University, Thunder Bay, ON, Canada.*
16:30	B1-5	**Weed suppressing effects of fall rye (*Secale*) cover crops in edible bean production.** H. Flood and M.H. Entz. *Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada.*
16:45	B1-6	**A proteome level investigation of *Brassica napus* and *Sclerotinia sclerotiorum* interaction.** Y. Liang, S. Srivastava, S. Strelkov, and N.N.V. Kav. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

B2. CBA/CSA student session 2 **Room: Salon C**

Moderator: Anne Légère

15:30 B2-1 **Molecular phylogeny of the North American eurybioid asters, *Oreostemma*, *Herrickia*, *Eurybia*, and *Triniteurybia* (Asteraceae, Astereae) using nuclear and chloroplast DNA regions.** S. Selliah and L. Brouillet. *Herbier Marie-Victorin, Institut de recherche en biologie végétale, Université de Montréal, Montréal, QC, Canada.*

15:45 B2-2 **The influence of a long-term black medic (*Medicago lupulina* cv. 'George') cover crop on arbuscular mycorrhizal fungi colonization and nutrient uptake in flax (*Linum usitatissimum*) grown under zero-tillage management.** M.S. Turmel, M. Entz, M. Tenuta, W. May, and G. Lafond. *Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada; (M.T.) Department of Soil Science, University of Manitoba, Winnipeg, MB, Canada; and (W.M. & G.L.) Agriculture and Agri-Food Canada, Indian Head Research Farm, Indian Head, SK, Canada.*

16:00 B2-3 **Evaluating flower visitors as pollinators of *Lythrum salicaria* (purple loosestrife).** W.D. Caswell and A.R. Davis. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada.*

16:15 B2-4 **The effect of black medic cover crop on N supplying power of prairie soils.** S. Naguleswaran, M.H. Entz, W. May, and G. Lafond. *Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada; and (W.M. & G.L.) Agriculture and Agri-Food Canada, Indian Head Research Farm, Indian Head, SK, Canada.*

16:30 B2-5 **Genetic variation and phytogeography of Nova Scotia's isolated populations of *Helianthemum canadense* (L.) Michx. as revealed with AFLP markers.** A.F. Yorke and R.C. Evans. *Department of Biology, Acadia University, Wolfville, NS, Canada.*

16:45 B2-6 **Growing Kura clover with barley and triticale: Effects on silage yield, weed pressure, and cereal diseases.** S.M. Kosinski, J.R. King, K.N. Harker, T.K. Turkington, and D. Spaner. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada; and (K.N.H. & T.K.T.) Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, AB, Canada.*

B3. CSPP student session 2 **Room: Salon D**

Moderator: Chris Todd

15:30	B3-1	**Natural transformation of *Acinetobacter* sp. with the *cp4 epsps* gene via homologous recombination.** R.G. Campbell, R.H. Gulden, D.J. Levy-Booth, M.M. Hart, J.R. Powell, K.E. Dunfield, J.T. Trevors, J.P. Klironomos, C.J. Swanton, and K.P. Pauls. *Department of Plant Agriculture, (D.J.L.-B., M.M.H. & J.T.T.) Department of Environmental Biology, (J.R.P. & J.P.K.) Department of Integrative Biology, and (K.E.D.) Department of Land Resource Science, University of Guelph, Guelph, ON, Canada.*
15:45	B3-2	**The two ABA binding proteins, FCA and ABAP1, share common origins.** S. Kumar, F.A. Razem, and R.D. Hill. *Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada.*
16:00	B3-3	**Characterization of a light harvesting mutant of *Chlamydomonas reinhardtii.*** L.L. Gray and K.E. Wilson. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada.*
16:15	B3-4	**Bioimaging of Arabidopsis ribosomal proteins RPL23aA and -B reveals preferential incorporation of RPL23aA during ribosome biogenesis.** R.F. Degenhardt and P.C. Bonham-Smith. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada.*
16:30	B3-5	**Tradeoffs between leaf longevity and photosynthetic rate in *Populus balsamifera* populations.** R.Y. Soolanayakanahally, S. Silim, and R.D. Guy. *Department of Forest Sciences, University of British Columbia, Vancouver, BC, Canada; and (S.S.) Shelterbelt Centre, PFRA-AAFC, Indian Head, SK, Canada.*
16:45	B3-6	**Ribosomal protein S15a: Dissecting transcriptional regulation in *Arabidopsis thaliana*.** J.L. Hulm and P.C. Bonham-Smith. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada.*
17:00	B3-7	**Characterization of a mitochondrial Arabidopsis glyoxylate/pyruvate-dependent GABA transaminase.** S.M. Clark and B.J. Shelp. *Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada.*

17:00 – 18:30 **Poster session with authors present (even numbers) (Salon A and Salon East) (Student poster judging)**

18:30 – 19:00 **Graduate student meeting (Salon B)**

18:30 **Dinner (on your own) and free evening**

19:00 – 21:00 **Wine Education (Prince Albert East and West Rooms, Hilton Garden Inn)**

19:00 – 22:00 **CSPP Board meeting (Vice Regal Hospitality Room, Hilton Garden Inn)**

19:00 – 23:30 **Graduate student social (Winston's English Pub & Grill, 243 – 21st Street East)**

07:30 – 08:30	Registration	Gallery Suite B (2)
07:30 – 08:30	Posters and trade show	Salon A and Salon East
08:30 – 10:00	**Special session A**	
	SA1. Natural products from horticultural crops (CSHS)	Gallery D
	SA2. Ontogeny of the flower: The next generation (CBA)	Gallery C
	SA3. Education in action (CBA/CSPP)	Blair Nelson Room
08:30 – 10:00	**Session C**	
	C1. Pest management 1	Gallery A
	C2. Plant development and improvement 1	Gallery B
09:00 – 10:00	**Campbell Scientific datalogger demonstration**	**Gallery Suite A (1)**
10:00 – 10:30	Coffee break, posters and trade show	Salon A and Salon East
10:30 – 11:30	**Zeiss microscopy demonstration**	**Gallery Suite A (1)**
10:30 – 12:00	**Special session B**	
	SB1. Progress in organic cropping systems (CSA)	Gallery C
	SB2. Emerging plant disease epidemics (CPS)	Gallery D
	SB3. Communicating plant science	Blair Nelson Room
10:30 – 12:00	**Session D**	
	D1. Plant responses to the environment 1	Gallery A
	D2. Plant development and improvement 2	Gallery B
12:00 – 13:00	CBA – Mycology Section	Gallery A (Bring your lunch)
12:00 – 13:00	CBA – Teaching Section	Gallery B (Bring your lunch)
12:00 – 13:00	CBA – Systematics & Phytogeography Section	Gallery D (Bring your lunch)
12:00 – 13:30	Lunch	Grand Salon and Salon B,C,D
12:00 – 13:30	Posters and trade show	Salon A and Salon East
13:30 – 15:00	**Special session C**	
	SC1. Designing a new agri-food industry 1	Gallery D
	SC2. Emerging barriers to marketing crops (CSA)	Blair Nelson Room
13:30 – 15:00	**Session E**	
	E1. Plant responses to the environment 2	Gallery A
	E2. Plant development and improvement 3	Gallery B
	E3. Pest management 2	Gallery C
15:00 – 15:30	Coffee break, posters and trade show	Salon A and Salon East
15:30 – 17:00	**Special session D**	
	SD1. Designing a new agri-food industry 2	Gallery D
	SD2. Natural products (CSPP)	Blair Nelson Room
15:30 – 17:00	**Session F**	
	F1. Plant development and improvement 4	Gallery A
	F2. Plant development and improvement 5	Gallery B
	F3. Plant responses to the environment 3	Gallery C
17:00 – 18:30	**Poster session with authors present** (odd #s)	**Salon A and Salon East**
17:00 – 19:00	CSA – General discussion of members	Gallery Suite A (1)
18:00 – 18:30	**CSHS Natural products special seminar**	**Blair Nelson Room**
19:00	Dinner (on your own)	
20:00 – 21:00	**Luella K. Weresub mycology lecture (CBA)**	**Gallery B**

07:30 – 08:30 Registration (Gallery Suite B (2))

07:30 – 08:30 Posters and trade show (Salon A and Salon East)

08:30 – 10:00 Special session A

SA1. Natural products from horticultural crops (CSHS) **Room: Gallery D**
Moderator: Shahrokh Khanizadeh

08:30 SA1-1 **Distribution and antioxidant properties of apple flavonols.** H.P.V. Rupasinghe. *Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, NS, Canada.*

09:00 SA1-2 **Novel techniques to improve functionality of horticultural foods and food ingredients.** H. Ramaswamy. *Department of Food Science, McGill University, Ste-Anne-de-Bellevue, QC, Canada.*

09:30 SA1-3 **Foods with added physiological function: Facts and fallacies.** P.J. Jones. *Director, Richardson Centre for Functional Foods and Nutraceuticals, and Professor, Departments of Food Science and Human Nutritional Sciences, University of Manitoba, Winnipeg, MB, Canada.*

SA2. Ontogeny of the flower: The next generation (CBA) **Room: Gallery C**
Moderators: Usher Posluszny, Rodger Evans

08:30 SA2-1 **Keys to innovation: Ontogenetic avenues to floral specialization.** L. Hufford. *School of Biological Sciences, Washington State University, Pullman, WA, USA.*

09:00 SA2-2 **Thinking outside the MADS-box: Development of inflorescence and flower in an evolutionary perspective.** M. Buzgo, S. Kim, B.A. Hauser, A.S. Chanderbali, P.S. Soltis, D.E. Soltis, D.G. Oppenheimer, H. Ma, J.H. Leebens-Mack, and C. dePamphilis. *Department of Botany, University of Florida, Gainesville, FL, USA; (H.M. & C.deP.) Penn State University, University Park, PA, USA; and (J.H.L.-M.) Department of Plant Biology, University of Georgia, Athens, GA, USA.*

09:30 SA2-3 **MADS-box genes: A key to understanding Rosaceae flowers?** R.C. Evans and E.M. Kramer. *Biology Department, Acadia University, Wolfville, NS, Canada; and (E.M.K.) Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA.*

SA3. Education in action (CBA/CSPP) **Room: Blair Nelson**
Moderators: Christine Maxwell, Greg Moorhead

08:30 SA3-1 **What will I do when I grow up?** M. Devine. *Performance Plants Inc., Saskatoon, SK, Canada.*

09:00 SA3-2 **Using scientific literature and interactive groups to teach plant ecology.** K.A. Frego. *Department of Biology, University of New Brunswick, Saint John, NB, Canada.*

09:30 SA3-3 **Maximizing feedback and evaluation while minimizing time and red ink.** S.M. Macfie. *Department of Biology, the University of Western Ontario, London, ON, Canada.*

08:30 – 10:00 Session C

C1. Pest management 1 **Room: Gallery A**
Moderator: Lone Buchwaldt

08:30 C1-1 **Variability of *Leptosphaeria maculans* in western Canada based on avirulence genes.** H.R. Kutcher, H. Brun, S.R. Rimmer, M. Balesdent, and T. Rouxel. *Agriculture and Agri-Food Canada, Melfort Experimental Farm, Melfort, SK, Canada; (H.B.) UMR 1099, BiOP3, Institut National de la Recherche Agronomique, Le Rheu, France; and (M.B. & T.R.) INRA – BIOGER, Versailles, France.*

08:45 C1-2 **Identification of *Penicillium* isolates associated with blue mould on apples in southern Ontario, using PCR-RFLP.** V. Popovic, K.W. Ellens, and D. Errampalli. *Agriculture and Agri-Food Canada, Southern Crop Protection and Food Research Centre, Vineland Station, ON, Canada.*

09:00 C1-3 **Induction of hydroxycinnamic acids in canola cultivars leads to differential responses to various pathogenicity groups of *Leptosphaeria maculans*.** A. El Hadrami, W.G.D. Fernando, and F. Daayf. *Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada.*

09:15 C1-4 **The Soybean Rust Sentinel Plot Program: Molecular identification, screening and tracking of *Phakopsora pachyrhizi*.** S. Hambleton, R. Tropiano, and A. Tenuta. *Agriculture and Agri-Food Canada, Eastern Cereal and Oilseed Research Centre, Ottawa, ON, Canada; and (A.T.) Ontario Ministry of Agriculture, Food and Rural Affairs, Ridgetown College, Ridgetown, ON, Canada.*

09:30 C1-5 **Marker based identification of *Lr34* in Canadian wheat cultivars.** B.D. McCallum and D. Somers. *Agriculture and Agri-Food Canada, Cereal Research Centre, Winnipeg, MB, Canada.*

09:45 C1-6 **Fruit breeding at the University of Saskatchewan.** R.H. Bors. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada.*

C2. Plant development and improvement 1 **Room: Gallery B**

Moderator: Jonathan Page

08:30	C2-1	**Inter simple sequence repeat (ISSR) markers to assess genetic diversity and relatedness within strawberry cultivars and breeding lines.** S.C. Debnath, S. Khanizadeh, A.R. Jamieson, and C. Kempler. *Agriculture and Agri-Food Canada, Atlantic Cool Climate Crop Research Centre, St. John's, NL, Canada; (S.K.) Agriculture and Agri-Food Canada, Horticultural Research and Development Centre, St-Jean-sur-Richelieu, QC, Canada; (A.R.J.) Agriculture and Agri-Food Canada, Atlantic Food and Horticulture Research Centre, Kentville, NS, Canada; and (C.K.) Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Agassiz, BC, Canada.*
08:45	C2-2	**How the antimalarial artemisinin is made in plants.** P.S. Covello, K.T. Teoh, D.R. Polichuk, D.W. Reed, and G. Nowak. *National Research Council, Plant Biotechnology Institute, Saskatoon, SK, Canada.*
09:00	C2-3	**Cellular localization and its molecular regulation of Arabidopsis cyclin-dependent kinase inhibitors.** D.A. Bird, Y. Zhou, M.M. Buruiana, L.C. Fowke, and H. Wang. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada; and (H.W.) Department of Biochemistry, University of Saskatchewan, Saskatoon, SK, Canada.*
09:15	C2-4	**Development of the soybean seed coat cuticle.** K. Ranathunge, S. Shao, C.A. Peterson, and M.A. Bernards. *Department of Biology, University of Waterloo, Waterloo, ON, Canada; and (S.S. & M.A.B.) Department of Biology, the University of Western Ontario, London, ON, Canada.*
09:30	C2-5	**Do members of the Lycopodiaceae possess endodermal Casparian bands?** D.E. Enstone and C.A. Peterson. *Department of Biology, University of Waterloo, Waterloo, ON, Canada.*
09:45	C2-6	**Proteomic analysis of mature tomato (*Lycopersicon esculentum*) and *Arabidopsis thaliana* pollen.** I.S. Sheoran, K.A. Sproule, A.R.S. Ross, D.J.H. Olson, and V.K. Sawhney. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada; and (A.R.S.R. & D.J.H.O.) National Research Council of Canada, Plant Biotechnology Institute, Saskatoon, SK, Canada.*

09:00 – 10:00 Campbell Scientific datalogger demonstration (Gallery Suite A (1))

10:00 – 10:30 Coffee break, posters and trade show (Salon A and Salon East)

10:30 – 11:30 Zeiss microscopy demonstration (Gallery Suite A (1))

10:30 – 12:00 Special session B

SB1. Progress in organic cropping systems (CSA) — Room: Gallery C

Moderator: Adrian Johnston

10:30 SB1-1 **Organic cropping in the semi-arid prairies: Opportunities, challenges and progress.** S.A. Brandt, E.N. Johnson, S.S. Malhi, R.P. Zentner, A.G. Thomas, and O.O. Olfert. *Agriculture and Agri-Food Canada, Scott Research Farm, Scott, SK, Canada; (S.S.M.) Agriculture and Agri-Food Canada, Melfort Research Farm, Melfort, SK, Canada; (R.P.Z.) Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada; and (A.G.T. & O.O.O.) Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada.*

11:00 SB1-2 **Soil-plant interactions in long-term organic cropping systems.** M. Entz, M. Tenuta, C. Welsh, A. Nelson, Y. Shen, and J. Froese. *Department of Plant Science and (M.T.) Department of Soil Science, University of Manitoba, Winnipeg, MB, Canada; (A.N.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada; and (Y.S.) Langzou University, Gansu Province, People's Republic of China.*

11:30 SB1-3 **Economic and social impacts of organic production systems.** R. McCrae, B. Frick, and R. Martin. *Organic Agriculture Centre of Canada, Truro, NS, Canada.*

SB2. Emerging plant disease epidemics (CPS) — Room: Gallery D

Moderator: Michael Celetti

10:30 SB2-1 **Introduction: The importance of emerging plant diseases in Canada.** M.J. Celetti and G.J. Boland. *Ontario Ministry of Agriculture, Food and Rural Affairs, University of Guelph, Guelph, ON, Canada; and (G.J.B.) Department of Environmental Biology, University of Guelph, Guelph, ON, Canada.*

10:40 SB2-2 **Emerging diseases in Canadian forests.** R. Wilson. *Ontario Ministry of Natural Resources, Forest Management Branch, Sault Ste. Marie, ON, Canada.*

11:00 SB2-3 **Emerging diseases of horticultural crops in Canada.** G.D. Jesperson and S. Sabaratnam. *British Columbia Ministry of Agriculture and Lands, Kelowna, BC, Canada; and (S.S.) British Columbia Ministry of Agriculture and Lands, Abbotsford, BC, Canada.*

11:20 SB2-4 **Emerging diseases of field crops in western Canada: Rusts, clubs, spots, staggers and blasts.** R.A.A. Morrall, R.J. Howard, P.G. Pearse, B.D. Gossen, and D.A. Kaminski. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada; (R.J.H.) Alberta Agriculture and Food, Brooks, AB, Canada; (P.G.P.) Saskatchewan Agriculture and Food, Regina, SK, Canada; (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada; and (D.A.K.) Manitoba Agriculture, Food and Rural Initiatives, Carman, MB, Canada.*

11:40 SB2-5 **SB2-5. The Canadian Plant Health response to emerging diseases: What role does CFIA play? What makes an emerging disease a quarantine pest?** M. Wood. *National Manager, Horticulture Section, Canadian Food Inspection Agency, Ottawa, ON, Canada.*
– Presented by T. Herman.

SB3. Communicating plant science **Room: Blair Nelson**
Moderators: Mary Leggett, Jill Thomson

10:30	SB3-1	**The future of science in education.** J. McVittie. *College of Education, University of Saskatchewan, Saskatoon, SK, Canada.*
11:00	SB3-2	**Biotech Week: A national perspective.** J. Tranberg. *Ag-West Bio Inc., Saskatoon, SK, Canada.*
11:30	SB3-3	**How to write and speak about science to nonscientists.** M. Robin. *Office of Research Communications, University of Saskatchewan, Saskatoon, SK, Canada.*

10:30 – 12:00 Session D

D1. Plant responses to the environment 1 **Room: Gallery A**
Moderator: Karen Tanino

10:30	D1-1	**Nitrogen fertilization of butternut squash (*Cucurbita moschata* [Duchesne ex Lam.] Duchesne ex Poir.): Yield, N uptake, and N use efficiency.** L.L. Van Eerd. *University of Guelph, Ridgetown Campus, Ridgetown, ON, Canada.*
10:45	D1-2	***Botrytis cinerea* manipulates the antagonistic effects between plant immune pathways to restore its disease.** M. El Oirdi and K. Bouarab. *Centre de Recherche en Amélioration Végétale, Département de Biologie, Université de Sherbrooke, Sherbrooke, QC, Canada.*
11:00	D1-3	**Ferric and cupric reductase activities by iron-limited cells of the green alga *Chlorella kessleri*: Quantification via oxygen electrode.** H.G. Weger, C.N. Walker, and M.B. Fink. *Department of Biology, University of Regina, Regina, SK, Canada.*
11:15	D1-4	**Functional analysis of poplar herbivore defense proteins and their effects on insect pests.** C.P. Constabel and I.T. Major. *Centre for Forest Biology and Department of Biology, University of Victoria, Victoria, BC, Canada.*
11:30	D1-5	**Mitochondrial anaerobic ATP synthesis using nitrite as an electron acceptor.** A.U. Igamberdiev, M. Stoimenova, and R.D. Hill. *Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada.*

D2. Plant development and improvement 2 **Room: Gallery B**

Moderator: Gavin Humphreys

10:30	D2-1	**Development of smut resistant hulless barley using molecular markers.** T.S. Grewal, B.G. Rossnagel, and G.J. Scoles. *Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada.*
10:45	D2-2	**Field performance of double haploid dill (*Anethum graveolens* L.).** D. Waterer and A. Ferrie. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada; and (A.F.) National Research Council, Plant Biotechnology Institute, Saskatoon, SK, Canada.*
11:00	D2-3	**Mapping quantitative trait loci controlling common bunt resistance in the spring wheat cross 'RL4452 × AC Domain'.** D.G. Humphreys, B. Fofana, S. Cloutier, C.A. McCartney, and D.J. Somers. *Agriculture and Agri-Food Canada, Cereal Research Centre, Winnipeg, MB, Canada; and (C.A.M.) Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada.*
11:15	D2-4	**Age-related resistance studies with the potential to improve biofuel production.** R.K. Cameron, J. Carviel, F. Al-Daoud, and A. Mohammad. *Department of Biology, McMaster University, Hamilton, ON, Canada.*
11:30	D2-5	**Mapping QTLs for pre-harvest sprouting tolerance in spring wheat: Implication in hard white wheat breeding.** B. Fofana, D.G. Humphreys, G. Rasul, S. Cloutier, S.M. Woods, O.M. Lukow, and D.J. Somers. *Agriculture and Agri-Food Canada, Cereal Research Centre, Winnipeg, MB, Canada.*

12:00 – 13:00 CBA – Mycology Section (Gallery A); Bring your lunch

12:00 – 13:00 CBA – Teaching Section (Gallery B); Bring your lunch

12:00 – 13:00 CBA – Systematics & Phytogeography Section (Gallery D); Bring your lunch

12:00 – 13:30 Lunch (Grand Salon and Salon B,C,D)

12:00 – 13:30 Posters and trade show (Salon A and Salon East)

13:30 – 15:00 Special session C

SC1. Designing a new agri-food industry 1 — Room: Gallery D

(Sponsored by Saskatchewan Wheat Pool)

Moderators: Coreen Franke, Mark Kuchuran

13:30		**Introduction and opening remarks**
13:35	SC1-1	**Trends, opportunities and challenges for agriculture as they relate to the emerging bio-economy.** P.A. O'Sullivan. *Ag-West Bio Inc., Saskatoon, SK, Canada.*
13:50	SC1-2	**Agriculture as a solution provider to health: The Flax Canada 2015 initiative.** K.C. Fitzpatrick. *Director of Health and Nutrition, Flax Canada 2015, Winnipeg, MB, Canada.*
14:20	SC1-3	**The good we get from grain™.** M. Pickard. *InfraReady Products (1998) Ltd., Saskatoon, SK, Canada.*
14:40	SC1-4	**Enhanced phytosterol ester biosynthesis in seed oil.** J. Zou. *National Research Council of Canada, Plant Biotechnology Institute, Saskatoon, SK, Canada.*

SC2. Emerging barriers to marketing crops (CSA) — Room: Blair Nelson

Moderator: Brian Rossnagel

13:30	SC2-1	**The good, the novel and the bad.** G.G. Rowland. *Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada.*
14:00	SC2-2	**Challenges for the export of Canadian crops.** P.A. Burnett. *Grain Research Laboratory, Canadian Grain Commission, Winnipeg, MB, Canada.*
14:30	SC2-3	**The changing market for potatoes: Challenges for the development and introduction of new varieties.** T.R. Tarn. *Agriculture and Agri-Food Canada, Potato Research Centre, Fredericton, NB, Canada.*

13:30 – 15:00 Session E

E1. Plant responses to the environment 2 **Room: Gallery A**
Moderator: Ken Wilson

13:30	E1-1	**Overexpression of damaged DNA binding protein 1A (DDB1A) enhances *Arabidopsis* DNA repair.** W.M. Al Khateeb and D.F. Schroeder. *Department of Botany, University of Manitoba, Winnipeg, MB, Canada.*
13:45	E1-2	**Non-targeted FT-ICR MS analysis of AM fungi growth stimulating carrot root exudates.** Y. Ferhatoglu, D.D. Douds, and G. Nagahashi. *Phenomenome Discoveries, Saskatoon, SK, Canada; and (D.D.D. & G.N.) USDA Agriculture Research Service, Eastern Regional Research Center, Wyndmoor, PA, USA.*
14:00	E1-3	**Transcriptional regulation of PR-5 proteins during fungal infection in *Prunus* spp.** A. El Kereamy, A. Taheri, D. Errampalli, K.P. Pauls, and S. Jayasankar. *Department of Plant Agriculture, University of Guelph, Vineland Station, ON, Canada; (D.E.) Agriculture and Agri-Food Canada, Vineland Station, ON, Canada; and (K.P.P.) Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada.*
14:15	E1-4	**Functional analyses of *Alpha-dioxygenase* in salt-stressed *Arabidopsis*.** T.S.T. Aung, A. Plant, and M. Hamberg. *Department of Biological Sciences, Simon Fraser University, Burnaby, BC, Canada; and (M.H.) Department of Medical Biochemistry and Biophysics, Karolinska Institute, Stockholm, Sweden.*
14:30	E1-5	**Detection of algal metabolic phenotypes by ^{1}H-NMR.** H.D. Bestman, J. Zee, and C. Preuss. *Department of Biology and the King's Centre for Molecular Structure, The King's University College, Edmonton, AB, Canada.*
14:45	E1-6	**Stomatal conductance and heat stress genetic mechanism.** N. Murtaza. *Department of Plant Breeding and Genetics, University College of Agriculture, Bahauddin Zakaryia University, Multan, Pakistan.*

E2. Plant development and improvement 3 — Room: Gallery B

Moderator: Yantai Gan

13:30	E2-1	**Genotypic variation in traits contributing to early seedling vigour in field grown barley.** A.O. Anyia, J.J. Slaski, P.R. Watson, and J.M. Nyachiro. *Alberta Research Council, Vegreville, AB, Canada; and (J.M.N.) Alberta Agriculture and Food, Lacombe, AB, Canada.*
13:45	E2-2	**Floral symmetry and nectary structure: Investigation of spurless, single-spurred and peloric, multi-spurred flowers of toadflax (*Linaria genistifolia* (L.) P. Mill.).** A.R. Davis and S. Vogel. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada; and (S.V.) Department of Morphology and Reproductive Ecology, Institute of Botany, University of Vienna, Vienna, Austria*.
14:00	E2-3	**Vegetable research at the University of Saskatchewan.** D. Waterer. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada.*
14:15	E2-4	**The *Arabidopsis autobahn* mutation causes defects to auxin transport and alters leaf vein pattern and phyllotaxis.** J. Garrett, J. Meservy, L. Tavernini, M. Blackshaw, and E.A. Schultz. *Department of Biological Sciences, University of Lethbridge, Lethbridge, AB, Canada.*
14:30	E2-5	**Functional characterization of four Arabidopsis *UEV1* genes and the involvement of *AtUEV1D* in DNA damage response.** R. Wen, J.A. Torres-Acosta, X. Lai, L. Pastushok, L. Newton, W. Xiao, and H. Wang. *Department of Microbiology and Immunology, University of Saskatchewan, Saskatoon, SK, Canada; and (J.A.T.-A. & H.W.) Department of Biochemistry, University of Saskatchewan, Saskatoon, SK, Canada.*
14:45	E2-6	**Hormonal interactions in fruit development.** J.A. Ozga, B.T. Ayele, and D.M. Reinecke. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

E3. Pest management 2 **Room: Gallery C**

Moderator: Curt McCartney

13:30	E3-1	**Comparative genomics to assess horizontal gene transfer between mycorrhizal fungi and plants.** T. Hsiang. *Department of Environmental Biology, University of Guelph, Guelph, ON, Canada.*
13:45	E3-2	**An extract from dwarf mistletoe (genus *Arceuthobium*) demonstrates antimicrobial activity against Gram-positive bacteria, including Methicillin Resistant *Staphylococcus aureus* (MRSA).** K.Y. Pernitsky and C.M. Ross. *Department of Biological Sciences, Thompson Rivers University, Kamloops, BC, Canada.*
14:00	E3-3	**Detection of *Pantoea stewartii* by Taqman real-time PCR.** J.T. Tambong, N. Mwange, M. Bergeron, T. Ding, and F. Mandy. *Agriculture and Agri-Food Canada, Eastern Cereal and Oilseed Research Centre, Ottawa, ON, Canada; and (M.B., T.D. & F.M.) Immunology Laboratory, Centre for Infectious Disease Prevention and Control, Ottawa, ON, Canada.*
14:15	E3-4	**Direct real-time PCR (DRT-PCR): Rapid and cost effective detection and its applications on different pathogen diagnosis.** W.-S. Kim, A.M. Svircev, and L.W. Stobbs. *Agriculture and Agri-Food Canada, Southern Crop Protection and Food Research Centre, Vineland, ON, Canada.*
14:30	E3-5	**Responses of lodgepole pine to infection by western gall rust.** J.M. Wolken and P.V. Blenis. *Department of Renewable Resources, University of Alberta, Edmonton, AB, Canada.*
14:45	E3-6	**Enzymatic browning in selected apple genotypes.** A.P.K. Joshi, S. Cheng, S. Khanizadeh, N.L. Pitts, and H.P.V. Rupasinghe. *Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, NS, Canada; and (S.K.) Agriculture and Agri-Food Canada, Horticultural Research and Development Centre, St-Jean-sur-Richelieu, QC, Canada.*

15:00 – 15:30 Coffee break, posters and trade show (Salon A and Salon East)

15:30 – 17:00 Special session D

SD1. Designing a new agri-food industry 2 **Room: Gallery D**

(Sponsored by Saskatchewan Wheat Pool)

Moderators: Coreen Franke, Mark Kuchuran

15:30 SD1-1 **Balancing product safety and product quality from laboratory to pilot plant.** A. Abdellatif. *Canagra Technologies Inc., Saskatoon, SK, Canada.*

15:50 SD1-2 **Biodiesel opportunities.** M. Reaney. *Department of Applied Microbiology and Food Science, University of Saskatchewan, Saskatoon, SK, Canada.*

16:10 SD1-3 **Maximizing the value of canola protein products: The problem, solutions and opportunities.** D.D. Maenz. *MCN BioProducts Inc., Saskatoon, SK, Canada.*

SD2. Natural products (CSPP) **Room: Blair Nelson**

Moderator: Patrick Covello

15:30 SD2-1 **The structure, functions and biosynthesis of suberin.** M.A. Bernards. *Department of Biology, the University of Western Ontario, London, ON, Canada.*

16:00 SD2-2 **Dissecting the nicotine biosynthetic pathway using gene silencing.** J.E. Page, E. Liu, and A.T. Todd. *National Research Council of Canada, Plant Biotechnology Institute, Saskatoon, SK, Canada.*

16:30 SD2-3 **Regulation of isoprenoid metabolism in medicinal plants.** A. Lane, K. Biswas, and S.S. Mahmoud. *Departments of Chemistry, and Earth and Environmental Sciences, University of British Columbia Okanagan, Kelowna, BC, Canada.*

15:30 – 17:00 Session F

F1. Plant development and improvement 4 **Room: Gallery A**
Moderator: Inder Sheoran

15:30 F1-1 **Selection for straw fibre in oilseed flax.** N.A. Coetzee and G.G. Rowland. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada.*

15:45 F1-2 **Identification of factors affecting isoflavonoid biosynthesis in soybean seeds.** S. Dhaubhadel. *Agriculture and Agri-Food Canada, Southern Crop Protection and Food Research Centre, London, ON, Canada.*

16:00 F1-3 **Differential regulation of ethylene perception elements during fruit ripening in plum (*Prunus salicina* L.).** I. El-Sharkawy, W.S. Kim, A. El-Kereamy, A.M. Svircev, D.C.W. Brown, and S. Jayasankar. *Department of Plant Agriculture, University of Guelph, Vineland Station, ON, Canada; (W.S.K. & A.M.S.) Agriculture and Agri-Food Canada, Vineland Station, ON, Canada; and (D.C.W.B.) Agriculture and Agri-Food Canada, Southern Crop Protection and Food Research Centre, London, ON, Canada.*

16:15 F1-4 **Developing a scale-up system for the micropropagation of thidiazuron-induced strawberry shoots using a bioreactor.** S.C. Debnath. *Agriculture and Agri-Food Canada, Atlantic Cool Climate Crop Research Centre, St. John's, NL, Canada.*

16:30 F1-5 **NSERC News / Nouvelles du CRSNG.** M.V. Lamarca. *Life Sciences and Special Research Opportunities / Sciences de la vie et Occasions spéciales de recherche, Research Grants and Scholarships / Subventions de recherche et Bourses, Ottawa, ON, Canada.*

F2. Plant development and improvement 5 — Room: Gallery B

Moderator: Hong Wang

15:30 F2-1 **Overview of research towards optimizing *Brassica* sp. as biodiesel feedstocks - A research theme in the "Green Crop Network".** J.K. Vessey, W. Keller, L. Kunst, P. McVetty, and H. Fei. *Department of Biology, Saint Mary's University, Halifax, NS, Canada; (W.K.) National Research Council of Canada, Plant Biotechnology Institute, Saskatoon, SK, Canada; (L.K.) Department of Botany, University of British Columbia, Vancouver, BC, Canada; and (P.McV.) Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada.*

15:45 F2-2 **Phylogenomic evidence for pterin-dependent enzymes in plants.** A.D. Hanson, A. Noiriel, and V. de Crécy-Lagard. *Horticultural Sciences Department, University of Florida, Gainesville, FL, USA; and (V. de C.-L.) Microbiology and Cell Science Department, University of Florida, Gainesville, FL, USA.*

16:00 F2-3 **Microarray analysis of phenylpropanoid gene expression.** V.S. Bhinu, U.A. Schäfer, R. Li, J. Huang, and A. Hannoufa. *Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada.*

16:15 F2-4 **Characterisation of *Ascochyta rabiei - Cicer arietinum* interaction for resolving the genetic basis of resistance.** H.M. Booker, G.K. Kishore, A. Sharpe, B. Tar'an, and L. Buchwaldt. *Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada; and (B.T.) Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada.*

16:30 F2-5 **A flavone-specific *O*-methyltransferase gene family in grain plants.** R.K. Ibrahim and J.M. Zhou. *Biology Department, Concordia University, Montréal, QC, Canada.*

16:45 F2-6 **Evaluation of environmental effects and stability of isoflavone content in soybean (*Glycine max* L. Merr.).** S.E. Murphy, L. Woodrow, and G.R. Ablett. *Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada; (L.W.) Agriculture and Agri-Food Canada, Harrow, ON, Canada; and (G.R.A.) Ridgetown Campus, University of Guelph, Ridgetown, ON, Canada.*

F3. Plant responses to the environment 3 **Room: Gallery C**
Moderator: Doug Waterer

15:30 F3-1 **Determination of dry matter and stability of carotenoids in kale and spinach during drying.** M.G. Lefsrud, D.A. Kopsell, C.E. Sams, R.M. Augé, J.B. Wills Jr., and A.J. Both. *Department of Bioresource Engineering, McGill University, Ste-Anne-de-Bellevue, QC, Canada; (D.A.K., C.E.S. & R.M.A.) Plant Sciences, University of Tennessee, Knoxville, TN, USA; (J.B.W.) Biosystems Engineering and Soil Science Departments, University of Tennessee, Knoxville, TN, USA; and (A.J.B.) Department of Bioresource Engineering, Rutgers University, New Brunswick, NJ, USA.*

15:45 F3-2 **Ecology of feral alfalfa (*Medicago sativa* L.) populations along the road verges of southern Manitoba.** M.V. Bagavathiannan, R.C. Van Acker, M.H. Entz, S. McLachlan, and L. Friesen. *Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada; (R.C.V.A.), Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada; and (S.M.) Department of Environment and Geography, University of Manitoba, Winnipeg, MB, Canada.*

16:00 F3-3 **Density fluctuations in *Pinus banksiana* Lamb. and *Picea mariana* [Mill.] BSP trees, in Nopiming Provincial Park, Manitoba.** M. Hoffer and J. Tardif. *Centre for Forest Interdisciplinary Research (C-FIR) and Department of Biology, University of Winnipeg, Winnipeg, MB, Canada.*

16:15 F3-4 **Influence of mycorrhizal fungi on growth and water relations in *Populus*.** J.A. Siemens and J.J. Zwiazek. *Department of Renewable Resources, University of Alberta, Edmonton, AB, Canada.*

16:30 F3-5 **Effects of summer CO_2 enrichment on leaf photosynthesis and fruit yield of greenhouse tomatoes.** Q. Wang, X. Hao, S. Khosla, and S. Borhan. *Greenhouse and Processing Crops Research Centre, Agriculture and Agri-Food Canada, Harrow, ON, Canada; and (S.K.) Ontario Ministry of Agriculture, Food and Rural Affairs, Harrow, ON, Canada.*

16:45 F3-6 **Neural networks to predict weekly yields of sweet peppers in a commercial greenhouse.** B.D. Hill and W.C. Lin. *Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada; and (W.C.L.) Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Agassiz, BC, Canada.*

17:00 – 18:30 Poster session with authors present (odd #s) (Salon A and Salon East)

17:00 – 19:00 CSA – General discussion of members (Gallery Suite A (1))

18:00 – 18:30 CSHS Natural products special seminar

CSHS Natural products special seminar **Room: Blair Nelson**
Moderator: Shahrokh Khanizadeh

18:00 SA1-4 **Exploring native Canadian plants for human health.** R. Cao. *Agriculture and Agri-Food Canada, Food Research Program, Guelph, ON, Canada.*

19:00 Dinner (on your own)

20:00 – 21:00 Special lecture

Luella K. Weresub mycology lecture (CBA) **Room: Gallery B**
Moderator: Jim Traquair

20:00 SL1-1 **Developing microorganisms as bioherbicides - research at the interface of science and art.** G. Peng, S.M. Boyetchko, K.L. Bailey, and R. Hynes. *Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada.*

07:30 – 08:30	Registration	Gallery Suite B (2)
07:30 – 08:30	Posters and trade show	Salon A and Salon East
08:30 – 10:00	**Plenary 2:** Plant health networks: The international experience	**Salon B,C,D**
10:00 – 10:30	Coffee break, posters and trade show	Salon A and Salon East
10:30 – 12:00	**Plenary 2** (continued)	**Salon B,C,D**
12:00 – 14:30	CPS luncheon, Annual General Meeting and awards	Gallery A
12:00 – 14:30	CSPP luncheon, Annual General Meeting and awards	Gallery B
12:00 – 14:30	CBA luncheon, Annual General Meeting and awards	Gallery C
12:00 – 14:30	CSA luncheon, Annual General Meeting and awards	Gallery D
12:00 – 15:00	CSHS luncheon, Annual General Meeting, awards and election	Gallery Suite A (1)
14:30 – 15:00	Coffee break, posters and trade show	Salon A and Salon East
15:00 – 17:00	**Special session E**	
	SE1. Plant ecology and invasive species (CWSS/CBA)	Gallery D
15:00 – 17:00	**Session G**	
	G1. Pest management 3	Gallery A
	G2. Plant responses to the environment 4	Gallery B
16:00 – 17:00	CSA Board meeting	Gallery Suite A (1)
17:00 – 18:30	**CSHS Organic Horticulture Forum**	**Gallery B**
17:00 – 18:00	CBA – Ecology Section	Gallery D
18:00 – 19:00	**Cocktails (cash bar)**	**Salon B,C,D**
19:00 – 23:30	**Banquet and live band entertainment**	**Salon B,C,D**

07:30 – 08:30 Registration (Gallery Suite B (2))

07:30 – 08:30 Posters and trade show (Salon A and Salon East)

08:30 – 10:00 Plenary 2

PL2. Plant health networks: The international experience **Room: Salon B,C,D**
Moderators: Bruce Gossen, Liz Foster

08:30		**Opening remarks and introduction of speakers.**
08:45	PL2-1	**The U.S. National Plant Diagnostic Network: Critical infrastructure to protect natural and agricultural plant systems.** J.P. Stack. *Biosecurity Research Institute, Kansas State University, Manhattan, KS, USA.*
09:15	PL2-2	**USDA National Plant Protection Laboratory Accreditation Program (NPPLAP): Regulatory-related testing and networked plant health diagnostic laboratories.** L. Levy, P.H. Berger, and P.J. Shiel. *USDA, APHIS, PPQ, CPHST, NPGBL, BARC-East, Beltsville, MD, USA; and USDA, APHIS, PPQ, CPHST, Raleigh, NC, USA.*
09:45		**Questions and answers.**

10:00 – 10:30 Coffee break, posters and trade show (Salon A and Salon East)

10:30 – 12:00 Plenary 2 (continued)

PL2. Plant health networks: The international experience **Room: Salon B,C,D**
Moderators: Bruce Gossen, Liz Foster

10:30	PL2-3	**Plant heath networks for diagnostics, surveillance and research: The Australian approach.** P.C. Pheloung. *Australian Government Department of Agriculture, Fisheries and Forestry, Canberra, Australia.*
11:00	PL2-4	**PL2-4. Canadian plant health expertise and capabilities: Networking for the future.** N.K. Nishikawa and E. Foster. *National Laboratory Operations, Science Branch, Canadian Food Inspection Agency, Ottawa, ON, Canada.*
11:30		**Panel discussion**

12:00 – 14:30 CPS luncheon, Annual General Meeting and awards (Gallery A)

12:00 – 14:30 CSPP luncheon, Annual General Meeting and awards (Gallery B)

12:00 – 14:30 CBA luncheon, Annual General Meeting and awards (Gallery C)

12:00 – 14:30 CSA luncheon, Annual General Meeting and awards (Gallery D)

12:00 – 15:00 CSHS luncheon, Annual General Meeting, awards and election (Gallery Suite A (1))

14:30 – 15:00 Coffee break, posters and trade show (Salon A and Salon East)

15:00 – 17:00 Special session E

SE1. Plant ecology and invasive species (CWSS/CBA) **Room: Gallery D**
Moderator: David Clements

15:00 SE1-1 **Prioritizing non-indigenous species management using a survey, monitoring and modeling framework.** L.J. Rew, E. Lehnhoff, and B.D. Maxwell. *Land Resources and Environmental Sciences Department, Montana State University, Bozeman, MT, USA.*

15:20 SE1-2 **Integrating climate and trait models to predict the invasiveness of exotic plants in Canada's Eastern Prairie region.** R. Otfinowski, N.C. Kenkel, and P. Dixon. *Department of Botany, University of Manitoba, Winnipeg, MB, Canada; and (P.D.) Parks Canada, Western Canada Service Center, Winnipeg, MB, Canada.*

15:40 SE1-3 **Crested wheatgrass invasion in western Canada: Consequences and management.** S.D. Wilson and B.M. Vaness. *Department of Biology, University of Regina, Regina, SK, Canada.*

16:00 SE1-4 **Invasive plant management and ecological issues in Alberta.** D.E. Cole, D. Oyarzun, T.H. Dietzler, and J.R. King. *Pest Management Branch, Alberta Agriculture and Food, Edmonton, AB, Canada; (D.O.) Rural Programs, Alberta Agriculture and Food, Edmonton, AB, Canada; (T.H.D.) Municipal District of Rocky View, Calgary, AB, Canada; and (J.R.K.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

16:20 SE1-5 **Plant community response to herbivory and disturbance: Lessons for restoration of Garry oak ecosystems.** E.K. Gonzales, D.R. Clements, and V.M. LeMay. *Department of Forest Sciences, University of British Columbia, Vancouver, BC, Canada; (D.R.C.) Department of Biology, Trinity Western University, Langley, BC, Canada; and (V.M.L.) Department of Forest Resources Management, University of British Columbia, Vancouver, BC, Canada.*

16:40 SE1-6 **The role of plant ecology in conceptualizing invasive species.** B.M.H. Larson. *Department of Environment and Resource Studies, University of Waterloo, Waterloo, ON, Canada.*

15:00 – 17:00 Session G

G1. Pest management 3 — Room: Gallery A

Moderator: Miao Liu

15:00 G1-1 **Implications of foliar diseases and possible control strategies in wild blueberry production.** D.C. Percival, L.I. Stewart, and P.D. Hildebrand. *Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, NS, Canada; and (P.D.H.) Agriculture and Agri-Food Canada, Atlantic Food and Horticulture Research Centre, Kentville, NS, Canada.*

15:15 G1-2 **Virulence of stem rust race TTKS on Canadian wheat cultivars.** T. Fetch Jr. *Agriculture and Agri-Food Canada, Cereal Research Centre, Winnipeg, MB, Canada.*

15:30 G1-3 **Detached leaf approach for disease resistance or pathogenicity test requires reevaluation: A lesson from *Arabidopsis-Colletotrichum* interaction.** G. Liu, R. Kennedy, D.L. Greenshields, G. Peng, L. Forseille, and Y. Wei. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada; and (G.P. & L.F.) Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada.*

15:45 G1-4 **Antibody microarray for the detection of grapevine and tree fruit viruses.** I. Abdullahi, M. Rott, C. Masters, and R. Johnson. *Centre for Plant Health, Canadian Food Inspection Agency, Sidney, BC, Canada.*

16:00 G1-5 **Agriculture and Agri-Food Canada develops carrot foliage trimmer for control of Sclerotinia rot in carrots.** K.R. Sanderson and R.D. Peters. *Agriculture and Agri-Food Canada, Crops and Livestock Research Centre, Charlottetown, PE, Canada.*

16:15 G1-6 **Microscopic study of germ tube fusion in wheat leaf rust (*Puccinia triticina* Eriks).** X. Wang and B.D. McCallum. *Agriculture and Agri-Food Canada, Cereal Research Centre, Winnipeg, MB, Canada.*

16:30 G1-7 **Identity of tar spot of maple in Canada.** T. Hsiang and L. Tian. *Department of Environmental Biology, University of Guelph, Guelph, ON, Canada.*

16:45 G1-8 **Revisiting the classification of crown rust fungus: An insight from rDNA sequences.** M. Liu, R. Tropiano, E. McCabe, J. Bergeron, and S. Hambleton. *Agriculture and Agri-Food Canada, Eastern Cereal and Oilseed Research Centre, Ottawa, ON, Canada.*

G2. Plant responses to the environment 4 **Room: Gallery B**

Moderator: Rob Gulden

15:00	G2-1	**Enhancing the economic viability of home gardens.** H. Elsadr and D. Waterer. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada.*
15:15	G2-2	**Cover crops, nitrogen cycling and weed dynamics in subsequent cucumber (*Cucumis sativus* L.) crop.** L.L. Van Eerd, D.E. Robinson, and A. Verhallen. *University of Guelph, Ridgetown Campus, Ridgetown, ON, Canada; and (A.V.) Ontario Ministry of Agriculture, Food and Rural Affairs, Ridgetown, ON, Canada.*
15:30	G2-3	**Enhancement of salinity tolerance by engineering chloride volatilization into plants.** P. Koonjul, S. Kaur, S. Babayeva, and H.S. Saini. *Institut de recherche en biologie végétale, Université de Montréal, Montréal, QC, Canada; and (H.S.S.) Faculty of Environmental Studies, University of Waterloo, Waterloo, ON, Canada.*
15:45	G2-4	**The characterization of two green algal isolates from a northern Saskatchewan uranium mine site.** A.M. Macdonald and K.E. Wilson. *Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada.*
16:00	G2-5	**Hay yields are declining on Canadian farms: A Saskatchewan perspective.** P.G. Jefferson and F. Selles. *Western Beef Development Centre, Humboldt, SK, Canada; and (F.S.) Agriculture and Agri-Food Canada, Brandon Research Centre, Brandon, MB, Canada.*
16:15	G2-6	**Flower-visitor constancy in tall-grass prairie ecosystems.** D.B. Robson. *The Manitoba Museum, Winnipeg, MB, Canada.*
16:30	G2-7	**Leaf life span and plant height as adaptive traits along gradients of productivity and disturbance.** P. Ryser and J. O'Hara. *Department of Biology, Laurentian University, Sudbury, ON, Canada.*

16:00 – 17:00 CSA board meeting (Gallery Suite A (1))

17:00 – 18:30 CSHS Organic Horticulture Forum

CSHS Organic Horticulture Forum **Room: Gallery B**

Moderator: David Ehret

17:00 **Panel discussion.** B. Frick, T. Forge, M. Dorais, G.H. Neilsen, and R.K. Prange. *Organic Agriculture Centre of Canada, Truro, NS, Canada; (T.F.) Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Agassiz, BC, Canada; (M.D.) Agriculture and Agri-Food Canada, Horticultural Research Centre, Université Laval, Sainte-Foy, QC, Canada; (G.H.N.) Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Summerland, BC, Canada; and (R.K.P.) Agriculture and Agri-Food Canada, Atlantic Food and Horticulture Research Centre, Kentville, NS, Canada.*

17:00 – 18:00 CBA – Ecology Section (Gallery D)

18:00 – 19:00 Cocktails (cash bar) (Salon B,C,D)

19:00 – 23:30 Banquet and live band entertainment (Salon B,C,D)

07:30 – 08:30	Registration	Gallery Suite B (2)
07:30 – 08:30	**Poster and trade show take-down**	**Salon A and Salon East**
08:00 – 12:00	**Post-conference morning field trips**	**Buses will be on the west side of TCU Place at 07:45**
	Field trip 1: University of Saskatchewan Agriculture Building and AAFC-Plant Gene Resources of Canada	
	Field trip 2: Canadian Light Source Synchrotron and Plant Science Greenhouse	
	Field trip 3: University of Saskatchewan Horticulture field plots and Patterson Garden	
08:30 – 10:00	**Special session F**	
	SF1. Organic horticulture: Separating fact from fantasy (CSHS)	Gallery A
	SF2. Phloem and long distance signalling (CSPP)	Gallery B
08:00 – 10:00	SF3. Nutrient cycling in the soil-plant system: Filling the gaps 1 (AAFC/CSA)	Gallery D
10:00 – 10:30	Coffee break; Poster and trade show take-down	Salon A and Salon East
10:30 – 12:00	**Special session G**	
	SG1. Floristics for the future (CBA)	Gallery A
	SG2. Linking plant pathology with industry (CPS)	Gallery B
10:20 – 12:00	SG3. Nutrient cycling in the soil-plant system: Filling the gaps 2 (AAFC/CSA)	Gallery D
12:00	**End of conference**	
12:00 – 16:00	**Post-conference afternoon field trips**	**Buses will be on the west side of TCU Place at 11:45**
	Field trip 1: University of Saskatchewan Agriculture Building and AAFC-Plant Gene Resources of Canada	
	Field trip 2: Canadian Light Source Synchrotron and Plant Science Greenhouse	
	Field trip 3: University of Saskatchewan Horticulture field plots and Patterson Garden	
12:30 – 14:30	CSPP Board meeting	Gallery B
12:30 – 14:30	CPS Board meeting	Hilton Garden Inn (Prince Albert East and West Rooms)
13:00 – 16:30	**CSA field trip:** U of S Kernen Crop Research Farm and AAFC-Saskatoon Research Centre Research Farm	**Bus will be on the west side of TCU Place at 12:45**
14:00 – 15:30	CBA Board meeting	Gallery Suite A (1)
15:30 – 17:30	Plant Canada Board meeting	Hilton Garden Inn (Prince Albert East and West Rooms)

07:30 – 08:30 Registration (Gallery Suite B (2))

07:30 – 08:30 Poster and trade show take-down (Salon A and Salon East)

08:00 – 12:00 Post-conference morning field trips
(Buses will be on the west side of TCU Place at 07:45)

08:00	Field trip 1	- University of Saskatchewan Agriculture Building - Agriculture and Agri-Food Canada, Plant Gene Resources of Canada
08:00	Field trip 2	- Canadian Light Source Synchrotron - Plant Science Greenhouse
08:00	Field trip 3	- University of Saskatchewan Horticulture field plots - Patterson Garden

08:30 – 10:00 Special session F

SF1. Organic horticulture: Separating fact from fantasy (CSHS) **Room: Gallery A**
Moderator: David Ehret

08:30	SF1-1	**Organic production of vegetables: State of the art and challenges.** M. Dorais. *Agriculture and Agri-Food Canada, Horticultural Research Centre, Université Laval, Sainte-Foy, QC, Canada.*
09:00	SF1-2	**Organic fruit production: Managing reality and perception.** G.H. Neilsen, D.T. Lowery, T. Forge, D. Neilsen, and D. Ehret. *Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Summerland, BC, Canada; and (T.F. & D.E.) Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Agassiz, BC, Canada.*
09:30	SF1-3	**Are organically-produced fruits and vegetables safer and more nutritious than conventionally-produced fruits and vegetables: A review of the literature.** R.K. Prange. *Agriculture and Agri-Food Canada, Atlantic Food and Horticulture Research Centre, Kentville, NS, Canada.*

SF2. Phloem and long distance signalling (CSPP) **Room: Gallery B**

Moderator: Carol Peterson

08:30 SF2-1 **How do molecules get into the phloem?** R. Turgeon. *Department of Biology, Cornell University, Ithaca, NY, USA.*

09:00 SF2-2 **Regulation of cell-to-cell and long-distance RNA trafficking.** B. Ding. *Department of Plant Cellular and Molecular Biology and Plant Biotechnology Center, Ohio State University, Columbus, OH, USA.*

09:30 SF2-3 **Phloem structure in *Eriophorum vaginatum* accommodates efficient nutrient recycling in nutrient-poor wetlands.** E. Cholewa. *Department of Biology, Nipissing University, North Bay, ON, Canada.*

SF3. Nutrient cycling in the soil-plant system: Filling the gaps 1 (AAFC/CSA) **Room: Gallery D**

Moderator: Chantal Hamel

08:00 **Welcome**

08:10 SF3-1 **Nitrogen cycling: Reducing losses from agricultural systems.** J.A. MacLeod and M. Grimmett. *Agriculture and Agri-Food Canada, Crops and Livestock Research Centre, Charlottetown, PE, Canada.*

08:40 SF3-2 **Behaviour and fate of phosphorus in soil: Changing concepts and research perspectives of soil phosphorus chemistry and fertility.** T.Q. Zhang and T. Forge. *Agriculture and Agri-Food Canada, Greenhouse and Processing Crops Research Centre, Harrow, ON, Canada; and (T.F.) Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Agassiz, BC, Canada.*

09:10 SF3-3 **Soil food web structure and the use of nematodes as indicators.** T.A. Forge, S. Bittman, C. Hamel, A. Nayyar, C. Landry, and T. Zhang. *Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Agassiz, BC, Canada; (C.H. & A.N.) Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada; (C.L.) Institut de Recherche et de Développement en Agroenvironnement, Sainte-Foy, QC, Canada; and (T.Z.) Agriculture and Agri-Food Canada, Greenhouse and Processing Crops Research Centre, Harrow, ON, Canada.*

09:40 SF3-4 **Immediate and residual effects of swine manure and its compost on soil phosphorus fractions in a clay loam soil under corn-soybean rotation.** A. Herath, T.Q. Zhang, C. Hamel, C.S. Tan, T. Welacky, and M.J. Goss. *Department of Land Resource Science, University of Guelph, Guelph, ON, Canada; (T.Q.Z., C.S.T. & T.W.) Agriculture and Agri-Food Canada, Greenhouse and Processing Crops Research Centre, Harrow, ON, Canada; and (C.H.) Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada.*

10:00 – 10:30 Coffee break; Poster and trade show take-down (Salon A and Salon East)

10:30 – 12:00 Special session G

SG1. Floristics for the future (CBA) — Room: Gallery A

Moderators: Tim Dickinson, Deborah Metsger

10:30 SG1-1 **Biodiversity and floristics: Gathering data to answer big questions.** A. Bruneau. *Département de Sciences biologiques, Université de Montréal, Montréal, QC, Canada.*

10:50 SG1-2 **Oil and water? Geospatial technologies, taxonomy, and collection databases: The case of E-Flora BC.** B. Klinkenberg. *Geography Department, University of British Columbia, Vancouver, BC, Canada.*

11:10 SG1-3 **Building on existing resources: Onwards, upwards, downwards, and sideways.** M.E. Barkworth. *Intermountain Herbarium, Department of Biology, Utah State University, Logan, UT, USA.*

11:30 SG1-4 **Panel discussion on the future of floristics in Canada.** Moderator: B. Ford. *Department of Botany, University of Manitoba, Winnipeg, MB, Canada.*

SG2. Linking plant pathology with industry (CPS) — Room: Gallery B

Moderator: Simon Shamoun

10:30 SG2-1 **The BioMal® story: The legacy of a government-industry partnership.** K.L. Bailey and M. Leggett. *Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada; and (M.L.) Philom Bios Inc., Saskatoon, SK, Canada.*

11:00 SG2-2 **From the forest to the lab bench and back again: The cooperative venture to launch the biocontrol fungus *Chondrostereum purpureum*.** W. Hintz, S.F. Shamoun, and P. de la Bastide. *Biology Department, University of Victoria, Victoria, BC, Canada; and (S.F.S.) Natural Resources Canada, Pacific Forestry Centre, Victoria, BC, Canada.*

11:30 SG2-3 **The role of Industry in facilitating the commercialization of biopesticides.** P. Marrone. *Marrone Organic Innovations Inc., Davis, CA, USA.*

SG3. Nutrient cycling in the soil-plant system: Filling the gaps 2 (AAFC/CSA) **Room: Gallery D**

Moderator: Chantal Hamel

10:20	SG3-1	**Phosphorus fertilization influence biological interactions in forage stands.** A. Nayyar, C. Hamel, T. Forge, F. Selles, and P. Jefferson. *Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada.*
10:40	SG3-2	**Crop fertilization can modify soil microbial community structure, function, and soil C to N ratio.** C. Hamel, A.F. Cruz, K. Hanson, F. Selles, and R. Zentner. *Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada.*
11:00	SG3-3	**The impact of cropping systems with differing intensities of grain legumes on soil quality.** G.P. Lafond, H. Hunter, R. Lemke, N. Lupwayi, and W.E. May. *Agriculture and Agri-Food Canada, Indian Head Research Farm, Indian Head, SK, Canada; (R.L.) Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada; (H.H.) Indian Head Agricultural Research Foundation, Indian Head, SK, Canada; and (N.L.) Agriculture and Agri-Food Canada, Beaverlodge Research Farm, Beaverlodge, AB, Canada.*
11:20	SG3-4	**Long term effects of dairy manure on grass: Production and soil nutrient shifts.** S. Bittman, T. Forge, C.G. Kowalenko, D.E. Hunt, F. Bounaix, and T. Zhang. *Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Agassiz, BC, Canada; and (T.Z.) Agriculture and Agri-Food Canada, Greenhouse and Processing Crops Research Centre, Harrow, ON, Canada.*
11:40	SG3-5	**Characterization and comparison of fungal and mycorrhizal communities following various P-fertilization in a maize/soybean rotation.** M.-S. Beauregard, C. Hamel, and M. St-Arnaud. *Institut de recherche en biologie végétale, Jardin botanique de Montréal, Montréal, QC, Canada; and (C.H.) Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada.*

12:00 End of conference

12:00 – 16:00 Post-conference afternoon field trips
(Buses will be on the west side of TCU Place at 11:45)

12:00	Field trip 1	- University of Saskatchewan Agriculture Building - Agriculture and Agri-Food Canada, Plant Gene Resources of Canada
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12:30 – 14:30 CSPP Board meeting (Gallery B)

12:30 – 14:30 CPS Board meeting (Prince Albert East and West Rooms, Hilton Garden Inn)

13:00 – 16:30 CSA field trip (Buses will be on the west side of TCU Place at 12:45)

13:00	CSA field trip	- University of Saskatchewan Kernen Crop Research Farm - Agriculture and Agri-Food Canada, Saskatoon Research Centre Research Farm

14:00 – 15:30 CBA Board meeting (Gallery Suite A (1))

15:30 – 17:30 Plant Canada Board meeting (Prince Albert East and West Rooms, Hilton Garden Inn)

ABSTRACTS

Plenary Sessions
and
Special Lectures

PLENARY 1

Natural products: Biology, chemistry, and application

PL1-1. Natural product-based insecticide development: Spinosad, Spinetoram and the future. P. Lewer, P.R. Graupner, D.R. Hahn, D.O. Duebelbeis, J.R. Gilbert, L.L. Karr, G.D. Crouse, and T.C. Sparks. *Dow AgroSciences, 9330 Zionsville Road, Indianapolis, IN 46268, USA.*
Natural products have a long history of providing leads and commercial products to control agricultural pests. We have developed a sophisticated approach to discovering new natural product-based insecticides from, for example, plants, fungi and bacteria, for development into commercial products. This will be illustrated by discussing elements of our discovery program. One important discovery from our program was a new family of spinosyns - the 21-butenyl-spinosyns - some of which had enhanced potency and spectrum relative to the "classical" (21-ethyl) spinosyns. An extensive mutation program based on the producing bacterium, *Saccharopolyspora pogona*, enabled production of gram quantities of a targeted demethylated analog, which was then synthetically-modified to yield yet more potent analogs. The biological evaluation of these compounds versus their Spinosyn A analogs and the selection of Spinetoram for advancement as a second-generation Spinosad-based product will be discussed.

PL1-2. Folate synthesis, storage, and salvage in relation to biofortification. A.D. Hanson and J.F. Gregory III. *(A.D.H.) Horticultural Sciences and (J.F.G.) Food Science and Human Nutrition Departments, University of Florida, Gainesville, FL 32611, USA.*
Plants are major sources of dietary folate, so that the processes whereby they make, break, and stockpile folates directly impact human health. Knowledge of these processes is enabling engineering of the amounts and types of plant folates. (1) Synthesis. All the plant folate synthesis enzymes are now cloned and characterized (including dihydroneopterin triphosphate pyrophosphatase, which had not been cloned from bacteria), and two plant folate transporters have been identified. Overexpressing GTP cyclohydrolase I or p-aminobenzoate (pABA) synthase in tomato fruit respectively boosts pterin or pABA production, and overexpressing both together increases folate content by >10-fold, so that a 100-g serving supplies the entire adult RDA. (2) Storage. It was thought that plant folates are confined to metabolic compartments, but this supposition has now been shown to be wrong. Leaf and beet vacuoles have been found to store a large fraction of the total tissue folate, which suggests the possibility of manipulating the storage process. Vacuolar folates include polyglutamates, which is paradoxical since the hydrolase that removes polyglutamyl tails is also vacuolar. This implies that vacuolar folates are effectively protected from hydrolysis, perhaps via binding to proteins. Such sequestration could affect bioavailability in humans. (3) Salvage. Plants can have unusually high folate breakdown rates – up to 10% per day in harvested fruits and vegetables – and such losses are clearly nutritionally significant. Breakdown seems normally to be opposed by active salvage pathways – i.e., the pterin and pABA-glutamate breakdown products are recycled to folate synthesis. Folate salvage processes have been little studied in any organism, yet they are probably ubiquitous in folate synthesizers, including human parasites (e.g., Plasmodium). As plants seem to have very active salvage pathways, they make good models in which to explore this area of biochemistry.

PL1-3. Associating gene discovery to biochemical function in the discovery of natural product pathways. V. De Luca, J. Murata, M. Magnotta, D. Levac, and J. Roepke. *Department of Biological Sciences, Brock University, 500 Glenridge Avenue, St. Catharines, ON L2S 3A1, Canada.*
Catharanthus roseus (Madagascar Periwinkle) has been the source of unique alkaloid drugs with powerful anticancer properties that have revolutionized the fight against cancers like infantile leukemia and Hodgkins disease. Vinblastine and vincristine drugs have saved countless numbers of lives over the last 45 years. Recent research activities have created a new generation of less toxic, more powerful and more effective analogs of vinblastine that will be introduced commercially in the next few years. This renewed commercial interest together with the our interest in complete identification of the pathways leading to the biosynthesis of *Catharanthus* alkaloids has prompted us to apply new and versatile techniques of laser capture micro-dissection technology and Carborundum abrasion technique to produce cell-type specific cDNA libraries (leaf epidermis, idioblast, laticifer, mesophyl and vasculature-specific cells) for EST analyses. This new technology combined with large-scale sequencing, plant transformation and RT-PCR has led to the identification the exact sites of alkaloid biosynthesis as well as the discovery of new candidate genes for this pathway. In the broader context, this new knowledge about biochemical specialization for manufacturing plant secondary metabolites is now being harnessed to increase production of these commercially relevant secondary metabolites by marker based selection of existing germplasm or by high throughput screening of mutagenized *Catharanthus* lines.

PLENARY 2

Plant health networks: The international experience

PL2-1. The U.S. National Plant Diagnostic Network: Critical infrastructure to protect natural and agricultural plant systems. J.P. Stack. *Biosecurity Research Institute, Kansas State University, Manhattan, KS 66506, USA.*

The National Plant Diagnostic Network (NPDN) is a consortium of five regional networks and a national database. NPDN (http://www.npdn.org) was established in June 2002 by the United States Department of Agriculture (USDA) as a key component of a national plant biosecurity program. A secure agricultural system requires rapid detection of outbreaks, accurate diagnoses of problems, secure communications, and early response capability to minimize impacts. Local, state, and national response plans to outbreaks are developed and implemented by state departments of agriculture and the USDA Animal and Plant Health Inspection Service. The land grant university system was recognized as having the necessary expertise and mission to facilitate early detection and preliminary diagnoses of pest and disease outbreaks. The United States was divided into five regions based upon climate, ecological zones, and similarity of agricultural production systems. Regional diagnostic centers at Cornell University (Northeast Region), Kansas State University (Great Plains Region), Michigan State University (North Central Region), University of California at Davis (Western Region), and the University of Florida (Southern Region) were established to coordinate diagnostics, communications, and training. The national database is located at Purdue University. NPDN Accomplishments include a national outbreak exercise program, standardized diagnostic protocols for select agents, training programs for first detectors, and a national secure communications system. NPDN is fully operational and has performed well in several outbreaks, including Asian Soybean Rust, Pink Hibiscus Mealy Bug, *Phytophthora ramorum* blight, and Plum Pox Virus.

PL2-2. USDA National Plant Protection Laboratory Accreditation Program (NPPLAP): Regulatory-related testing and networked plant health diagnostic laboratories. L. Levy, P.H. Berger, and P.J. Shiel. *USDA, APHIS, PPQ, CPHST, NPGBL, BARC-East, Building-580, Beltsville, MD 20705, USA; and USDA, APHIS, PPQ, CPHST, Suite 400, 1730 Varsity Drive, Raleigh, NC 27606, USA.*

The purpose of the National Plant Protection Laboratory Accreditation Program (NPPLAP) is to provide a structured, authoritative system for laboratories to carry out diagnostic tests on high consequence plant pathogens or pests of regulatory concern to U.S. agriculture and natural resource health and security. The goal of this process is to increase laboratory capacity for diagnostic determinations, enhancing the ability of APHIS PPQ to provide timely response and management for introductions of plant diseases and pests. A key issue was identification and engagement of one or more laboratories with the needed expertise and equipment to conduct the complicated molecular diagnostics needed to make regulatory determinations. Once accomplished, increased speed and reliability of diagnostic tests while adding surge capacity in the event of an extraordinary emergency can be developed. The current program occurs in two phases, allowing for accreditation of the lab and then subsequent certification of individual diagnosticians through proficiency testing. Certification of individuals allows tracking of individual performance. The NPPLAP ensures that the highest quality tests are performed consistently across accredited laboratories using validated methods. It serves to increase national laboratory capacity, capabilities, quality, and will facilitate rapid and accurate detection, leading to a quicker response by regulatory agencies and stakeholders.

PL2-3. Plant health networks for diagnostics, surveillance and research: The Australian approach. P.C. Pheloung. *Australian Government Department of Agriculture, Fisheries and Forestry, G.P.O. Box 858, Canberra ACT 2601, Australia.*

Australia recognises the importance of establishing good connections between those with plant health expertise and those with policy setting and operational responsibility for protecting Australia's plant health status. The benefits include the capacity to quickly establish the nature of a new plant pest threat and respond accordingly, and to demonstrate freedom from plant pests that affect trade, both domestically and internationally. Under a general national plant health strategy, attempts have been made to implement the elements of a plant health network, with partial success. The constitutional division of responsibility between the Federal, State and Territory Governments dictates how networks can be established and maintained, as does the extent to which the private sector accepts some degree of responsibility for plant health issues. The two-fold challenges to the development of effective networks have been to achieve widespread and ongoing voluntary participation by individuals, and a willingness of stakeholder organisations to commit resources and share responsibility. Some progress has been made towards developing diagnostic protocols for a number of *emergency plant pests* (EPP). The growing use of internet based information systems has led to the development of multi-user interactive systems to facilitate access to and knowledge of expertise, plant pest specimen data, surveillance activities and diagnostic tools. Cooperative Research Centres (CRC) in Australia have been an effective means of linking Universities, State and Federal research institutions in order to collaboratively undertake projects guided by national research priorities. A

CRC for National Plant Biosecurity created in 2005 should contribute substantially to Australia's capacity to deal with plant health issues.

PL2-4. Canadian plant health expertise and capabilities: Networking for the future. N.K. Nishikawa and E. Foster. *National Laboratory Operations, Science Branch, Canadian Food Inspection Agency, 159 Cleopatra Dr., Ottawa, ON K1A 0Y9, Canada.*
The Action Plan for Terrestrial Plants and Plant Pests was developed in 2005 as part of the Invasive Alien Species (IAS) Strategy for Canada. One of the Action Plan's priorities is the formation of a technical network within the scientific community to strengthen linkages among those concerned with protecting plant resources in Canada. The Canadian Food Inspection Agency (CFIA)'s Science Branch is leading the development of a plant health diagnostic network as part of the plant protection network initiative (PlantProNet). As a first step in developing this network, the CFIA has contacted provinces to identify regional plant health diagnostic issues. We are also assessing the range and capacity of expertise on plant pests currently available in Canada, and identifying and connecting with stakeholders in the agricultural and forestry sectors. In addition, the CFIA has been in contact with regulatory counterparts from the USA and other trading partners to share information on best practices and future directions for their plant health networks.

SPECIAL LECTURES

Luella K. Weresub mycology lecture (CBA)

SL1-1. Developing microorganisms as bioherbicides - research at the interface of science and art. G. Peng, S.M. Boyetchko, K.L. Bailey, and R. Hynes. *Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*
Microbial bioherbicides which primarily contain fungi and bacteria as the active ingredient are being developed as additional tools for integrated weed management. Although potential benefits of these products to crop/plant industries and to environment are well recognized, commercial use has been delayed by a range of technical difficulties and regulatory complexities that emerged during the research and development process. To increase the probability of success, a critical mass of expertise is required that can take the research through an intertwining pathway of science, engineering, and regulatory challenges. Most bioherbicide agents cause damage to weeds, but achieving consistent efficacy under varying field conditions can be a different story. Success may follow a lengthy process of making small incremental steps that are unique for each weed-bioherbicide system. In the early stages, the research can skip back and forth between discoveries and proof of concept, but it is likely that critical technologies such as fermentation, formulation, and application make an efficacious organism into a potential "product". Regulatory requirements can also appear daunting and expensive. However, the science conducted forms the backbone for the strategies used to address the regulatory concerns, especially risk assessment. This presentation will highlight some of the challenges in research and development of microbial bioherbicides based on our own experiences to highlight new strategies and potential technologies that have evolved.

ABSTRACTS

Special Sessions
with
Invited Speakers

SPECIAL SESSION A

SA1. Natural products from horticultural crops (CSHS)

SA1-1. Distribution and antioxidant properties of apple flavonols. H.P.V. Rupasinghe. *Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, NS B2N 5E3, Canada.*
Apples are rich in many health-enhancing constituents including dietary phenolics mainly flavonoids and phenolic acids. Over 60 different phenolic compounds have been identified from apples that consisted of sub-classes of flavonoids, mainly flavonols, flavanols, anthocyanins, and proanthocyanidins. Scientific evidence revealed that apple flavonoids reduce the risk of cardiovascular disease, various cancers, and neurological disorders. In apple fruit, flavonols are present as quercetin (q) glycosides exclusively in the peel. Based on the evaluation of 27 apple genotypes, the major flavonols present in apple skin are q-3-galactoside, q-3-rhamnoside, q-3-glucoside, q-3-rutinoside, and q-3-peltatoside. The most abundant flavonol in skin tissue was q-3-galactoside, which represented about 45% of total flavonols in the skin. The total flavonol content and profiles among apple cultivars are distinct. The total flavonol content of scab resistance 'Novamac' (356 mg/100 g DW), and 'Nova Spy' (282 mg/100 g DW) was the highest among tested genotypes. Supercritical fluid extraction, ultrasound assistant solvent extraction and countercurrent extraction were compared for the extraction efficiency of flavonols. Structural modification of flavonol aglycone (q) greatly influenced the antioxidant properties of apple flavonols. Among nine major polyphenolics, q-3-glucoside possesses the greatest ability to protect the human neuronal cell line, SY-SH5Y from oxidative insult (H_2O_2) *in vitro*.

SA1-2. Novel techniques to improve functionality of horticultural foods and food ingredients. H. Ramaswamy. *Department of Food Science, McGill University, Ste Anne de Bellevue, QC, Canada.*
Many horticultural/plant products are consumed/used for their neutraceutical/functional values. This could range from simple addition of nutrients to the human diet to providing functionally ingredients for many applications. Many novel techniques have been used to improve the neutraceutical value or functionality of horticultural/plant foods and food ingredients. These techniques could offer various means of improving neutraceutical/functional properties of foods/food ingredients such as improving the of neutraceutical value of proteins by modification of their secondary and tertiary structures, improving their functional properties such a water binding, emulsification, rheological (visco-elastic & textural), ahessive and film making properties, as well as providing better processing scenarios to reduce their destruction. This presentation will examine the use of some novel processes such as high pressure processing, extrusion cooking and film casting techniques to effect improvements in the neutraceutical/ functional properties of horticultural/plant foods and food ingredients.

SA1-3. Foods with added physiological function: Facts and fallacies. P.J. Jones. *Richardson Centre for Functional Foods and Nutraceuticals, and Departments of Food Science and Human Nutritional Sciences, 196 Innovation Drive, University of Manitoba, Winnipeg, MB, Canada.*
Functional foods provide additional physiological benefit beyond that of meeting basic nutritional needs. Such foods are similar in appearance to, or may be, a conventional food, are consumed as part of a usual diet, and are demonstrated to have physiological benefits and/or reduce the risk of chronic disease beyond basic nutritional functions. Several factors have converged to bring functional foods to the limelight. First, consumers appear to be more interested then in the past on the relationship between diet and disease; as average life-spans increase there is interest in protecting youth and fitness. In addition, skepticism about traditional pharmacological medicine has prompted the public's self-empowerment to better take control of their own wellness through healthy food choices. Second, several countries now possess legislation to allow health claim statements to be placed directly on food products. Health claims have opened the door for food companies to manufacture foods which appeal to this market sector. Third, high personal health care costs in some countries have driven consumers and legislators to adopt and encourage health prevention strategies such as functional foods. Fourth, clearer understanding of the metabolic causes of diseases and surrogate indicators for risk of such diseases has led to a more solid grounding for establishing the role of various functional foods in improving health and reducing disease mortality and morbidity. Despite several success stories in the functional foods arena, certain problem areas remain. In summary, functional foods are the direction of foods of the future, serving up new opportunities to improve population health.

SA1-4. Exploring native Canadian plants for human health. R. Cao. *Food Research Program, Agriculture and Agri-Food Canada, 93 Stone Road West, Guelph, ON N1G 5C9, Canada.*
The boundary between medicine and food is not always clear in many ancient cultures. Many plants have traditionally been used in both culinary and healing practices. Herbs, in particular have been shown the duo functionality. Scientific information on herbal medicines is limited, and the majority has been related to exotic plants. On the other hand, most attention has been focussed on only a few herbal plants in Canada, such as American ginseng, echinacea, St. John's Wort and feverfew. Thorough investigations have not been carried out for many other native Canadian plants in terms of their

chemical composition, biological activity and potential use for disease prevention. Also, from the marketing point of view, many of the existing herbs have only a small niche in the market place, so overproduction and consequent price depression can happen easily as we have seen in the ginseng industry. There is obviously a need in multidisciplinary collaborations among herbalists, botanists, chemists and other scientists, as introducing native plants into mass production require knowledge in environmental impact, genetic variability and the effects of other factors on the bioactive components. This presentation is intended to present an overview of the needs, challenges of such an approach with examples from our own recent research on two native plants, Osage orange (*Maclura pomifera* (Raf.) Schneid.) and the inside-out flower (*Vancouveria hexandra*), and their antioxidative phytochemicals.

SA2. Ontogeny of the flower: The next generation (CBA)

SA2-1. Keys to innovation: Ontogenetic avenues to floral specialization. L. Hufford. *School of Biological Sciences, Washington State University, Pullman, WA, USA.*
Abstract not provided.

SA2-2. Thinking outside the MADS-box: Development of inflorescence and flower in an evolutionary perspective. M. Buzgo, S. Kim, B.A. Hauser, A.S. Chanderbali, P.S. Soltis, D.E. Soltis, D.G. Oppenheimer, H. Ma, J.H. Leebens-Mack, and C. dePamphilis. *Department of Botany, University of Florida, P.O. Box 118526, Gainesville, FL 32611, USA; (H.M. & C.deP.) Penn State University, 405D Life Sciences Bldg., University Park, PA 16802, USA; and (J.H.L.-M.) Department of Plant Biology, University of Georgia, 2502 Miller Plant SCI, Athens, GA 30602-7271, USA.*
We tested the ABC model of gene regulation of floral organ identity in basal angiosperms. The results are that gene expression and features in basal angiosperms ("Fading Borders") differ from model organisms, and this pattern in basal angiosperms may represent the condition present in the earliest flowering plants. Further, the definition of the border of the flower is not clear-cut, and the only reliable clue is the absence of an axillary meristem in all floral organs. Nevertheless, this feature is absolutely stable in all flowering plants, only broken in mutations of genes like *APETALA1*, *APETALA2* or *AGL24* - the so called A class genes. The future question will be whether this correlation represents a strong underlying constraint of development and an ancient acquisition of flowering plants. Therefore, A class genes are essential for understanding the origin of the flower, and studies need to involve genes involved in shoot apical meristem development.

SA2-3. MADS-box genes: A key to understanding Rosaceae flowers? R.C. Evans and E.M. Kramer. *Biology Department, Acadia University, 24 University Ave., Wolfville, NS B4P 2R6, Canada; and (E.M.K.) Department of Organismic and Evolutionary Biology, Harvard University, 16 Divinity Ave., Cambridge, MA 02138, USA.*
Once restricted to the study of *Arabidopsis* and *Antirrhinum*, using developmental genes for the study of plant evolution (evo-devo) has increased considerably in the past several years. The ABC(DE) model of floral development, along with the apparent conservation of the genes that underpin this model, have allowed studies to move away from traditional model organisms in an effort to understand the developmental genetic basis for angiosperm floral diversity. The rose family (Rosaceae) present an interesting group in which to study developmental genes as their flowers produce a floral tube (hypanthium), and while most taxa have perigynous flowers some produce epigynous flowers through fusion of ovary and hypanthium. Our work uses patterns of 'B' (*pistillata* (*PI*), *apetala3* (eu*AP3*), and *TOMATO MADS BOX GENE* 6 (*TM6*)) and 'C' (*Agamous* (*AG*)) class gene expression as a means to study the genetic basis of hypanthium development, as well as differences between perigynous and epigynous flowers. The Rosaceae hypanthium is believed to be either appendicular (phylogenetic fusion of sepal, petal and stamen bases), or receptacular (extension of vegetative receptacle tissue) in origin. If the former, one possible outcome would be to observe 'B' and 'C' class expression in the developing hypanthium. Preliminary results show expression on the floral apex as it is pulled up with the developing hypanthium and second, third and fourth whorl organs are initiated. No distinct patterns of expression in hypanthium tissues are observed during its development. Our results are compared with previous analyses of floral development genes in Rosaceae.

SA3. Education in action (CBA/CSPP)

SA3-1. What will I do when I grow up? M. Devine. *Performance Plants Inc., 101-108 Research Drive, Saskatoon, SK S7N 3R3, Canada.*
Most of us would agree that careers in science are challenging and rewarding, although they are not necessarily predictable. Broadly speaking, there are two avenues to success: to be a real expert (not just competent) in a specific area, such that your expertise is in demand; if you are world-renowned in subject X, and subject X is of broad importance, you are likely to be in a good position. Alternatively, you could have a specific field of expertise but also to be generally competent in a broad range of related fields (for example, a molecular biologist but also knowledgeable about anatomy, ecology, crop physiology, etc.). In either role you must be able to share your

knowledge and expertise coherently with a wide range of people, not just fellow scientists. You also need to be able to participate in, and ultimately lead teams, often bringing diverse expertise together, both scientific and non-scientific (e.g. technical, business, marketing, etc.). Finally, flexibility is important; you must be able to anticipate outcomes and adapt quickly to seize new opportunities and evolve into new roles. My experience tells me that the above applies equally to all sectors: academic, government research, and private sector.

SA3-2. Using scientific literature and interactive groups to teach plant ecology. K.A. Frego. *Department of Biology, University of New Brunswick, P.O. Box 5050, Saint John, NB E2L 4L5, Canada.*

When this upper-year course was allotted 90-minute classes, the students' (and my) need for classroom variety was added to my desire to further develop undergraduates' familiarity with primary literature, and to avoid an expensive plant ecology textbook. My objective was to incorporate primary literature and peer teaching with lecture material and experimental lab exercises. For a given topic (e.g. edaphic factors, plant-animal interactions), I provided an introductory lecture to set the context, and assigned readings from the primary literature. Each student was a member of two permanent working groups: 'reading' and 'teaching'. In their first configuration, reading groups of 5 who read the same paper(s) first met for 10-15 minutes to discuss and clarify their understanding of the paper. The students then reshuffled into teaching groups that comprised one member from each of the reading groups. These peer teaching groups then taught one another the salient points of their particular papers, and the group as a whole extracted major patterns, concepts and examples. The whole class then pulled together the topic while I facilitated with blackboard notes. For my part, this approach required extensive preparation, and a flexible approach in synthesizing at the end, but made me quite redundant during the group work time. Students were unanimously enthused about the approach, and reported greater comfort with primary literature.

SA3-3. Maximizing feedback and evaluation while minimizing time and red ink. S.M. Macfie. *Department of Biology, the University of Western Ontario, London, ON N6A 5B7, Canada.*

Are you reluctant to increase the number of grading-intensive assignments and exams in your classes for fear of spending hours with a red pen in hand? Many educators bemoan the reduced number of oral presentations and written (short-answer or essay-style) examinations that are required of today's students, but feel helpless in the wake of increasing class sizes. For those educators who persist in giving more time-intensive assignments, the temptation exists to reduce written evaluation to a few scribbles and a grade, or to delay feedback until the end of term. However, timely and constructive feedback is essential to effective learning, and one must wonder if rushed evaluations are worth the time spent. I suspect they are not. One solution is to replace a multitude of forms of evaluation with computer-graded, multiple choice exams. I do not propose that we abandon this convenient style of evaluation because I believe that carefully constructed multiple choice questions can effectively evaluate a student's ability to recall, reason and think critically. However, I also believe students are short-changed if they are not given feedback while they explore and express their ideas and understandings. In this session, I will share my time-saving strategies for methods of evaluation and feedback that extend beyond the dreaded multiple choice exam.

SPECIAL SESSION B

SB1. Progress in organic cropping systems (CSA)

SB1-1. Organic cropping in the semi-arid prairies: Opportunities, challenges and progress. S.A. Brandt, E.N. Johnson, S.S. Malhi, R.P. Zentner, A.G. Thomas, and O.O. Olfert. *Agriculture and Agri-Food Canada (AAFC) Scott Research Farm, P.O. Box 8, Scott, SK S0K 4A0, Canada; (S.S.M.) AAFC Melfort Research Farm, P.O. Box 1240, Melfort, SK S0E 1E0, Canada; (R.P.Z.) AAFC Swift Current Research Centre, P.O. Box 1031, Swift Current, SK S9H 3X2, Canada; and (A.G.T. & O.O.O.) AAFC Saskatoon Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Organic agriculture is expanding worldwide in response to increasing demand for organic food and growing concerns about environmental degradation. Maintaining soil productivity, controlling weeds, and using appropriate crop rotations are important production issues facing organic agriculture in the semi-arid region of the Canadian Prairies. Lower input costs plus price premiums normally more than offset lower yields in organic vs. conventional agriculture. Recent research in this region demonstrated the favourable economic performance and energy efficiency of organic systems. Yield losses due to weeds can be high, but cultural practices that increase crop competitiveness or physically damage weeds have proven effective. Practices that utilize biological N_2 fixation have been successful in replacing nitrogen removed in organic crops. Composted livestock manure has shown greater potential in restoring soil P than other strategies such as rock phosphate application. Maintaining sufficient residue cover to control soil erosion is a challenge in organic systems, particularly in dry cycles. Practices that reduce tillage for organic crops typically compromise weed control. Soil arthropod biodiversity indicators that are sensitive to pesticides are favoured, in contrast to those

sensitive to tillage. In the short term, economic returns in this region remain very promising if weeds can be managed and the crop commands a sufficiently large organic price premium. Long- term sustainability of organic systems, however, will depend on controlling soil erosion and using cost-effective means of replacing nutrients. The application of livestock manure will be instrumental in building and sustaining successful organic production systems in the future.

SB1-2. Soil-plant interactions in long-term organic cropping systems. M. Entz, M. Tenuta, C. Welsh, A. Nelson, Y. Shen, and J. Froese. *Faculty of Agricultural and Food Sciences, University of Manitoba, Winnipeg, MB, Canada; (A.N.) Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada; and (Y.S.) Langzou University, Gansu Province, People's Republic of China.*
The Glenlea study was started in 1992 in order that organic crop production systems could be compared with newer (conventional) systems. The study includes two farming systems (grain only; grain-forage combination) that are both managed using organic and conventional methods. Subplots include manure treatments. Measurements include crop productivity, pests, soil quality, energy balance, insect biodiversity and crop quality. Results indicate that soils (0 to 15 cm) in the organic plots contain less carbon than under conventional management. Surprisingly, the organic soils remain less erodible than conventional soils; this was attributed to greater mycorrhizal infection and diversity in organic plots. After 14 years, soil P deficiency was detected in the forage-grain no manure plots only. Organic plots have sufficient N for crop production; however conventional plots are at much higher risk of N leaching due to high late-season nitrate-N soil levels. Seed micronutrient concentration in flax and wheat crops was often higher, and never lower, under organic compared with conventional management. Weed flora has changed over 15 years; there is some evidence that weed species capable of mycorrhizal association are increasing while non-mycorrhizal weeds are declining.

SB1-3. Economic and social impacts of organic production systems. R. McCrae, B. Frick, and R. Martin. *Organic Agriculture Centre of Canada, Truro, NS, Canada.*
Abstract not provided.

SB2. Emerging plant disease epidemics (CPS)

SB2-1. Introduction: The importance of emerging plant diseases in Canada. M.J. Celetti and G.J. Boland. *Ontario Ministry of Agriculture, Food and Rural Affairs, University of Guelph, Guelph, ON N1G 2W1, Canada; and (G.J.B.) Department of Environmental Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*
Plant diseases are an important component of plant health worldwide, and cause billions of dollars in economic losses in agriculture and forestry each year. The terms new, emerging and reemerging plant pathogens refer to pathogens that have been introduced to a new region within five years, established pathogens that are increasing in incidence or prevalence within twenty years, and pathogens that are reemerging due to changes in the pathogen, host, disease management practices, or environment, respectively. Collectively these are referred to as emerging plant diseases. Recent examples of economically important emerging diseases in North America include karnal bunt, plum pox potyvirus, potato late blight, ramorum blight or sudden oak death, and soybean rust. In addition to causing direct economic losses, emerging diseases also reduce export revenues because of our inability to meet phytosanitary requirements for international trade. With increased international trade and travel, it is becoming more important to reduce the threat of emerging diseases through improved inspection of goods and better methods for pathogen detection. In the following symposium, examples of emerging and reemerging diseases and their impact on Canadian agriculture and forestry will be examined.

SB2-2. Emerging diseases in Canadian forests. R. Wilson. *Ontario Ministry of Natural Resources, Forest Management Branch, 70 Foster Dr., Suite 400, Sault Ste. Marie, ON P6A 6V5, Canada.*
Over the last century exotic fungal diseases such as white pine blister rust, Dutch elm disease, beech bark disease and American chestnut blight have ravaged eastern forests causing great economic losses, long term ecological impacts and challenging urban and forest managers. These diseases were introduced into North America on infected nursery stock or on infected lumber and have become widely established. Approaches to forest pest management have largely been ad hoc, reactive and often regional in addressing immediate and short-term priorities. So what have we learned from our past experiences in addressing exotic alien pests? Many emerging forest diseases maybe also linked to nursery stock or infected wood products. This presentation will examine three diseases on our doorstep: sudden oak death, oak wilt and butternut canker, assess the severity of their impacts and examine the proposed National Forest Pest Strategy approach in dealing with threats posed by native and exotic alien pests.

SB2-3. Emerging diseases of horticultural crops in Canada. G.D. Jesperson and S. Sabaratnam. *British Columbia Ministry of Agriculture and Lands, 200 – 1690 Powick Road, Kelowna, BC V1X 7G5, Canada; and (S.S.) British Columbia Ministry of Agriculture and Lands, 1767 Angus Campbell Road, Abbotsford, BC V3G 2M3, Canada.*

Emerging diseases are a significant threat to horticultural industries nationally and internationally. Emerging diseases may include diseases caused by new or recently introduced pathogens, diseases that have increased in incidence within the last 20 years, and diseases that are re-emerging due to changes in management practices, cultivars or climatic conditions. Examples of recently introduced or emerging pathogens that have significantly impacted horticultural crops in Canada include Plum pox virus, Blueberry scorch virus, bois noir phytoplasma, ramorum blight and dieback (*Phytophthora ramorum* Werres, de Cock & Man), chrysanthemum white rust (*Puccinia horiana* Henn), potato bacterial wilt (*Ralstonia solanacearum* (Smith) Yabuuchi et al.) and potato wart (*Synchytrium endobioticum* (Schilberzky) Percival). Phytophthora blight (*Phytophthora capsici* Leonian) and cucurbit downy mildew (*Pseudoperonospora cubensis* (Berk. & M.A. Curtis) Rostovzev) are emerging diseases in the United States that threaten many vegetable crops in Canada. Fire blight of apple and pear, caused by *Erwinia amylovora* (Burrill) Winslow et al. is an example of a long-established disease that is re-emerging due to changes in crop management practices. An overview of the impact of key emerging diseases to horticultural crops will be presented.

SB2-4. Emerging diseases of field crops in western Canada: Rusts, clubs, spots, staggers and blasts. R.A.A. Morrall, R.J. Howard, P.G. Pearse, B.D. Gossen, and D.A. Kaminski. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; (R.J.H.) Alberta Agriculture and Food, 301 Horticultural Station Road East, Brooks, AB T1R 1E6, Canada; (P.G.P.) Saskatchewan Agriculture and Food, 3085 Albert Street, Regina, SK S4S 0B1, Canada; (B.D.G.) Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; and (D.A.K.) Manitoba Agriculture, Food and Rural Initiatives, P.O. Box 1149, Carman, MB R0G 0J0, Canada.*
Plant diseases increase in importance (i.e. emerge) due to many factors, such as introduction of exotic pathogens or hosts, and changes in pathogen or host genotypes, the environment, consumer perception, scientific knowledge, or quarantine regulations. For example, *Puccinia striiformis* has become more common on prairie wheat since 2001, probably due to a combination of adaptation to warmer environmental conditions and climate change. *Plasmodiophora brassicae*, first identified on canola near Edmonton in 2003, appears to be spreading rapidly. The longevity of its resting spores makes disease management extremely difficult. *Ascochyta pisi* has re-emerged on field pea in some locations due to the high susceptibility of certain cultivars and possibly the importation of infested seed from Europe. Fungal endophytes in some forage grasses (grown mainly for seed) can cause severe health problems if fed to livestock. With above-average moisture, flowers of caraway and coriander are blasted by fungal pathogens (*Ascochyta* and *Aureobasidium* spp.) that dramatically reduce yield and quality of these novel crops.

SB2-5. The Canadian Plant Health response to emerging diseases: What role does CFIA play? What makes an emerging disease a quarantine pest? M. Wood. *National Manager, Horticulture Section, Canadian Food Inspection Agency, 59 Camelot Drive, Ottawa, ON K1A 0Y9, Canada.*
The Canadian Food Inspection Agency (CFIA) Plant Health Division is the National Plant Protection Organization for Canada. CFIA is responsible for identifying pests of quarantine significance and for determining the appropriate level of protection or reaction based not only upon science but economic impacts as well. The CFIA, together with stakeholders including researchers, provincial governments, industry groups and citizens play an important role in the process of determining which emerging pests become quarantine pests under a National Plant Health Strategy. The directions, the changing roles of stakeholders and the contribution by Canadian plant pathologists to the development of the proposed National Plant Health Strategy will be discussed.

SB3. Communicating plant science

SB3-1. The future of science in education. J. McVittie. *College of Education, University of Saskatchewan, Saskatoon, SK, Canada.*
Abstract not provided.

SB3-2. Biotech Week: A national perspective. J. Tranberg. *Ag-West Bio Inc., Saskatoon, SK, Canada.*
Abstract not provided.

SB3-3. How to write and speak about science to nonscientists. M. Robin. *Office of Research Communications, University of Saskatchewan, Saskatoon, SK, Canada.*
Abstract not provided.

SPECIAL SESSION C

SC1. Designing a new agri-food industry 1 *(Sponsored by Saskatchewan Wheat Pool)*

SC1-1. Trends, opportunities and challenges for agriculture as they relate to the emerging bio-economy. P.A. O'Sullivan. *Ag-West Bio Inc., Saskatoon, SK, Canada.*
Abstract not provided.

SC1-2. Agriculture as a solution provider to health: The Flax Canada 2015 initiative. K.C. Fitzpatrick. *Director of Health and Nutrition, Flax Canada 2015, 465 – 167 Lombard Avenue, Winnipeg, MB R3B 0T6, Canada.*
The agricultural industry has two foundation pillars on which to build for the future: improvements in human health and sustainable development. Projected future costs of health care delivery will negatively impact funds available for other high priority public issues and needs. It is becoming increasingly important that all industries, which can positively impact cost reduction, do so by: keeping people healthier longer and out of the health care system and preventing disease by encouraging healthier lifestyles through product services and information, and developing new technologies that will reduce health care costs in Canada, and that can be marketed to the world. FC2015 is a unique government-industry initiative that has as a major objective the development of new commercial products and the utilization of value-added components. The vision of FC2015 is to ensure that Canada is recognized as the global leader in the development and commercialization of human and animal based health, animal feed, fiber and industrial products from flax. A goal of FC2015 is to deliver a $6 billion annual reduction in health care costs. A primary target for flax development over the next decade is the commercialization of innovative health promoting foods, food ingredients and supplement products. This presentation will describe how FC2015 is positioning flax as an agricultural solution to reducing health care costs in Canada.

SC1-3. The good we get from grain™. M. Pickard. *InfraReady Products (1998) Ltd., 850C 56th St. E., Saskatoon, SK S7K 5Y8, Canada.*
Innovation is the lifeblood of the Canadian Agri-Food industry. For an industrial food manufacturer, business vitality and success flows from a steady stream of fresh ideas and new opportunities. In this presentation the key success factors of InfraReady Products will be presented with an emphasis on transformational innovation to capture the Good We Get from Grain™.

SC1-4. Enhanced phytosterol ester biosynthesis in seed oil. J. Zou. *National Research Council of Canada, Plant Biotechnology Institute, Saskatoon, SK, Canada.*
Abstract not provided.

SC2. Emerging barriers to marketing crops (CSA)

SC2-1. The good, the novel and the bad. G.G. Rowland. *Crop Development Centre, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.*
Before the acronym PNT (Plant with a Novel Trait) appeared in Federal Government documents around 1994, Canada had given the world triticale and canola. Thousands of crop varieties and breeding lines in some 175 species that had been developed through mutation breeding and interspecific hybridization were released by government agencies around the world. Natural mutations found within agricultural species were being incorporated into many crop varieties. Then Canada developed a definition of a PNT that caught in it traditional gene discovery, mutation breeding and interspecific hybridization. These methods or techniques were to be regulated by the Canadian Food Inspection Agency (CFIA), Health Canada and Environment Canada. We now have an ambiguous plant breeding environment that regulates novel developments by these traditional techniques. Other countries have not followed Canada's "lead" which has left us in an uncompetitive position where innovation and commercialization is stymied.

SC2-2. Challenges for the export of Canadian crops. P.A. Burnett. *Grain Research Laboratory, Canadian Grain Commission, 1404-303 Main Street, Winnipeg, MB R3C 3G8, Canada.*
Customers of Canadian grains (crops) have specific quality and safety demand for the commodities they import. Some of these parameters are real but others could be construed as obstacles to trade. Advances in processing technology and their incumbent changes to the traditional production methods, results in increasing challenges to the suppliers in ensuring the proper quality parameters of their respective commodities. Examples discussed to illustrate this will include trace elements, chemical residues, mycotoxins and changing quality requirements in a range of crops.

SC2-3. The changing market for potatoes: Challenges for the development and introduction of new varieties. T.R. Tarn. *Potato Research Centre, Agriculture and Agri-Food Canada, P.O. Box 20280, Fredericton, NB E3B 4Z7, Canada.*
The potato (*Solanum tuberosum* L.) is the fourth ranked world crop, Canada's most important vegetable and is a food full of good nutrients. Canada ranks second in the world in exports of frozen French fries. At the same time frozen French fries and potato chips are considered "junk" foods and their association with obesity has caused a decline in potato consumption. Traditional fresh market consumption is threatened by changing population demographics and consumer preferences. Against this background the industry is exploring opportunities to enhance existing markets and develop new value chains. The success of these opportunities is dependent on new cultivars. Further enhanced nutritional quality and lower glycemic index are fresh market requirements. Standards for processed potatoes continue to increase and the development of a potato starch industry appears increasingly likely. Some of these changes involve breeding for new traits and use of new germplasm. Common cultivars are susceptible to the major diseases

and pests of potato. In 1995 Monsanto launched a series of genetically modified potatoes that included resistance to the Colorado potato beetle. Fast food companies would not sell French fries made from these potatoes, processors would not process them and the GMO cultivars were withdrawn from production. Biotechnology can make major contributions to potato improvement but the market place is still not ready.

SPECIAL SESSION D

SD1. Designing a new agri-food industry 2 *(Sponsored by Saskatchewan Wheat Pool)*

SD1-1. Balancing product safety and product quality from laboratory to pilot plant. A. Abdellatif. *Canagra Technologies Inc., P.O. Box 22065, RPO Wildwood, Saskatoon, SK S7H 5P1, Canada.*
Development of a new bio product involves a scaling up of the process from the laboratory to the pilot plant. Processing at the pilot plant, however, is considerably more complex and difficult to control than in the laboratory. Key factors affecting the product quality and safety include identification, assessment and control of hazards; integration, cleaning and sorting of raw materials; optimization of heating rates, mixing rates and holding times; and excessive agitation and particle size. Planning pilot plant production at the laboratory stage increases effectiveness of the process. At this stage, selection of equipment, process conditions, sampling points, product specification, and regulatory compliance must be considered. Verification and validation of planning in the laboratory may then be realized in the pilot plant.

SD1-2. Biodiesel opportunities. M. Reaney. *Department of Applied Microbiology and Food Science, University of Saskatchewan, Saskatoon, SK, Canada.*
Abstract not provided.

SD1-3. Maximizing the value of canola protein products: The problem, solutions and opportunities. D.D. Maenz. *MCN BioProducts Inc., 860-410 22nd St. E., Saskatoon, SK S7K 5T6, Canada.*
Conventional processing of canola (*Brassica napus*) generates a high-valued oil plus a low-valued protein containing meal. The meal is generally used as a feed ingredient for livestock and the low value is a direct result of high levels of fiber and antinutritional factors such as phytic acid. One method of increasing the value of canola is to develop a process to concentrate the protein into high valued products low in fiber and antinutritional factors. MCN BioProducts Inc. has developed a proprietary process for the production of canola protein concentrate (CPC). CPC contains 0 detectable phytic acid, less than 5 μmole/g of total glucosinolates, and has a dry matter protein concentrate of greater than 60%. The balance of essential amino acids on a % of nitrogen basis in the protein concentrate products resembled that of the starting material. Studies in rainbow trout, Atlantic salmon and shrimp have shown that CPC can replace up to 50% of the fishmeal component of the diet without compromising feed intake or weight gain. The composition and feeding trials results indicate that CPC has considerable commercial potential. Cost-effective fractionation of the seed to generate high valued protein concentrates along with high valued oil has the potential to improve and stabilize canola crush margins.

SD2. Natural products (CSPP)

SD2-1. The structure, functions and biosynthesis of suberin. M.A. Bernards. *Department of Biology, the University of Western Ontario, London, ON N6A 5B7, Canada.*
Suberin is a cell wall-associated biopolymer found in specific cell types including root epidermis, root endodermis (including Casparian bands), bundle sheath cells, and the periderm (bark) of woody species and underground organs (e.g., tubers). Suberin is unique and distinct from other non-carbohydrate cell wall biopolymers such as lignin and cutin because (1) it contains two distinct polymeric domains: poly(phenolic) and poly(aliphatic); (2) each domain has a unique chemical composition; and (3) suberin is found only in specialized cells. Suberin functions as a physical barrier, preventing water loss, regulating solute transport and providing protection against pathogens. It is also a component of the wound-healing process in plants; indeed, one prevalent model system used to study suberization is the potato (*Solanum tuberosum* L.) tuber, which upon wounding, undergoes a massive re-arrangement of metabolism, leading to the formation of the phenolic and aliphatic monomers. This involves two disparate metabolic pathways: lipid metabolism and phenolic metabolism. Our research has focused on identifying unique metabolic steps associated with the biosynthesis of both phenolic and aliphatic suberin monomers, as well as the macromolecular assembly of the poly(phenolic) domain. We have identified a number of unique/critical metabolic steps in suberin monomer biosynthesis, and are working toward cloning the genes encoding the enzymes involved. With these we will be able to study more precisely the coordinate regulation of critical steps in suberin biosynthesis.

SD2-2. Dissecting the nicotine biosynthetic pathway using gene silencing. J.E. Page, E. Liu, and A.T. Todd. *National Research Council of Canada, Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0B6, Canada.*

Virus-induced gene silencing (VIGS) is a functional genomics tool for rapidly generating gene expression knockouts in plants. Plants infected with a virus containing a target host gene fragment direct an antiviral RNA silencing response against their own mRNA, leading to a loss-of-function phenotype for the target gene. We used VIGS vectors based on tobacco rattle virus (TRV) to dissect alkaloid metabolism in the model plant *Nicotiana benthamiana* (Solanaceae). This effort has focused on cDNAs that encode enzymes of the nicotine biosynthetic pathway, as well as transcription factors that control nicotine accumulation. We silenced genes predicted to encode several nicotine biosynthetic enzymes including *N*-methylputrescine oxidase (MPO), which catalyzes an as yet unknown step in nicotine formation, and an isoflavone reductase-like protein (IR) suggested to be involved in the nicotine pathway. Silencing of MPO or IR expression resulted in substantial reductions in nicotine levels, indicating that the encoded enzymes function in the nicotine pathway. An *in vitro* assay of purified, recombinant MPO showed that it oxidizes *N*-methylputrescine to the key pathway intermediate to yield *N*-methylpyrrolinium ion. The catalytic function of IR is not clear at this time although the enzyme appears to be involved in the NAD cycle. Using an EST genomics based screen, we have also identified six transcription factors that regulate constitutive or jasmonate induced nicotine levels. Their characterization via VIGS and stable transgenic analysis is currently in progress.

SD2-3. Regulation of isoprenoid metabolism in medicinal plants. A. Lane, K. Biswas, and S.S. Mahmoud. *Departments of Chemistry, and Earth and Environmental Sciences, University of British Columbia Okanagan, 3333 University Way, Kelowna, BC V1V 1V7, Canada.*
Isoprenoids, or terpenoids, are the largest class of plant natural products. They are essential for the growth and development of all plants, and also have extensive applications as food additives, cosmetics, and industrial raw materials. Terpenoids also impart potent medicinal and health promoting properties to numerous herbs and medicinal plants. Despite significant progress in describing genes and elucidation of the metabolic pathways responsible for the biosynthesis of terpenoids, our current understanding of cellular, molecular and biochemical factors that control production of these compounds are poorly understood. We are investigating regulation of terpenoid biosynthesis in higher plants, using lavender [Lavandula, a common herb of the mint family (Lamiacea)], as a model system. Lavenders accumulate large quantities of essential oils that contains over 100 mono- and sesquiterpenes, with linalool representing the most abundant constituent of the oil. We have recently obtained sequence information for approximately 15,000 ESTs from the essential oil producing parts of English Lavender (*L. angustifolia*). A preliminary homology-based analysis has revealed that our EST collection contains over 500 clones representing genes involved in all known steps of isoprenoid biosynthetic pathways in this plant. We are using microarray analysis to identify structural and regulatory genes that control linalool production in this plant.

SPECIAL SESSION E

SE1. Plant ecology and invasive species (CWSS/CBA)

SE1-1. Prioritizing non-indigenous species management using a survey, monitoring and modeling framework. L.J. Rew, E. Lehnhoff, and B.D. Maxwell. *Land Resources and Environmental Sciences Department, Montana State University, Bozeman, MT 59717, USA.*
Few areas have sufficient resources to target every non-indigenous species (NIS) patch/population. Conceptually, management of NIS can be regarded as having three main phases: inventory/survey, monitoring and management. Although all three phases can be performed simultaneously, considering them as different phases is important for theoretical, methodological, and logistical reasons. The first phase, inventory/survey, determines which species are present and their distribution within the environment. Data can be used to develop probability of occurrence or risk maps, which help select patches for monitoring, the second phase. Monitoring provides information on how patches are changing with time and what their impact on the ecosystem may be. Populations identified by the first phase and determined to be invasive by the second phase, should then be subject to a number of different management practices and resulting population dynamics monitored as part of an adaptive management approach. This final monitoring phase should evaluate the effectiveness of the control practices at reducing NIS distribution and impact, but also the impact of both the NIS and management practice on the surrounding system (vegetation and soil, etc.). We will demonstrate the use of the framework to prioritize management for a number of NIS, as well as describe the field techniques and analysis methods used, in the northern area of the Greater Yellowstone Ecosystem.

SE1-2. Integrating climate and trait models to predict the invasiveness of exotic plants in Canada's Eastern Prairie region. R. Otfinowski, N.C. Kenkel, and P. Dixon. *Department of Botany, University of Manitoba, 505-Buller Building, Winnipeg, MB R3T 2N2, Canada; and (P.D.) Parks Canada, Western Canada Service Center, 145-McDermot Avenue, Winnipeg, MB R3B 0R9, Canada.*
Invasive exotic species threaten the biodiversity and function of native ecosystems around the world. Existing models, attempting to predict successful invaders, often

emphasize isolated stages of biological invasions and fail to formalize interactions between exotic species and recipient environments. By integrating the climatic range and biological traits of exotic vascular plants in Canada's Eastern Prairie Region, we present a model in which invasiveness is predicted from each species' ability to establish and proliferate within natural areas. Based on climate, our model identified 155 new potential invaders of Riding Mountain National Park, including 42 species currently absent from Manitoba; however, its success in predicting establishment ranged from 30–80% and depended on the extent of human disturbance. Within natural areas, proliferation of exotic plants was correlated with perenniality and vegetative reproduction, and in Manitoba, many species in this category included escaped forages and ornamentals. Our results demonstrate that exotic plants will continue to threaten natural ecosystems in the Eastern Prairie Region. By integrating establishment and proliferation, key stages in the progress of biological invasions, our model offers a novel approach in the quantification and mitigation of these threats that promises application in other regions of Canada.

SE1-3. Crested wheatgrass invasion in western Canada: Consequences and management. S.D. Wilson and B.M. Vaness. *Department of Biology, University of Regina, Regina, SK S4S 0A2, Canada.*
Crested wheatgrass (*Agropyron cristatum* L.) is a tussock-forming C_3 grass introduced from Eurasia for soil stabilization and pasture productivity enhancement. It invades both cultivated fields and native prairie, reducing diversity and possibly altering ecosystem function. Recent important findings include 1) restoration of abandoned fields with native species slows crested wheatgrass invasion; 2) invasion of native prairie can be slowed by both grazing and herbicide application; and 3) native grasses sequester more carbon at shallow depths than does crested wheatgrass, but this difference diminishes at greater depths. Continuing research in this area is focused on the consequences of crested wheatgrass invasion for soil resource availability and spatial heterogeneity.

SE1-4. Invasive plant management and ecological issues in Alberta. D.E. Cole, D. Oyarzun, T.H. Dietzler, and J.R. King. *Pest Management Branch, Alberta Agriculture and Food, 17507 Fort Road NW, Edmonton, AB T5Y 6H3, Canada; (D.O.) Rural Programs, Alberta Agriculture and Food, 7000 – 113 Street, Edmonton, AB T6H 5T6, Canada; (T.H.D.) Municipal District of Rocky View, 911 – 32 Avenue NE, Calgary, AB T2E 6X6, Canada; and (J.R.K.) Agricultural, Food and Nutritional Science, Agriculture and Forestry Centre, University of Alberta, Edmonton, AB T6G 2P5, Canada.*
A plant species is considered invasive if it is non-native and its introduction is likely to cause economic or environmental harm or harm to human health. Invasive plant species have infested and negatively affected pastures, rangelands, hay lands, nature reserves and non-crop land in Alberta for over a hundred years and continue to invade new areas. The introduction, movement and attempts at eradication of several invasive plant species in Alberta is reviewed. Now, more tools and different approaches are available to better manage invasive species, especially for new species invading previously un-infested areas. Surveying, mapping, early detection, weather monitoring and risk assessment programs are available for interagency and intercontinental cooperative efforts. Preventative measures and maintaining competitive desirable plant communities without disturbance are key to excluding new invasive plant species. The most critical element required for successful invasive plant management is widespread interest and concern for invasive plants and their effect on the environment and society.

SE1-5. Plant community response to herbivory and disturbance: Lessons for restoration of Garry oak ecosystems. E.K. Gonzales, D.R. Clements, and V.M. LeMay. *Department of Forest Sciences, Faculty of Forestry, University of British Columbia, Vancouver, BC V6T 1Z4, Canada; (D.R.C.) Department of Biology, Trinity Western University, 7600 Glover Road, Langley, BC V2Y 1Y1, Canada; and (V.M.L.) Department of Forest Resources Management, Faculty of Forestry, University of British Columbia, Vancouver, BC V6T 1Z4, Canada.*
Non-native plants dominate many natural communities subject to anthropogenic disturbance such as endangered Garry oak ecosystems on Vancouver Island and the nearby Gulf Islands. Given the pronounced abundance of non-native grasses in these meadows, competition is thought to be the primary driver of plant community composition. Non-native annual grasses such as *Anthoxanthum odoratum* may compete for soil moisture while non-native perennial grasses such as *Dactylis glomerata* produce dense clumps and litter that may inhibit germination and establishment of other species. Concurrent with the introduction of non-native plants, however, was an increase in black-tailed deer and the introduction of sheep. Herbivores selectively favour palatable species, such as native lilies including *Camassia leichtlinii*, and may facilitate non-native plant species dominance. We quantified the effects of two restoration techniques, fencing and biomass removal (clipping), crossed in a factorial experiment. After three years, we compared differences in biomass between seven plant functional groups with general linear mixed models. Clipping reduced the biomass of non-native perennial graminoids and had a positive effect on native annual forbs. Herbivory limited native but not non-native plant species. The date of biomass collection also contributed significantly to the variance of native species but not non-native species. Many native species in Garry oak ecosystems are ephemeral while the litter produced by non-native grasses is persistent. Our results suggest that both fencing and

clipping benefit native biomass, provided that clipping occurs during native species senescence.

SE1-6. The role of plant ecology in conceptualizing invasive species. B.M.H. Larson. *Department of Environment and Resource Studies, University of Waterloo, Waterloo, ON N2L 3G1, Canada.*
Invasive plant species have tremendous economic costs and dramatic effects on ecological systems. Accordingly, this symposium presupposes that these species pose a "threat to native species and ecosystems" and it thus focuses on solutions and associated actions that we might take. I instead argue that this "threat" is not a straightforward ecological claim and that we need to reconceptualize the problem to act more effectively. Invasion biology rests on a duality between nature/non-human/native and culture/human/non-native that is very difficult to defend from the perspective of ecologically-motivated systems thinking. In particular, it assumes that there is an enduring "native" something that is under threat from humans, when in fact there is abundant evidence that humans are thoroughly embedded within natural (ecological) systems. A number of lines of ecological research have also shown that it is misguided to assign causal primacy to invasive species as opposed to multiple interacting causal agents. These agents include human-caused disturbances and global warming, which may swamp the effects of invasive species per se. For these and other reasons, some ecologists have argued that ecological change is inevitable and that our concerns about invasive species are largely unwarranted. I discuss these issues and offer some suggestions for how plant ecologists might avoid cynicism in the course of their research through appropriate advocacy and engagement with stakeholders dealing with local invasive species.

SPECIAL SESSION F

SF1. Organic horticulture: Separating fact from fantasy (CSHS)

SF1-1. Organic production of vegetables: State of the art and challenges. M. Dorais. *Agriculture and Agri-Food Canada, Horticultural Research Centre, Laval University, QC G1K 7P4, Canada.*
In light of the growing concern of Canadians about animal waste, environmental pollution from fertilizers, water quality and greenhouse gas effects, as well as their growing interest in organically grown foods (20% annual growth in North America), the development of sustainable organic production systems for vegetable crops is essential for consumer satisfaction and Canadian grower competitiveness. The target of this presentation is to review recent research results on the importance of appropriate soil properties, fertilizers and irrigation management on soil activity, plant growth and environmental health as well as product quality in term of nutritional value and safety issue. Species and cultivar selection, the use of grafting and plant growth promoters will also be discussed. This presentation will identify new challenges that organic growers have to fulfil in the face of a global market and public awareness of health attributes of food, and then conclude by identifying several prospects for future research with emphasis on the AAFC research program.

SF1-2. Organic fruit production: Managing reality and perception. G.H. Neilsen, D.T. Lowery, T. Forge, D. Neilsen, and D. Ehret. *Pacific Agri-Food Research Centre, Summerland, BC V0H IZ0, Canada; and (T.F. & D.E.) Pacific Agri-Food Research Centre, Agassiz, BC VOM 1A0, Canada.*
Organic production excludes inputs of synthetic chemicals and fertilizers and uses naturally derived products as defined by organic certification programs. Organic production has been advocated due to its potential to reduce the environmental impact of agricultural production systems. Interest has been further stimulated by public perception of personal health benefits associated with organic food and an increased premium to producers at a time of otherwise low product prices. For producers, the 'organic challenge' is considerable due to societal demands for appealing, high quality fruit and a historical tradition of intensive management, including liberal use of protective chemicals. This presentation will provide examples from field production of horticultural fruit crops in British Columbia, including small fruit, wine grapes and tree fruits where producers are rising to the challenge. Emphasis will be placed on strategies to address the challenges of supplying adequate nutrients and controlling weeds, insects and pathogens including the use of 'organic-friendly' cultivars, soil amendments and mulches, non-herbicide weed control, green manure cover crops and solarization and organic-compatible insect and disease control strategies. Approaches will be assessed relative to effectiveness and environmental impact. The presentation will conclude by identifying major limitations to organic production and illustrate several promising research possibilities from AAFC-research programs.

SF1-3. Are organically-produced fruits and vegetables safer and more nutritious than conventionally-produced fruits and vegetables: A review of the literature. R.K. Prange. *Agriculture and Agri-Food Canada, Atlantic Food and Horticulture Research Centre, Kentville, NS B4N 1J5, Canada.*
The increasing consumption of 'organic' fruits and vegetables is partly due to the perception that 'organically-grown' fruits and vegetables are safer and have more nutritional value than their 'conventionally-grown' counterparts. This presentation will review the scientific

information on the effect of organic production on major food safety factors, eg synthetic pesticides, nitrate, environmental pollutants, natural plant toxins, biological pesticides, pathogenic microbes and mycotoxins, and on food quality factors, eg sensory attributes (appearance, texture, taste and aroma), nutritive values, and chemical constituents. The published research suggests that organic production can reduce synthetic pesticide and nitrate content (in nitrophilic vegetables only), has no effect on environmental pollutant content and its effects on natural plant toxins, biological pesticides, pathogenic microbes and mycotoxins are unknown. There is some evidence that the trend to increasing yield in conventional production has resulted in a reduction of some quality factors, which may be mitigated by the lower yields associated with organic production. Much of the published literature on the effect of organic production methods is conflicting or inconclusive, partly because many of the research and nutritional publications do not recognize the wide variability within horticultural crops, regardless of production method. Scientific progress in comparing organically- and conventionally-grown fruits and vegetables will be achieved with more horticulturally-oriented research, using standard protocols applied to both production methods.

SF2. Phloem and long distance signalling (CSPP)

SF2-1. How do molecules get into the phloem? R. Turgeon. *Department of Plant Biology, Cornell University, Ithaca, NY 14853, USA.*

Signal molecules must enter the phloem before they can be transported over long distances in the translocation stream. The pathways of entry are limited and are the same as those used to load photosynthetically derived carbohydrates in leaves. One pathway of carbohydrate loading is through the apoplast. In many species, sucrose enters the cell wall space and is actively loaded into the sieve elements (SE) and/or companion cells (CC). This route could be used by signal molecules, but requires specific transporters. A second route of carbohydrate loading is symplastic, through the plasmodesmata-linked cytosol of cells, all the way from the mesophyll to the SE/CC complex. This is an inherently passive and non-selective strategy that could account for the mobility of many signals. Yet a third carbohydrate loading strategy is synthesis of transport compounds within the phloem itself. One way to determine if signals, or other exotic compounds, can be mobilized this way is to synthesize them under the control of a phloem-specific promoter. For this purpose we use the galactinol synthase (GAS) promoter, which is active only in the companion cells of minor veins and thus can be used to introduce molecules specifically into this cell type. In one study, CONSTANS (CO), a nuclear protein that plays a central role in the flowering response, substituted for photoperiod and initiated flowering when synthesis was driven by the GAS promoter in the minor veins of Arabidopsis.

SF2-2. Regulation of cell-to-cell and long-distance RNA trafficking. B. Ding. *Department of Plant Cellular and Molecular Biology and Plant Biotechnology Center, Ohio State University, Columbus, OH 43210, USA.*

In plants, ample evidence suggests the existence of an RNA trafficking machinery that transports diverse RNAs from cell to cell and from organ to organ. RNA trafficking has important functions in regulating development, spread of viral and viroid infection, and plant defense responses via RNA silencing. An eminent question is how trafficking of an RNA across specific cellular boundaries and in different directions is regulated at the molecular level. Viroids present simple models to study the trafficking mechanisms. Without encoding any proteins, a viroid RNA must have evolved sequence/structural features to be directly recognized by the preexisting cellular machinery to accomplish functions associated with infection. These include trafficking/localization to proper subcellular sites to accomplish replication within a cell and trafficking across various cellular boundaries to establish systemic infection. Studies on *Potato spindle tuber viroid* (PSTVd) contributed evidence that trafficking of an RNA within the phloem may not simply follow source-to-sink pattern of diffusion but is rather regulated. Further studies identified a bipartite RNA motif that is necessary and sufficient for trafficking from bundle sheath to mesophyll in young tobacco leaves. This motif is not required for trafficking in the reverse direction (i.e., from mesophyll to bundle sheath) or between other cell types. The requirement for this motif diminishes during leaf development. More recently, a motif with a well-understood tertiary structure was found to be required for PSTVd to traffic from the bundle sheath into the phloem for long distance trafficking. These data indicate that an RNA can possess multiple motifs for trafficking across distinct cellular/tissue boundaries. Several labs have identified viroid-interacting proteins that can be further investigated for their potential roles in viroid trafficking and infection. Future studies to identify additional viroid RNA motifs and cellular factors should contribute further insights into the molecular mechanisms that regulate RNA trafficking.

SF2-3. Phloem structure in *Eriophorum vaginatum* accommodates efficient nutrient recycling in nutrient-poor wetlands. E. Cholewa. *Department of Biology, Nipissing University, 100 College Drive, North Bay, ON P1B 8L7, Canada.*

Eriophorum vaginatum is a tussock forming sedge that grows abundantly in nutrient-poor wetlands. Previous studies reported that *E. vaginatum* survived for 20 years in crude oil spills in Alaska and persistently stored ^{137}Cs from the Chernobyl accident in its tissues. This indicates that it

must recycle nutrients. We located extensive populations of *E. vaginatum* near Sudbury, ON, where a long history of mining and industrial activities have resulted in an ideal study site to search for native plant species resistant to heavy metals. We are revealing the structure of the corm, an overwintering storage organ, where starch-storing cortex surrounds a central vascular cylinder enclosed by a typical endodermis. In the vascular cylinder, phloem is located in vertical amphivasal vascular bundles and has a symplastic connection to unusual vascular sclerenchyma through transfer cells. In addition, we have found an atypical horizontal vascular ring internal to the endodermis that complements phloem transport. ICP-MS analysis revealed high levels of metals in the contaminated soils from Sudbury, however, corms collected from these sites excluded most of the metals from their tissues with the exception of Al. CLSM analysis revealed that accumulated Al is located mostly in the phloem. Since *E. vaginatum* does not display Al toxicity, we will investigate the role of phloem in the mechanism of Al tolerance in this species. This research may lead to the use of *E. vaginatum* in biostabilization and revegetation of contaminated wetlands in the northern hemisphere.

SF3. Nutrient cycling in the soil-plant system: Filling the gaps 1 (AAFC/CSA)

SF3-1. Nitrogen cycling: Reducing losses from agricultural systems. J.A. MacLeod and M. Grimmett. *Agriculture and Agri-Food Canada, Crops and Livestock Research Centre, Charlottetown, PE, Canada.*
Abstract not provided.

SF3-2. Behaviour and fate of phosphorus in soil: Changing concepts and research perspectives of soil phosphorus chemistry and fertility. T.Q. Zhang and T. Forge. *Greenhouse and Processing Crops Research Centre, Agriculture and Agri-Food Canada (AAFC), Harrow, ON N0R 1G0, Canada; and (T.F.) Pacific Agri-Food Research Centre, AAFC, Agassiz, BC, Canada.*
Soil phosphorus (P), a primary nutrient that is essential to the completion of plant life-cycle, has received increasing attention in the past decade due to concerns on water quality. Phosphorus in soil exists in inorganic and organic forms binding to soil components through adsorption, precipitation, and microbial immobilization. Long-term application and low solubility of P in soil has cumulatively increased the complexity of its behaviours and cycling pathways. Recent studies have revealed that residual fertilizer/manure P in soil is mainly in labile and moderately labile inorganic forms. Moderately labile P is reversible, and thus soil residual P can be re-usable by crops, a concept controversial to the traditional belief that soil residual P is irreversibly "fixed". However, the agronomic value of residual P may be limited to timely meet crop needs. A supplemental P fertilization strategy must be developed and implemented. Leaching and preferential flow can be significant pathways for P loss from soil to water resource, in addition to surface runoff and erosion that were well realized. New technologies including NMR and synchrotron-based X-ray absorption spectroscopy enable scientists to characterize P compounds in manure, water and soil, determine both short- and long-term P transformation pathways, and pinpoint P sources in different ecosystems. Soil P cycling must be revisited to wisely use P resource in an economically beneficial and environmentally responsible manner.

SF3-3. Soil food web structure and the use of nematodes as indicators. T.A. Forge, S. Bittman, C. Hamel, A. Nayyar, C. Landry, and T. Zhang. *Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1000, 6947 Highway 7, Agassiz, BC V0M 1A0, Canada; (C.H. & A.N.) Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, Swift Current, SK S9H 3X2, Canada; (C.L.) IRDA, 2700 Einstein Bl 305.1, Sainte-Foy, QC, Canada; and (T.Z.) Agriculture and Agri-Food Canada, Harrow, ON N0R 1G0, Canada.*
Nutrient mineralization is influenced by the structure of the soil food web, which is comprised of the microbial biomass (primary decomposers) and various groups of invertebrate secondary and tertiary consumers. Crop and soil management practices affect nutrient availability and conditions for root growth in-part through changes in structure of the soil food web. Soil nematode communities include fungivore, bacterivore, omnivore and predator feeding groups in addition to the well-known plant-parasites. Because nematodes, as a group, perform multiple functions within the food web, some aspects of food web status (e.g. degree of enrichment, relative importance of bacterial -vs- fungal decomposition pathways, functional diversity) can be inferred from data on nematode community structure. Nematode communities from several long-term field experiments were analyzed as part of the GAPS project. These experiments included: Agassiz, BC (manure -vs- fertilizer on grass), Swift Current, SK (mixed -vs- monoculture forage production), Harrow, ON (compost -vs- raw manure on corn), and St. Lambert, QC (variable manure application rates to corn and grass). Nematode community analyses revealed significant treatment effects on soil food web structure in all experiments. The nature and implications of the treatment-induced changes in structure of soil nematode communities, and the food webs they represent, will be discussed for each experiment in relation to changes in other soil biological properties. At Agassiz, Swift Current and St. Lambert, there were significant changes in population densities of some key species of plant-parasitic nematodes that are likely having significant direct effects on crop productivity.

SF3-4. Immediate and residual effects of swine manure and its compost on soil phosphorus fractions in a clay loam soil under corn-soybean rotation. A. Herath, T.Q. Zhang, C. Hamel, C.S. Tan, T. Welacky, and M.J. Goss. *Department of Land Resource Science, University of Guelph, Guelph, ON N1G 2W1, Canada; (T.Q.Z., C.S.T. & T.W.) Agriculture and Agri-Food Canada, 2585 County Road 20, Harrow, ON N0R 1G0, Canada; and (C.H.) Agriculture and Agri-Food Canada, P.O. Box 1030, 1 Airport Road, Swift Current, SK S9H 3X2, Canada.*
Efficiency of applied P may be improved through in-depth understanding of soil P dynamics in relation to management practices. The objective of this study was to compare swine manure sources on soil P dynamics. A field experiment was conducted in Brookston clay loam soil, under corn (*Zea mays* L.) and soybean (*Glycine max* L.) rotation in 2004 and 2005. Treatments included three sources of swine manure [liquid (LM), solid (SM), and liquid composted with wheat straw (MC)], inorganic fertilizer P (IP), and a control (CK). Treatments were applied only to the corn phase. Soils were sampled after corn harvest to determine the immediate effects and after soybean harvest to determine the residual effects. Soil samples were analyzed for P fractions using the modified Hedley's procedure. Addition of SM and MC increased soil labile inorganic P (Pi), including water extractable Pi and bicarbonate extractable Pi, and moderately labile Pi in the corn phase. The effects were either similar to or higher than inorganic fertilizer P. In the soybean phase of the following year, both labile-Pi and moderately labile-Pi increased, indicating the transformation of other forms of P in soil. Addition of LM also increased the labile-Pi and moderately labile-Pi, but at a lower extent relative to SM and MC. Regardless of the sources, added P didn't influence both moderately stable and stable forms of soil P within the two-year period. Changes of soil P varied with the sources of swine manure, of which both agronomic and environmental impacts can differ.

SPECIAL SESSION G

SG1. Floristics for the future (CBA)

SG1-1. Biodiversity and floristics: Gathering data to answer big questions. A. Bruneau. *Département de Sciences biologiques, Université de Montréal, Montréal, QC, Canada.*
Abstract not provided.

SG1-2. Oil and water? Geospatial technologies, taxonomy, and collection databases: The case of E-Flora BC. B. Klinkenberg. *Geography Department, University of British Columbia, Vancouver, BC, Canada.*
Abstract not provided.

SG1-3. Building on existing resources: Onwards, upwards, downwards, and sideways. M.E. Barkworth. *Intermountain Herbarium, Department of Biology, Utah State University, Logan, UT 84322-5305, USA.*
Realizing the potential of combining floristic knowledge with digital technology creates new needs. These include communicating our knowledge to a broader audience, publicizing the questions that seem amenable to resolution through research, and ensuring the rapid dissemination of new knowledge. None of these tasks is trivial. Multi-entry identification keys, often cited as a magic bullet, require considerable effort to overcome the introduction of an inflexible and unthinking object between author and user. Fact sheets that can be used to confirm or refute an identification need to show the diagnostic features, and the images they contain should be linked to a voucher specimen. On the plus side, the number of images they include, or are linked to, is unlimited. Publicizing questions will aid students (and others) looking for research projects and could promote interaction between generations. Increasing the rate at which research findings are disseminated could be as simple as agreeing to post our publications to a common Web site. In this talk, I shall draw on my experience in editing the two grass volumes in the *Flora of North America* series and our current work in developing a one volume version from the two that will be published in the fall of 2007. Despite the relatively short time since publication of the two FNA volumes, the new volume will include three new generic names and one new subspecies.

SG2. Linking plant pathology with industry (CPS)

SG2-1. The BioMal® story: The legacy of a government-industry partnership. K.L. Bailey and M. Leggett. *Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; and (M.L.) Philom Bios Inc., 3935 Thatcher Avenue, Saskatoon, SK S7R 1A3, Canada.*
The concept of utilizing plant pathogens to benefit mankind and the environment has intrigued scientists for over four decades. In particular, a search for microbial herbicides that could be used to mitigate the development of herbicide resistance, lessen dependency on chemical herbicides, and reduce exposure to chemical herbicides, was initiated as a new scientific direction for the Canadian government. In the 1980's, a fungal pathogen (*Colletotrichum gloeosporioides* (Penzig) Saccardo f. sp. *malvae*) was isolated from round-leaved mallow, *Malva pusilla* Smith. It provided 60–90% control of mallow in field crops when applied as a foliar spray under optimum conditions. However, there is a big gap between proof-of-concept and production of the final product. An experienced business/industry partner was needed. Philom

Bios Inc. stepped forward at a very early stage to take on the risks of commercialization. The first Canadian microbial pest control product was borne from this joint venture, registered in 1992 as BioMal®. In this presentation, we will present focus on the history of BioMal®, the scientific and technological challenges encountered during its development, and the long-term relationships that were built among the partners along the way.

SG2-2. From the forest to the lab bench and back again: The cooperative venture to launch the biocontrol fungus *Chondrostereum purpureum*. W. Hintz, S.F. Shamoun, and P. de la Bastide. *University of Victoria, Victoria, BC, Canada; and (S.F.S.) Natural Resources Canada-Canadian Forestry Service, Pacific Forestry Centre, Victoria, BC, Canada.*
Abstract not provided.

SG2-3. The role of Industry in facilitating the commercialization of biopesticides. P. Marrone. *Marrone Organic Innovations Inc., Davis, CA, USA.*
Abstract not provided.

SG3. Nutrient cycling in the soil-plant system: Filling the gaps 2 (AAFC/CSA)

SG3-1. Phosphorus fertilization influence biological interactions in forage stands. A. Nayyar, C. Hamel, T. Forge, F. Selles, and P. Jefferson. *Agriculture and Agri-Food Canada, Swift Current, SK S9H 3X2, Canada.*
Effect of P fertilization (0, 20 and 40 kg P_2O_5 ha^{-1}) on AM fungal development and microbial interactions was studied in an eight year old field experiment with monoculture (alfalfa) and mixed (alfalfa and Russian wild rye) forage stands located in Saskatchewan. Soil was sampled three times. Yield of alfalfa monoculture was unaffected by P rates but that of mix stands was reduced at 0 and 20 kg P_2O_5 ha^{-1}. P input had no effect on the active soil microbial biomass despite increase in soil PO_4-P and NO_3-N fluxes. However, backward stepwise discriminant analysis of PLFA profiles revealed different soil microbial community structure in two forage stands. AM root colonization level was reduced with P fertilization and was lower in mixed than in monoculture. Microbial activity in soil was also reduced by P rates. Total nematode counts, nematode diversity as indicated by Simpson and Shannon-Winer indices and mycophagous nematode counts were unaffected by P inputs but were higher in mixed as compared to monoculture. We conclude that long-term P fertilization did not influence soil microbial community structure and nematode diversity but did reduce root colonization and microbial activity. The unexpected decrease in yield of mixed stand at 0 and 20 kg P_2O_5 ha^{-1} is likely due to the combined effect of reduced colonization, change in microbial community structure and high mycophagous nematode counts.

SG3-2. Crop fertilization can modify soil microbial community structure, function, and soil C to N ratio. C. Hamel, A.F. Cruz, K. Hanson, F. Selles, and R. Zentner. *Semiarid Prairie Agricultural Research Centre, P.O. Box 1030, Airport Road, Swift Current, SK S9H 3X2, Canada.*
The nutrient limiting microbial biomass and activity was sought at a time of rapid plant growth and high nutrient demand, in plots of a long-term fertilization experiment. Crops received the recommended amount of N and P fertilizer (NP), no N fertilizer (no-N), or no P fertilizer (no-P) since 1967. No-P reduced markedly soil available P, but did not reduce wheat biomass or soil microbial biomass C. No-N had very little effect on soil conditions, but created N shortage in planted soils. Fertilization treatments influenced the overall soil microbial community structure. Incubation soils under fallow and growing wheat for 48 h with a solution glucose, NH_4NO_3, or KH_2PO_4 did not enhanced SMB-C more than addition of water alone, indicating that none of C, N and P were limiting growth, under the conditions of the test. Specific phosphatase and nitrogenase activities were not affected by treatments. Lower specific denitrification rate in planted no-N treated soils was explained by low substrate (NO_3^-) availability, but higher specific activity in planted NP soils could not be explained by higher substrate or C availability, suggesting that the observed variation in this soil function was related to the nature of the soil microbial community. Crop fertilization can modify soil microbial community structure, the dynamics of some microbially driven soil processes, and modify soil C to N ratio.

SG3-3. The impact of cropping systems with differing intensities of grain legumes on soil quality. G.P. Lafond, H. Hunter, R. Lemke, N. Lupwayi, and W.E. May. *Indian Head Research Farm, P.O. Box 760, Indian Head, SK S0G 2K0, Canada; (R.L.) Swift Current Research Center, P.O. Box 1030, Swift Current, SK S9H 3X2, Canada; (H.H.) Indian Head Agricultural Research Foundation, P.O. Box 156, Indian Head, SK S0G 2K0, Canada; and (N.L.) Beaverlodge Research Farm, P.O. Box 29, Beaverlodge, AB T0C 0C0, Canada.*
The benefits of grain legumes on subsequent cereal crops are well recognized in cropping systems. The lower C/N ratio of grain legumes compared to cereals will increase the rate of residue decomposition. This increased rate of residue decomposition will affect the rate of nutrient cycling, soil microbial activity and diversity, soil organic carbon and nitrogen and possibly nitrous oxide emissions. The objective of the study is to compare the effects of cropping systems with different intensities of grain legumes (continuous pea vs wheat-pea vs wheat-wheat-pea) under no-till on soil quality and microbiology, carbon sequestration and nitrous oxide emissions. Increasing the frequency of grain legumes did not increase nitrous oxide

emissions during the pea phase of the cropping sequence and were lower overall than the emissions from the wheat phase. We did observe higher nitrous oxide emissions with wheat on pea stubble than wheat on wheat stubble but the overall rates were still low. Changing the frequency of grain legumes did not reveal any differences in the rate of carbon sequestration but the trend was for more carbon to be sequestered with continuous pea. Over the 11 year period, the rate of carbon sequestration was 313 kg C ha^{-1} $year^{-1}$. Only 10% of carbon sequestered on an annual basis was required to offset the N_2O emissions observed during that period. Soil microbial biomass in the rhizosphere decreased as the intensity of field pea increased on the cropping systems and the same was observed for β-glucosidase enzyme activity. Enzyme activity was greater in wheat than field pea rhizosphere and adding nitrogen also increased the activity. Microbial diversity was greater in pea rhizosphere than wheat rhizosphere, but activities were similar in bulk soil. Microbial diversity was greater in field pea than wheat rhizosphere, but there was no effect of rotation.

SG3-4. Long term effects of dairy manure on grass: Production and soil nutrient shifts. S. Bittman, T. Forge, C.G. Kowalenko, D.E. Hunt, F. Bounaix, and T. Zhang. *Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1000, Agassiz, BC V0M 1A0, Canada; and (T.Z.) Greenhouse and Processing Crops Research Centre, Agriculture and Agri-Food Canada, 2585 County Road 20, Harrow, ON N0R 1G0, Canada.*

A long-term study was initiated in 1994 to test whether applying dairy slurry on grass with an advanced application technique can replace mineral fertilizer in coastal BC. This paper reports on the effects on herbage production and shifts in soil nutrients. Dairy slurry was applied to tall fescue (*Festuca arundinacea* Schreb.) with a sleigh-foot banding applicator which limits ammonia loss. Manure application rates were 400 and 800 kg total-N ha^{-1} (200-400 kg mineral-N) in 4 equal doses or fertilizer (NH_4NO_3) at 200 and 400 kg N ha^{-1}. At high application rates of both manure and fertilizer, annual N uptake averaged 400 kg ha^{-1}. For manure, about 30% of applied N was stored in the soil organic matter compared to 14-22% for fertilizer. A third of applied manure N could not be accounted for in crop or soil, compared to 10-27% for fertilizer. Leaching accounted for most of the N loss from the fertilized plots compared to volatilization and denitrification for manure treatments. Application of dairy manure with 'BMP' method resulted in high herbage yields but accumulation of soil N, C and P. GAPS-related research is characterizing P fractions and dynamics in relation to biological activity.

SG3-5. Characterization and comparison of fungal and mycorrhizal communities following various P-fertilization in a maize/soybean rotation. M.-S. Beauregard, C. Hamel, and M. St-Arnaud. *Institut de recherche en biologie végétale, Jardin botanique de Montréal, 4001 East Sherbrooke street, Montreal, QC H1X 2B2, Canada; and (C.H.) Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, 1 Airport Road, P.O. Box 1030, Swift Current, SK S9H 2X3, Canada.*

Beneficial impacts of the relationships between plants and fungi on nutrient cycling, soil structure, environmental and pathogen stresses have been documented in several ecosystems. In agriculture, specific groups of fungi including those forming arbuscular mycorrhizae may have a greater influence on plant nutrition due to the limited solubility of phosphorus (P). Although intensively managed agricultural soils are fertilized, little is known about the effects of P-inputs on fungi diversity and relation with nutrient cycling. The evaluation of diverse fungal groups based on isolation or identification of spores sieved directly from the soil is highly time-consuming and biased toward sporulating taxa. The use of culture-independent DNA-based techniques has helped to overcome these technical constraints. From 2004 to 2006, total soil DNA was extracted and a PCR-Denaturing Gradient Gel Electrophoresis approach was used to profile annually the dominant fungal and endomycorrhizal ribotypes in a maize/soybean rotation. The impacts of plant phenology as well as organic or mineral P-fertilization on crop associated fungi also was defined. Over the 135 soil samples studied, 24 distinct fungal and 15 arbuscular mycorrhizal ribotypes were identified. Community structure of arbuscular mycorrhizal fungi varied within and between fertilization treatments, indicating that specific taxonomic units are not only related to the type of fertilizer. AMF ribotype assemblage changed with time without a clear seasonal trend, while some fungal sequence variants were clearly related to the sampling date. Variations related to crop within rotation indicated some level of plant specificity in mycorrhizal and other fungi.

ABSTRACTS

Contributed Oral Presentations

SESSION A

A1. CPS student session 1

A1-1. Evaluation of new sources of resistance to anthracnose in lentil. S. Vail and A. Vandenberg. *Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*
Recently released lentil (*Lens culinaris*) cultivars grown in the Canadian prairies are resistant only to race Ct1 of anthracnose caused by *Colletotrichum truncatum*. None are resistant to the more aggressive Ct0 race, for which resistance is scarce in the cultivated lentil gene pool. The accession VIR 421 and a family of breeding lines from the Crop Development Centre (3155S) were identified as potential sources of *L. culinaris* Ct0 resistance. Wild *Lens* relatives are also possible sources of resistance to race Ct0. A population of recombinant inbred lines was developed from an interspecific cross between susceptible *L. culinaris* cultivar 'Eston' and Ct1/Ct0 resistant *L. ervoides* accession L01-827A. An indoor study examined the differences in development of disease between genotypes of vegetative seedlings *versus* flowering plants. The interspecific line LR59-81 and VIR 421 had the highest level of resistance throughout the lifecycle of lentil. The breeding line 3155S-4 appeared to have more resistance to Ct0 compared to current varieties of lentil. Field evaluation of resistance was conducted throughout the summer of 2006. Examination of disease progression showed that resistance derived from the wild species was higher, especially as the plants aged. Resistance from the *L. culinaris* sources had similar disease development compared to Ct1 resistant genotypes. Genotypes within the cultivated gene pool provide the most readily accessible source of resistance and transfer of resistance from highly resistant interspecific lines is underway through an intense backcrossing program.

A1-2. Incidence, virulence and symptoms of *Botryodiplodia* and *Fusarium* in root rot diseases of cassava. S. Aigbe, S.U. Remison, and R. Bandyopadhyay. *Department of Crop Science, Ambrose Alli University, PMB 14, Ekpoma, Nigeria; and (R.B.) International Institute of Tropical Agriculture, PMB 5320, Ibadan, Nigeria.*
The incidence, virulence and symptoms of Botryodiplodia and Fusarium root rot diseases in cassava were examined. *Botryodiplodia theobromae*, *Fusarium oxysporum* and *Fusarium solani* were isolated from diseased cassava storage roots. Results showed that *B. theobromae* had the highest incidence of 57% while *F. solani* and *F. oxysporum* had 55 and 41%, respectively. In the same trend, the pathogenicity studies carried out showed *B. theobromae* to be more virulent at 100% disease severity while *F. solani* and *F. oxysporum* had 25 and 7% respectively. The Repeated experiments confirmed a close relationship between percentage incidence and virulence. All inoculated storage roots exhibited characteristic symptoms identical to those found in infected field; *B. theobromae* rotted tissue was grayish yellow to grayish green, *F. oxysporum* rotted tissue was light purple and *F. solani* rotted tissue was pale yellow brown.

A1-3. The plant signalling components EDS1 and SGT1 enhance the disease caused by the necrotrophic pathogen *Botrytis cinerea*. M. El Oirdi and K. Bouarab. *Centre de Recherche en Amélioration Végétale, Département de Biologie, Faculté des Sciences, Université de Sherbrooke, 2500 Boulevard de l'Université, Sherbrooke, QC J1K 2R1, Canada.*
Botrytis cinerea is a necrotrophic fungus which causes grey mould on a wide range of food plants especially grapevines, tomato, soft fruits, and vegetables. This disease brings about important economic losses, either in pre- and post-harvest crops. Successful protection of host plants against this pathogen is severely hampered by the lack of resistance genes in the hosts and the considerable phenotypic diversity of the fungus. Our results show that *B. cinerea* induces the expression levels of two plant signalling components *EDS1* and *SGT1* which have been shown to be essential for the resistance against biotrophic pathogens. By using Virus Induced Gene Silencing, we also show that *EDS1* and *SGT1* enhance the disease induced by *B. cinerea* in *N. benthamiana*. This work highlight a new strategy used by *B. cinerea* to establish its disease.

A1-4. Silencing mediates plant immunity induced by an elicitor. V. Dufour, M. Langlois, F. Daayf, S. Kauffmann, O. Voinnet, and K. Bouarab. *Centre de Recherche en Amélioration Végétale, Département de Biologie, Facultés des Sciences, Université de Sherbrooke, 2500 Boulevard de l'Université, Sherbrooke, QC J1K 2R1, Canada; (F.D. & S.K.) Department of Plant Science, 222 Agriculture Building, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; and (O.V.) Institut de Biologie Moléculaire des Plantes CNRS UPR 2357, 12, rue du Général Zimmer, 67084 Strasbourg Cedex, France.*
Plants attract a variety of intruders, from viruses, bacteria and fungi to insects. To protect themselves, plants have an armoury of defense mechanisms, including the hypersensitive response, the release of pathogenesis related proteins and antimicrobial secondary metabolites. The virulence protein P19 from several viruses is known to suppress the posttranscriptional gene silencing. Here we show that the suppressor of silencing P19 acts as an activator of plant immune responses and its elicitor effect requires its dimerization and the interaction with Small Interfering RNA. To our knowledge this is the first report showing that an elicitor of disease resistance mechanisms requires its dimerization and Small Interfering RNA for its activity. This finding may provide a powerful tool for discovering the common ways between silencing and disease resistance mechanisms induced by general and specific elicitors.

A1-5. Evaluation of promoter activity and over-expression of a rice peroxidase gene in transgenic carrot (*Daucus carota* L.). O. Wally, J. Jayaraj, and Z.K. Punja. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada.*

There is substantial evidence that suggests peroxidases are involved in plant defence against pathogens. Precise control of gene expression is crucial for maximizing resistance of the transgenic plants to fungal diseases. Expression levels of three constitutive promoters (CaMV 35S, double 35s (D35S), and Arabidopsis (*ubq3*) ubiquitin) and three tissue specific promoters (mannopine synthase, agropine synthase and *rol*D) were quantified in carrot tissues using *Gus*A expression. Histological staining and flurometric assays were performed on 5 independent lines for each promoter construct. The *ubq3* promoters had the highest GUS activities in carrot roots, while *ubq3* and D35S had the highest activities in shoots. A class III peroxidase gene (*POC1*) isolated from incompatible *Xanthamonas* infected rice, was over-expressed in carrot driven by the ubiquitin promoter with *bar* as the selectable marker. Resistance to two fungal pathogens in 7 transgenic lines was tested using detached petiole assays. Five of the *POC1* over-expressing lines had significant tolerance to *Botrytis cinerea* (95-65% reduction in disease symptoms after 7 days compared to controls). These same lines had 55-70% reduction in development of *Sclerotinia sclerotiorum*. Resistance to the root pathogen *Alternaria radicina*, was measured on harvested 4 month old roots at room temperature. Surface lesion sizes were reduced by 50-80% after 8 days on the 3 POC1 lines tested, the lesion unlike the controls were completely superficial with the pathogen being unable to establish infection beyond the outermost periderm layer.

A1-6. Detection of antibiotic-related genes of *Bacillus* species using polymerase chain reaction. S.N.P. Athukorala, W.G.D. Fernando, K.Y. Rashid, and T. de Kievit. *Department of Plant Science and (T. de K.) Department of Microbiology, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; and (K.Y.R.) Cereal Research Centre, Agriculture and Agri-Food Canada, Morden, MB R6M 1Y5, Canada.*

Although many *Bacillus* species are known to be good antibiotic producers capable of acting as biocontrol agents, the underlying antimicrobial mechanisms are often poorly understood. In this study, 21 *Bacillus* strains, demonstrating over 50% mycelial inhibition against *S. sclerotiorum* as well as significant control in plant assays, were examined for the presence of antibiotic biosynthetic genes. Primers specific for bacillomycin D, iturin A, surfactin, mycosubtilin, fengycin and zwittermicin A were used to amplify biosynthetic genes from these bacteria using polymerase chain reaction. The majority of strains (19/21) harbored surfactin and iturin A biosynthetic genes. Three strains (*B. subtilis* 3057, *B. amyloliquefaciens* BS6, *B. mycoides* 4079) were positive for bacillomycin D; however only one strain (*B. subtilis* H) showed the presence of fengycin biosynthetic gene. The zwittermicin A gene was detected in *B. mycoides* S, *B. thuringiensis* BS8 and *B. amyloliquefaciens* BS6. Sequence analysis of purified PCR products revealed homology with corresponding genes from other organisms in the GenBank database. Production of antibiotics will be confirmed through gas chromatography. This study will help to elucidate mechanisms underlying *Bacillus* biocontrol. Furthermore, it will enable us to develop rational strategies for the application of the antagonists and their metabolites within an agroecosystem.

A2. CBA/CSA student session 1

A2-1. Developmental morphology of several vine members of the Cucurbitaceae. T. Zitnak and U. Posluszny. *Department of Integrative Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Apical meristem development and branching of many Cucurbitaceae species is of interest due to the node's complex nature; however few ontogenetic studies exist to provide a morphological framework for investigation. This study provides a set of morphological characteristics by examining the ontogeny of several species of vine-forming Cucurbitaceae with different tendril architecture. Shoot architecture, phyllotactic patterns of the apical complex, and floral development were examined. Early ontogeny of the apical complex was determined using epi-illumination light microscopy and scanning electron microscopy. Results for *Sicyos angulatus* (L.) and *Ecballium elaterium* (L.) were compared to a similar published study of *Echinocystis lobata* (Michaud). For all species examined, each leaf primordium has a complex axillary structure that is offset from the leaf axil. This axillary complex undergoes a series of asymmetric divisions which give rise to structures in a set spatial sequence: a male inflorescence, female inflorescence, axillary bud and, with the exception of *E. elaterium*, a tendril. The axillary bud does not undergo dormancy but develops into either a compressed, quiescent shoot or continues growth to produce a branch. All 3 species have the same spatial sequence of axillary structures. However, each species displays different timing patterns for the initiation and development of these structures. Some of these timing patterns appear to correspond to the pattern of production of male and female flowers.

A2-2. Leaflet separation in *Chamaedorea seifrizii*. J. Nowak, N.G. Dengler, and U. Posluszny. *Department of Molecular and Cellular Biology, University of Guelph, Guelph, ON N1G 2W1, Canada; and (N.G.D.) Department*

of Botany, University of Toronto, Toronto, ON M5S 3B2, Canada.

Palms have evolved a unique process for compound leaf formation that is unlike any observed in other plants. The overall leaf development consists of two main processes: 1) plication formation through differential growth and 2) leaflet separation that has been described as abscission and more recently as an abscission-like process. This study has primarily focussed on determining the sequence of events occurring during leaflet separation in *Chamaedorea seifrizii* Burrett. This process consists of three steps. First, schizogeny occurs reducing the number of cell layers at the abaxial ridges in young leaf primordia. This occurs concurrently with the development of the separation site also located at the abaxial ridges. Second, the outermost cells on leaflet margins that participate in separation develop into an epidermal layer with a thick cuticle. There is also the deposition of the aliphatic components of suberin and/or cutin within the outer cell walls directly below the epidermal layer. Finally, mechanical rupture due to expansion growth aids the final separation of leaflet tips forming compound leaves with completely separated leaflets. These results indicate that an abscission-like process in *C. seifrizii* is responsible for compound leaf formation.

A2-3. Soil fertility and mycorrhizal association influences on lodgepole pine and interior hybrid spruce seedling growth. C. Wagg, B. Husband, H.B. Massicotte, and R.L. Peterson. *Department of Integrative Biology, University of Guelph, Guelph, ON N1G 2W1, Canada; (H.B.M.) Ecosystem Science and Management Program, University of Northern British Columbia, Prince George, BC V2N 4Z9, Canada; and (R.L.P.) Department of Molecular and Cellular Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*

In most plant communities mycorrhizal associations function as a major component for soil water and nutrient acquisition. Lodgepole pine (*Pinus contorta* Dougl. var. *latifolia* Engelm.) and interior hybrid spruce (*Picea glauca* (Moench) Voss × *Picea engelmannii* Parry ex Engelm.) are ectomycorrhizal hosts that co-occur in the interior wetbelt forests of British Columbia, which exhibit variation in growth across an elevation gradient. In this study, we evaluated how forest soil, seed origin, and mycorrhizal communities influence lodgepole pine and interior hybrid spruce growth. Using a complete factorial design, seeds of both species obtained from three elevational populations was germinated and grown for six months in soil collected from each of these forest sites at the University of Guelph Phytotron. Seed mass and germination rates differed among the three elevations. The root-shoot ratio and total dry mass of the seedlings were influenced by the forest soil as well as the mycorrhizal fungal associations present between the three forest soils. The differing effects of soil properties and mycorrhizal communities on seedling growth are discussed as potential influences on local adaptation.

A2-4. Screening for flax (*Linum usitatissimum* L.) dual purpose traits (seed oil and stem fibre) under western Canadian growing conditions. S. Mitra and G.G. Rowland. *Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*

Resurgence of fibre flax for natural fibres, as well as, already established markets for seed oil raises the question whether the same plant can be used for both purposes. Previous studies have shown the possibility of identifying and developing dual purpose varieties (Foster *et al.*, 1997). Ninety five recombinant inbred lines (RILs) were developed by crossing two diverse parents, one a fibre variety 'Viking' and the other a linseed mutant 'E1747' with good seed oil properties. The population was evaluated at one location (Saskatoon (Saskatchewan)) in 2005 and at 3 locations (Saskatoon, Floral and Melfort (Saskatchewan)) in 2006. Traits under study included stem fibre percentage, plant height at maturity, total seed oil percentage, total protein percentage and seed fatty acid composition. Variation among genotypes was found to be highly significant at all locations. Genotype x location interaction was also found to be highly significant for stem fibre percentage. There was no significant correlation found between oil traits and stem fibre percentage confirming earlier reports. The population will also be screened using two seed oil related molecular markers, as well as, fibre related markers to assist selection of dual purpose lines. Evaluation of the population both phenotypically and using molecular tools will help identify and further develop dual purpose varieties under western Canadian farming conditions.

A2-5. Hybrid origin of *Symphyotrichum anticostense* (Asteraceae: Astereae) based on three nuclear markers. J. Vaezi and L. Brouillet. *Institut de recherche en biologie végétale (IRBV), Université de Montréal, 4101 Sherbrooke Est, Montréal, QC H1X 2B2, Canada.*

Hybridization process is an usual event in *Symphyotrichum*. *S. anticostense* (Fernald) Nesom is a neo-endemic, rare species from northeastern North America, mostly in the Gulf of St. Lawrence region. It has been proposed to be an allo-decaploid species (2n=10x=80), hypothetically derived from a hybrid between *S. boreale* (T. & G.) Prov., possibly tetraploid (2*n*=4x=32), and *S. novi-belgii* (L.) Nesom, a hexaploid (2*n*=6x=48). In this study, we are using three molecular markers from nuclear genome, ITS, glyceraldehyde-3-phosphate dehydrogenase (GAPDH), and myo-inositol phosphate synthase (MIPS), to demonstrate the hybrid nature of the taxon and its relationships to the putative parents, and explore the possibility of multiple origins of the allopolyploid. ITS sequences of *S. anticostense*, despite concerted evolution and recombination, retain traces of

both parents. The GAPDH and MIPS trees show incongruence in the relationships among individuals. Given the recently divergent evolution of *Symphyotrichum*, this conflict could have resulted from incomplete lineage sorting of alleles with respect to speciation events. Nonetheless, alleles from both parents are detected in the allopolyploid. This is not definite proof, however, of the parentage of the allopolyploid because of incomplete lineage sorting within the genus and the ploidy level of the presumed parents. The relationships shown by these markers are complex but raise the possibility of multiple geographic origins for *S. anticostense*.

A2-6. Evaluating regrowth traits of three bromegrass (*Bromus*) species in the field. Biligetu and B.E. Coulman. *Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*
Bromegrass species are widely grown for hay, pasture and land reclamation. Smooth brome (*Bromus inermis*) and meadow brome (*Bromus riparius*) are two commonly cultivated species and hybrid brome (*B. riparius* X *B. inermis*) has recently been released in Canada. Understanding regrowth traits is useful for determining optimum cutting management and maximizing yield. The objective of this study was to compare the regrowth yield and plant characteristics of the three bromegrass species following defoliation at different stages of development. Forty-six days (700 GDD) after defoliation to 5 cm at the vegetative stage, the LAI (2.55) of smooth brome was significantly lower than that of meadow (3.43) and hybrid (3.36) brome. After 1465 GDD of regrowth, live tiller numbers of meadow, smooth and hybrid brome increased 132%, 14%, and 67%, respectively over pre-defoliation values. Forty-six days (750 GDD) after defoliation to 5 cm at the stem elongation stage, the LAI of the three bromegrasses was lower than for the vegetative defoliation treatment, with meadow brome having the highest LAI. Live tiller numbers were reduced by 23%, 58%, 46% for meadow, smooth and hybrid bromegrass compared to numbers present pre-defoliation. Meadow and hybrid brome showed greater regrowth dry matter yields than smooth brome after all defoliation treatments ($p<0.05$). The percentage of reproductive tillers in undefoliated smooth and hybrid brome was higher than for meadow brome.

A3. CSPP student session 1

A3-1. Disruption of adenosine metabolism leads to altered cytokinin profiles. S.C. Farrow, S. Schoor, K. Engel, R.J.N. Emery, and B.A. Moffatt. *Department of Biology, Trent University, 1600 West Bank Drive, Peterborough, ON K9J 7B8, Canada; and (S.S., K.E. & B.A.M.) Department of Biology, University of Waterloo, 200 University Avenue West, Waterloo, ON N2L 3G1, Canada.*
Through riboside phosphorylation and N^6-deamination, adenosine kinase (ADK) and adenosine deaminase (ADA), respectively, are responsible for the salvage of adenosine (Ado) in vertebrate organisms. To establish the role of these enzymes in plant nucleotide metabolism, *Arabidopsis* lines with reduced ADK activity were created by gene silencing (sADK lines) and a TDNA insertion line of a putative ADA gene was identified; these lines were crossed to disrupt both routes of Ado recycling (sADK, ADA^-). Several aspects of the sADK phenotype were consistent with changes in cytokinin (CK) activity including delayed senescence, decreased branching and altered shoot meristem elongation. This phenotype was enhanced by the introduction of the ADA mutation. We used liquid chromatography-tandem mass spectrometry to quantitatively determine CK and adenylate riboside and nucleotide levels in these lines. Interestingly, CK profiles of ADK and ADA lines differed markedly from the WT. Specifically, trans-Zeatin riboside concentration was much greater in the sADK lines, while ADA mutant lines showed drastically increased CK nucleotides levels. These results provide the first evidence for ADA activity in *Arabidopsis* and also demonstrate that both ADK and ADA play key roles in CK metabolism.

A3-2. A redox-regulated transactivation domain in NPR1 controls *PR-1* activation when recruited to a TGA2-NPR1 complex. A. Rochon, P. Boyle, T. Wignes, P.R. Fobert, and C. Despres. *Department of Biological Sciences, Brock University, 500 Glenridge Avenue, St. Catharines, ON L2S 3A1, Canada; and (T.W. & P.R.F.) National Research Council of Canada, Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada.*
Systemic acquired resistance (SAR) is a broad-spectrum, long lasting defense pathway induced in Arabidopsis after avirulent pathogen attack. The SAR pathway is typified by the accumulation of salicylic acid (SA) and the induction of pathogenesis related genes such as *PR-1*. An integral protein in this pathway, in part responsible for linking SA accumulation to *PR-1* induction, is NPR1 (Nonexpressor of pathogenesis-related gene 1). NPR1 is believed to exert its control in the SAR pathway through interaction with TGA transcription factors. Here, we use a series of *in vivo* plant assays to demonstrate that TGA2 is an autonomous repressor that is incorporated into a transactivating complex with NPR1 after SA treatment. In order to study this transactivating complex, deletions and point mutations in the C-terminus of NPR1 were created. With these constructs, we were able to show that NPR1 contains a C-terminal transactivating domain comprising two cysteine residues that must be oxidized for transactivation to occur. Additionally, the oxidation of these cysteines is also required for the transcriptional activation of the *PR-1* gene by the TGA2-NPR1 complex. These data further our

understanding of the mechanism by which TGA2 and NPR1 activate *PR-1*.

A3-3. Towards the identification of common bacterial blight resistance genes in *Phaseolus vulgaris*. G. Perry, Y. Reinprecht, J. Chan, and K.P. Pauls. *Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada.*

Infection by plant pathogens is a significant limitation to the yield and quality of common dry bean (*Phaseolus vulgaris* L.), an important pulse crop in Canada, cultivated throughout the central and Prairie Provinces. Common bacterial blight (CBB) presents itself as brown lesion on seeds, leaves and pods, and is caused by *Xanthomonas axonopodis* pv. *phaseoli*. Recently, a CBB-resistant cultivar, OAC-Rex was developed from a cross between *P. vulgaris* and a CBB-resistant accession of *Phaseolus acutifolius*. Another CBB-resistant line, HR67, was produced from a separate cross between *P. vulgaris* and *P. acutifolius*. OAC-Rex represents the first CBB resistant cultivar released in North America, however the genes responsible for this resistance not yet been identified. Binary-bacterial artificial chromosome (BiBAC) libraries were created to aid in the identification of the CBB-resistance genes in OAC-Rex and HR67. The libraries were screened with CBB resistance-associated molecular markers identified by previous studies, and the identified clones were analyzed using a gel-based restriction fingerprinting method for assembly into contigs. The fragments at the extreme ends of the contigs will be used to re-probe the libraries and expand the coverage of the contig. The unique clones will be transiently expressed in susceptible bean lines using *Agrobacterium tumefaciens*, and the plants will be infected with *X. axonopodis*. Clones containing genes for CBB resistance should cause a significantly reduced *X. axonopodis*-induced lesion. The inserts will be sequenced and analyzed to identify potential resistance genes.

A3-4. Characterization of DNA elements involved in carotenoid biosynthesis in *Arabidopsis thaliana*. K. Narayanan, G. Khachatourians, B. Yu, S. Wei, D. Hegedus, and A. Hannoufa. *(K.N., G.K. & B.Y.) Department of Applied Microbiology and Food Science, University of Saskatchewan, Saskatoon, SK, Canada; and (K.N., B.Y., S.W., D.H. & A.H.) Agriculture and Agri-Food Canada, Saskatoon Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Carotenoids are secondary metabolites that are widely distributed in nature. They have both agronomic and economic values as they are exploited for their colors in many crops, ornamental plants, cosmetic and food industries. The biological, agronomic and economic values of carotenoids have created much needed attention to study their biosynthetic pathway and its regulation. The availability of T-DNA tagged *Arabidopsis thaliana* mutant lines at AAFC-Saskatoon provides an opportunity to uncover the regulatory mechanisms involved in carotenoid biosynthesis. Currently, little is known about methods to screen mutants for alterations in carotenoid profiles. Therefore developing effective methods for high throughput screening of carotenoid mutants is a crucial step. In this study we report three methods currently used for screening *A. thaliana* mutants for altered carotenoid profiles. The first method involves visual screening based on the seed coat color; the second method relies on seedling phenotypes of pale green leaves with stunted growth. The third method uses norflurazon (an herbicide inhibiting phytoene desaturase enzyme involved in the carotenoid biosynthetic pathway) for screening carotenoid mutants. We will report on the carotenoid profiles of selected mutants and their molecular characterisation.

A3-5. Identification and differential regulation of phloem proteins in *Populus*. N.J. Dafoe and C.P. Constabel. *Department of Biology, University of Victoria, P.O. Box 3020, Station CSC, Victoria, BC V8W 3N5, Canada.*

Phloem is responsible for the transport of sugars and other organic compounds throughout the plant. Sieve elements, the specialized phloem cells specifically involved in phloem transport, are enucleate at maturity; however, they have a surprisingly large proteome, estimated to be between 100 and 600 proteins. To date the identity and function of these proteins has remained relatively obscure; although advances in proteomic technology have facilitated the identification of many phloem proteins. The majority of studies on phloem proteins have been limited to annual plants such as cucurbits or *Brassica napus*. The first objective of our study was to identify phloem proteins in *Populus*, a forest tree and model woody plant. Using 2D gel electrophoresis, we identified approximately 100 protein spots. With a combination of SDS-PAGE and LC-MS/MS, we were able to identify 81 poplar phloem proteins, the majority of which appear to function in defense. A major question to be addressed in order to understand the function of phloem is if these phloem proteins are differentially regulated in response to abiotic or biotic stresses. A second objective of our study was to identify poplar phloem proteins that were differentially regulated in response to wounding. Using 2D gel electrophoresis, two proteins were consistently upregulated 24 hours post-wounding. We are currently in the process of examining these proteins in order to further elucidate their function within the phloem.

A3-6. Characterization of a MRP transporter linked to cadmium accumulation in durum wheat grain. D.M. Silver, N.S. Harris, and G.J. Taylor. *Department of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9, Canada.*

Accumulation of cadmium (Cd) in durum wheat grain (*Triticum turgidum* L. ssp. *durum*) poses a potential human health risk and could endanger Canadian wheat exports.

Studies using low- and high-Cd accumulating near-isogenic lines (NILs) indicate that differences in root-to-shoot translocation and shoot-to-grain remobilization are key steps in grain Cd accumulation. Based on these observations, the simplest mechanistic explanation is that Cd sequestration occurs in roots and shoots. Microarray analysis of root tissue from these NILs identified a putative multidrug resistant-associated protein (MRP) gene, *TtMRP3*, which was upregulated in the low-Cd isoline. MRP homologues in yeast (ScYCF1) and Arabidopsis (AtMRP3) are involved Cd detoxification via glutathionated-conjugate transport into the vacuole, suggesting that TtMRP3 could reduce Cd availability for root-to-shoot translocation in the low-Cd isoline. Screening *Triticum* expressed sequence tag databases using the full-length rice MRP (*OsMRP3*) mRNA yielded 90% coverage of *TtMRP3*, excluding the 5′-end. The remaining sequence was isolated using rolling circle amplification-rapid amplification of cDNA ends. The complete *TtMRP3* coding sequence is 4506 bp and the translated product has >90% similarity to OsMRP3. Current work includes testing TtMRP3 for rescue of Cd tolerance in a yeast Cd-hypersensitive mutant, *ycf1Δ*, by heterologous expression.

SESSION B

B1. CPS student session 2

B1-1. Differences in the infection process on lentil tissue between races Ct0 and Ct1 of *Colletotrichum truncatum*. J. Wang and S. Banniza. *Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*

Colletotrichum truncatum (Schwein) Andrus & Moore causes lentil (*Lens culinaris* Medik.) anthracnose, which is a serious disease in western Canada. Two races of this pathogen, Ct0 and Ct1, have been identified in Canada. To investigate differences in the infection process between the two races, observations were carried out using detached leaflets of the Ct1-resistant cultivar 'CDC Robin' and the fully susceptible cultivar 'Eston'. Leaflets of both cultivars were inoculated with three race Ct0 isolates and three race Ct1 isolates, and incubated for 24, 36, 48, 60, and 72 hours postinoculation (hpi). Microscopy of infected leaflets showed that invasion of epidermal cells started with the formation of an infection vesicle at the penetration site, which was followed by the generation and growth of larger primary hyphae within epidermal cells. From those, thinner secondary hyphae developed that spread to surrounding cells by crossing cell walls. The development of infection structures of race Ct0 isolates was similar to that of infection structures of race Ct1 isolates on 'Eston'. However, on 'CDC Robin' infection vesicles of isolates belonging to race Ct1 appeared to be smaller at 24 hpi, and secondary hyphae were less developed at 72 hpi compared to the infection structures of race Ct0 isolates. This may indicate that growth and development of infection structures of race Ct1 isolates were inhibited on 'CDC Robin' compared to those of race Ct0 isolates.

B1-2. Karyotyping of *Pyrenophora tritici-repentis* reveals extensive chromosomal length polymorphism and independent locations of *ToxA* and *ToxB* genes. R. Aboukhaddour, S. Cloutier, G.M. Ballance, G. Hausner, and L. Lamari. *Department of Plant Science, 66 Dafoe Road, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; (S.C.) Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada; and (G.H.) Department of Microbiology, 418 Buller Building, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*

The fungus *Pyrenophora tritici-repentis* (Died.) causes tan spot, an important leaf disease of wheat worldwide. The pathogen produces multiple host selective toxins. *ToxA* and *ToxB* genes encode the necrosis-inducing Ptr ToxA and the chlorosis-inducing Ptr ToxB, respectively. The karyotype of 52 isolates of *P. tritici-repentis* from different races and geographical origins was determined by isolating protoplasts, releasing intact chromosomes in agarose plugs and subsequently separating them by pulsed field gel electrophoresis. The study revealed the presence of 5 to 9 chromosomes. Genome size ranged from 15 to 29 Mb and chromosome size ranged from 1.3 to 5.7 Mb. Considerable variation was observed in karyotype patterns among the *P. tritici-repentis* isolates tested. The differences between these patterns might be due to changes in chromosome structure involving translocation, deletion, duplication and/or acquisition of alien chromosomes. Southern hybridization with *ToxA* and *ToxB* revealed that the toxin genes are located on different chromosomes. These results suggest that *ToxA* and *ToxB* are of separate origin and have probably evolved independently.

B1-3. Retargeting of autophagosomes in *Arabidopsis* in response to powdery mildew infection. R.M. Kennedy and Y. Wei. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*

Autophagy is a non-selective degredative pathway that is conserved in eukaryotic organisms. It has been implicated as both a pro-survival strategy and a cell death mechanism. In *Arabidopsis thaliana* (L.) Heynh, autophagy is induced during nutrient depravation. Cell contents, such as cytoplasm and organelles, are sequestered in double membraned autophagosomes and delivered to the vacuole for breakdown. Products of this decomposition, such as amino acids, are released back into the cell to maintain cellular function. RT-PCR analysis of nine autophagy genes in *Arabidopsis*, *ATG1*, *ATG3*, *ATG4a*, *ATG4b*, *ATG5*, *ATG7*, *ATG8e*, *ATG9* and *ATG12a*, revealed accumulation of these transcripts during an *Erysiphe*

cichoracearum infection time course. We used confocal microscopy to visualize autophagy in vivo and observed autophagosomes accumulating at infection sites. Three autophagy mutants, *atg4ab*, *atg5-1*, *atg9-1* and *atg9-6* displayed fewer fungal penetrations at 2 days post infection compared to wild type. Together the data suggests that the redirection of autophagosomes to the infection sites could be a susceptibility factor for biotrophic parasitism.

B1-4. Fungal associates of the bronze birch borer on urban birch. S.P.K. Andersen. *Faculty of Forestry and the Forest Environment, Lakehead University, 955 Oliver Road, Thunder Bay, ON P7B 5E1, Canada.*
Birch decline is a serious problem commonly encountered in urban environments. It is often initiated by stress brought on by drought or poor growing conditions and commonly results in infestations by the bronze birch borer (*Agrilus anxius*). The larvae of these wood-boring insects produce galleries under the bark which girdle and presumably kill the tree. Although several studies have been published on fungal associates of wood-boring beetles, none have been published to date on fungal associates of the bronze birch borer. Isolations were taken from bronze birch borer-infested white birch (*Betula papyrifera*) in order to determine whether any fungal associations were present. A total of eight trees visibly infested with the bronze birch borer were removed from the urban centre of Thunder Bay during the summer of 2005 and used in this study. Trees were cut into small logs and bagged. Isolations were taken from both the beetle galleries and beetle frass directly from the logs and washings were performed on any larva that had been removed. Many fungi grew out in culture, including species in the genera *Melanconium* and *Cytospora* which are often associated with cankers and/or decline in birch. This could suggest that fungi found on birch that were once thought to be secondary pathogens may actually play a more serious role in birch decline. At this time no guarantee can be made that these fungi are specifically associated with the bronze birch borer as further studies are necessary in order to investigate this potential relationship.

B1-5. Weed suppressing effects of fall rye (*Secale*) cover crops in edible bean production. H. Flood and M.H. Entz. *Department of Plant Science, Faculty of Agriculture, University of Manitoba, Winnipeg, MB, Canada.*
The ability of certain plants to control their surroundings by suppressing the germination and growth of other plants has long been observed by farmers and scientists. The nature of these plant-to-plant effects (allelopathy) is less well known. Fall rye is recognized as a plant with allelopathic properties. Research on weed control benefits of fall rye cover crops has been conducted in several Canadian provinces. Fall rye cover crops are sometimes used in low residue crops to prevent soil erosion and improve soil structure. The objective of the present study was to examine effects of fall rye cover crops on weed density, water balance and growth and yield of edible bean crops in Manitoba. Field experiments were conducted at two Manitoba locations in 2006. Two rye termination times were used: Soil incorporation when rye produced 1500 kg/ha (site 1) and 500 kg/ha (site 2) dry matter and when rye produced 3500 kg/ha (site 1) and 1500 kg/ha (site 2) dry matter. Rye treatments resulted in 60 to 70% fewer broadleaved weeds and 25 to 60% fewer grass weeds at time of full bean soil emergence. Soil incorporation when rye produced greater biomass resulted in 25 to 40% fewer weeds compared to incorporation when rye produced less biomass. Bean yields were subsequently less affected at higher rye incorporation rates with losses averaged at 20%. These preliminary results suggest that rye cover crops provide weed suppression in an edible bean crop. Future work will involve a repeat of the field experiments (2007) and research to isolate allochemicals present in fall rye residues.

B1-6. A proteome level investigation of *Brassica napus* and *Sclerotinia sclerotiorum* interaction. Y. Liang, S. Srivastava, S. Strelkov, and N.N.V. Kav. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.*
Sclerotinia stem rot, caused by the ubiquitous necrotrophic pathogen *Sclerotinia sclerotiorum*, is one of the most serious diseases of canola affecting Canola yield throughout the world. It has been observed that upon infection of Canola leaves by Sclerotinia, the first signs of necrosis can be observed around 12 h post-inoculation and spreads relatively rapidly by 24 h. Therefore, it was our hypothesis that the period from 12 h to 24 h may be crucial for investigating the molecular changes that accompany disease progression. A proteome-level investigation of infected *B. napus* leaves at five time points (6, 12, 24, 36, and 48 h post-inoculation) was conducted using 2D gel electrophoresis. This investigation revealed 12 and 22 spots whose intensities were observed to be up- and down-regulated, respectively. The identities of these proteins were established using ESI-Q-ToF MS/MS and included uroporphyrinogen decarboxylase, ATPase, glyceraldehyde -3-phosphate dehydrogenase and peroxidase, which are known to play crucial roles in various plant processes. In addition, peroxidase enzyme activity assays at various time points after infection with *S. sclerotiorum* supported our proteome-level observations and suggested that the plant's antioxidant defense systems are enhanced during infection. Our results from these proteome-level experiments will be presented and discussed within the context of host-pathogen interactions, and may lead to the development of molecular strategies to engineer host resistance to this pathogen.

B2. CBA/CSA student session 2

B2-1. Molecular phylogeny of the North American eurybioid asters, *Oreostemma*, *Herrickia*, *Eurybia*, and *Triniteurybia* (Asteraceae, Astereae) using nuclear and chloroplast DNA regions. S. Selliah and L. Brouillet. *Herbier Marie-Victorin, Institut de recherche en biologie végétale (Dép. de sciences biologiques), Université de Montréal, 4101 rue Sherbrooke Est, Montréal, QC H1X 2B2, Canada.*

The aster genera *Oreostemma*, *Herrickia*, *Eurybia*, and *Triniteurybia*, collectively called the eurybioid grade, belong to the North American clade of tribe *Astereae*, at the base of the *Machaerantherinae*. The taxonomic relationships of the eurybioid grade, based on morphology, has been uncertain. A phylogenetic study based on nuclear ribosomal DNA (ITS and 3′ETS) data was unable to fully resolve phylogenetic relationships within this lineage and showed slight incongruence between the regions. In order to obtain a better understanding of the evolutionary history of the eurybioid grade, more variable markers were needed. Because few rapidly-evolving, low copy nuclear genes have been developed for *Asteraceae*, we optimised a marker originally charaterized in the *Leguminosae*, part of the cyclic nucleotide gated channel gene (CNGC4). The region between exons 5 and 7 (on the *Arabidopsis* sequence) was cloned and sequenced; the exons were easily aligned, but the introns proved very variable and parts had to be excluded. Though less variable than ribosomal or nuclear regions, three chloroplastic regions (combined in analyses) were used to provide data from an independent dataset: trn*L-F*, trn*C*-ycf6, and trn*S-G*. Parsimony and Bayesian analyses were performed on each dataset separately. Results are generally congruent with the ITS-ETS analyses, but resolution was improved in the CNGC4 analysis, despite incomplete lineage sorting. The following relationships appear to be confirmed: *Symphyotrichinae* (*Oreostemma* (*Herrickia* (*Eurybia* (*Triniteurybia* (*Machaerantherinae*))))). The eurybioid grade, a group with x = 9 that inhabits mainly humid to mesic habitats in temperate western and eastern North America, appears to be sister to the more xeric-adapted, southwestern, x = 5 *Machaerantherinae*.

B2-2. The influence of a long-term black medic (*Medicago lupulina* cv. 'George') cover crop on arbuscular mycorrhizal fungi colonization and nutrient uptake in flax (*Linum usitatissimum*) grown under zero-tillage management. M.S. Turmel, M. Entz, M. Tenuta, W. May, and G. Lafond. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; (M.T.) Department of Soil Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; and (W.M. & G.L.) Agriculture and Agri-Food Canada, Indian Head, SK S0G 2K0, Canada.*

Cover cropping was investigated as a method of increasing arbuscular mycorrhizal fungi (AMF) colonization and early nutrient uptake in flax (*Linum usitatissimum*). The presence of black medic (*Medicago lupulina* cv. 'George') in a flax - wheat (*Triticum aestivum*) - oat (*Avena sativa*) rotation was tested in long-term field experiments established in Manitoba and Saskatchewan in 2000 and 2002, respectively. The black medic cover crop had no influence on the early AMF colonization. When all site years were combined early flax concentrations of N, P, K and Zn were increased in the cover crop treatment, however, the cover crop had no effect on the total flax uptake of N, P, K, S, Ca, Mg, Zn, and Mn. The early flax uptake of Cu and Fe was decreased in the cover crop treatment. At one of the four site years total flax P uptake was increased by the cover crop though there was no effect on total N uptake. This research suggests that long-term cover cropping with black medic may have an effect on nutrient uptake in flax that is not directly related to changes in AMF colonization.

B2-3. Evaluating flower visitors as pollinators of *Lythrum salicaria* (purple loosestrife). W.D. Caswell and A.R. Davis. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*

Purple loosestrife (*Lythrum salicaria*) is an invasive perennial herb of wetlands that became established in Saskatchewan during the 1970's. Little is known about the reproductive biology of this species within the province, which is unfortunate due to its invasive nature, and the work being invested into its removal from Saskatchewan wetlands. Plants of *L. salicaria* have a complex breeding system, being heterostylous. Experimental pollinations by hand have confirmed that the species is strongly self-incompatible. In 2006, we studied the effectiveness of various insect visitors to virgin flowers of *L. salicaria* in the field by exposing previously non-visited (bagged) flowers to a single visit by the first-arriving insect. Later, using aniline-blue staining and fluorescence microscopy in the lab, we counted the number of pollen tubes that had grown down the style to the ovary. This quantification allowed a ranking of the effectiveness of individual insect species as pollinators. Single visits by sweat bees (Halictidae), bumble bees (*Bombus* spp.) and the European honey bee (*Apis mellifera*) yielded the highest number of pollen tubes per style (mean > 20, over all floral morphs), whereas non-bee visitors usually did not cross-pollinate *Lythrum*. Records of the frequency of flower visits revealed that bumble bees were the most abundant visitors to *L. salicaria*, followed by *A. mellifera*, sweat bees, hover flies, and a single butterfly (Pieridae). These data will help to establish a better understanding of applied aspects of pollination in this introduced species.

B2-4. The effect of black medic cover crop on N supplying power of prairie soils. S. Naguleswaran, M.H. Entz, W. May, and G. Lafond. *Department of Plant Science, University of Manitoba, 222 Agriculture Building,*

Winnipeg, MB R3T 2N2, Canada; and (W.M. & G.L.) Agriculture and Agri-Food Canada, Indian Head, SK S0G 2K0, Canada.

Black medic (*Medicago lupilina* L.) is a self-regenerating annual legume cover crop, which is able to produce persistent seed bank. It has wide adaptability for soils and environment. However, it has not been fully explored in Canadian Prairies due to lack of information. The objective of this research was to evaluate the effect of black medic on N supplying power of Prairie soils. A bioassay was conducted in a growth chamber at the University of Manitoba by using soils from 2 long-term black medic rotations: University of Manitoba Research Station in Winnipeg, Manitoba and the Agriculture and Agri-Food Canada Research Station in Indian Head, Saskatchewan. Wheat, oat and canola crops were grown in a series and tissue N and crop biomass was measured to quantify the total aboveground N uptake. After 5 years for Winnipeg and 4 years for Indian Head rotations, for the first time residual N amounts were significantly differed from medic and non-medic treatments. Black medic supplied 33.4 kg/ha N for Winnipeg soil and 32.9 kg/ha N for Indian Head soil. Portion of this residual N may come from biological N fixation and rest is biomass N. These long-term accumulated residual N is a good indicator to estimate the yearly basis accumulation which is an important factor to determine the annual N fertilizer recommendation for subsequent crops in rotations with black medic.

B2-5. Genetic variation and phytogeography of Nova Scotia's isolated populations of *Helianthemum canadense* (L.) Michx. as revealed with AFLP markers. A.F. Yorke and R.C. Evans. *Department of Biology, Acadia University, 24 University Avenue, Wolfville, NS B4P 2R6, Canada.*

Helianthemum canadense (L.) Michx., a perennial herb found on sand barrens in Nova Scotia, is provincially ranked as "critically imperiled", but has only "sensitive" status nationally. It has a special breeding biology, as plants produce self- and cross-pollinated offspring from two flower types on the same plant in a single season. Randomly selected individuals from populations in Nova Scotia, Maine, New Hampshire, and Quebec were examined to provide insight into the genetic diversity of Nova Scotia *H. canadense* populations. Amplified fragment length polymorphisms (AFLPs) were used to generate genetic diversity data. Data were analyzed with Analysis of Molecular Variance (AMOVA) and Principal Coordinates Analysis (PCoA). Neighbour-joining trees were also generated to illustrate relationships between individuals and populations. Variability within Nova Scotia populations was found to be relatively low. Two regions within Nova Scotia were identified as genetically distinct from one another. New England populations showed the most evidence of gene flow among them. Results indicate that Nova Scotia populations of *H. canadense* are genetically unique from the nearest populations in Canada and the United States. The two regions in Nova Scotia may have been isolated from other populations in North America for a significant amount of time, and could possibly have arisen from two separate post-glacial colonization events in the province.

B2-6. Growing Kura clover with barley and triticale: Effects on silage yield, weed pressure, and cereal diseases. S.M. Kosinski, J.R. King, K.N. Harker, T.K. Turkington, and D. Spaner. *Department of Agricultural, Food and Nutritional Science, University of Alberta, 4-10 Ag/For Building, Edmonton, AB T6G 2P5, Canada; and (K.N.H. & T.K.T.) Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C&E Trail, Lacombe, AB T4L 1W1, Canada.*

Farmers are interested in sustainable crop production systems that reduce the application of chemical fertilizers and pesticides. Perennial legume living mulches may provide nitrogen, compete with weeds, and reduce disease incidence in an interseeded cereal. The objectives of this experiment were to investigate the potential of a kura clover (*Trifolium ambiguum* M. Bieb) living mulch to supply nitrogen to barley (*Hordeum vulgare* L.) and triticale (X *Triticosecale* Wittmack) silage crops, and to decrease cereal diseases and weed pressure. Field experiments were conducted in 2006 at Edmonton and Lacombe, Alberta. Treatments included two cereal rotations, three levels of nitrogen fertilization, and spring herbicide suppression of the clover. Initial results indicate that the presence of the living mulch significantly reduced weed numbers and early season leaf diseases in barley. Triticale silage yields were not significantly different between the non-living mulch and living mulch plots in Edmonton, while barley silage yields were not significantly different between the non-living mulch and suppressed living mulch plots in Lacombe. Further study will be completed in 2007 on the nitrogen transfer potential of kura clover in this silage system.

B3. CSPP student session 2

B3-1. Natural transformation of *Acinetobacter* sp. with the *cp4 epsps* gene via homologous recombination. R.G. Campbell, R.H. Gulden, D.J. Levy-Booth, M.M. Hart, J.R. Powell, K.E. Dunfield, J.T. Trevors, J.P. Klironomos, C.J. Swanton, and K.P. Pauls. *Department of Plant Agriculture, (D.J.L.-B., M.M.H. & J.T.T.) Department of Environmental Biology, (J.R.P. & J.P.K.) Department of Integrative Biology, and (K.E.D.) Department of Land Resource Science, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Glyphosate [*N*-(phosphonomethyl)glycine] prevents the biosynthesis of aromatic amino acids by inhibiting 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS).

Roundup Ready® (RR) soybean [*Glycine max* (L.) Merr.] contains *cp4 epsps*, a glyphosate-resistant version of the gene. *Acinetobacter* sp. is a ubiquitous microorganism in the plant rhizosphere that has been shown to be naturally competent to take up DNA. The purpose of the current work was to test for the movement of DNA from transgenic plants to soil microorganisms using *cp4 epsps* as the target gene. The *cp4 epsps* gene was extracted from RR soybeans and ligated into the multi-cloning site on the broad-host range plasmid pRANGER-BTB-3® (pRANGER:*cp4 epsps*). A *cp4 epsps* gene containing a 222 base pair internal deletion was also ligated to pRANGER (pRANGER:Δ_{222} *cp4 epsps*). These two constructs, along with the original pRANGER plasmid, were electroporated separately into *Acinetobacter* sp. BD413. *Acinetobacter* pRANGER:*cp4 epsps* had an increased tolerance to glyphosate, growing on M9 plates + arabinose containing 1 mM glyphosate. *Acinetobacter* pRANGER:Δ_{222} *cp4 epsps* was exposed to an intact *cp4 epsps* gene and plated onto selective M9 medium to detect and quantify natural transformation of *Acinetobacter* sp. BD413 via homologous recombination.

B3-2. The two ABA binding proteins, FCA and ABAP1, share common origins. S. Kumar, F.A. Razem, and R.D. Hill. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*
The plant hormone abscisic acid (ABA) is considered to be a survival hormone regulating normal and stress-induced processes during different stages of plant development. Several of the ABA-mediated processes are brought about by changes in gene expression and post-transcriptional/ translational modifications of its target genes. Although earlier studies reported that several of the ABA response genes encode RNA-binding or RNA-processing proteins, none had been shown to be functional in binding ABA until recently, when the RNA-binding protein Flowering Time Control Protein A (FCA) was characterized as the first ABA receptor mediating ABA involvement in floral transition and root development. The identification of FCA as a receptor provided the first direct link between ABA and RNA processing. FCA shares homology at the C-terminus with ABAP1, an ABA-binding protein that was isolated from barley aleurone tissues and is involved in modulating barley germination and dormancy. *ABAP1* lacks the two RNA recognition motifs found in FCA, although its transcript level is regulated by alternative splicing of a pre-mRNA, likely in a similar fashion to *FCA*. Northern blots on barley mRNA with *ABAP1* specific probes detected both *FCA* and *ABAP1*. Comparative sequence analysis of *ABAP1* to rice *FCA* points towards the possible origin of *ABAP1* from *FCA*. Kozak sequences, which determine the translation start site on mRNA, are present on *FCA* mRNA at sites that can give rise to *ABAP1* from *FCA*. It therefore highlights a unique case where one gene gives rise to two different proteins in different plants controlling similar/different functions.

B3-3. Characterization of a light harvesting mutant of *Chlamydomonas reinhardtii*. L.L. Gray and K.E. Wilson. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*
The light harvesting complex (LHC) and its associated pigments absorb the majority of light energy required for photoautotrophic growth in photosynthetic eukaryotes. Structurally, the LHC is well characterized, but little is known about how individual LHC components are assembled. Our research aims to identify protein factors required to create a functional LHC by utilizing a *Chlamydomonas reinhardtii* line with a *ΔpsaF* mutation. This mutation causes a buildup of electrons as they enter photosystem I, causing high-light sensitivity. Our hypothesis is that secondary mutations which lead to high-light survival may be the result of LHC assembly defects. Suppressor mutants were created by random insertional-mutagenesis of the *ΔpsaF* line's nuclear genome; the C50 line was selected for further investigation. The C50 line exhibits approximately wild type chlorophyll levels and chlorophyll a:b ratio, suggesting normal LHC assembly. However, light-saturation curves suggest the C50 line has reduced LHC levels. Quantification of specific LHC proteins by Western blot indicate the C50 line has reduced LHCa levels. These investigations suggest this line is the first known LHC knockdown in *Chlamydomonas*.

B3-4. Bioimaging of Arabidopsis ribosomal proteins RPL23aA and -B reveals preferential incorporation of RPL23aA during ribosome biogenesis. R.F. Degenhardt and P.C. Bonham-Smith. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*
The ribosome is the largest cellular enzyme and is responsible for catalyzing protein synthesis. In the model plant *Arabidopsis thaliana*, it is comprised of 81 ribosomal proteins (r-proteins) and four ribosomal RNAs. Intriguingly, every r-protein is encoded by more than one gene, yet only one gene product can be incorporated into any given ribosome, suggesting that many r-protein genes may be functionally redundant. To investigate r-protein gene redundancy, we tagged both members of the *RPL23a* r-protein family (RPL23aA and -B) with fluorescent proteins and visualized their localization patterns in a heterologous tobacco system. When tagged r-proteins were expressed alone or with a known nucleolar-targeted protein, both RPL23aA and -B localized to the nucleolus, where ribosome subunit biogenesis occurs. However, despite having 94% amino acid sequence identity, the *RPL23a* family members exhibited different affinities for nucleolar accumulation. When we co-expressed both members, tagged with different fluorescent proteins, in the same cell, RPL23aA predominated and partially excluded RPL23aB from the nucleolus. Our results suggest that

RPL23aB functions in an auxiliary capacity and may be incorporated into the ribosome infrequently.

B3-5. Tradeoffs between leaf longevity and photosynthetic rate in *Populus balsamifera* populations. R.Y. Soolanayakanahally, S. Silim, and R.D. Guy. *Department of Forest Sciences, 2424 Main Mall, University of British Columbia, Vancouver, BC V6T 1Z4, Canada; and (S.S.) Shelterbelt Centre, PFRA-AAFC, Indian Head, SK S0G 2K0, Canada.*
Latitude represents a complex environmental gradient, along which photoperiod, temperature and growing season length can all be expected to vary. Twenty-one native populations of *Populus balsamifera* were selected from a wide range of environments in North America to investigate genetic variation in photosynthetic rates and other adaptive traits. Light-saturated photosynthetic assimilation (A), foliar nitrogen content (N) and carbon isotope composition ($\delta^{13}C$) varied significantly with latitude. Transpiration (E) and stomatal conductance (g_s) were negatively related to latitude, but not significantly so. The first axis of a canonical correlation analysis revealed that A and measures of instantaneous water use efficiency (A/E and A/g_s) vary positively with climatic predictors of "*borealness*", particularly latitude (but also longitude), frost free days and mean annual temperature. In contrast, leaf area, photosynthetic nitrogen use-efficiency (PNUE) and shoot biomass loaded strongly and negatively on this axis, being higher in southern populations with longer growing seasons. These patterns illustrate a general relationship whereby photosynthetic rate is inversely proportional to leaf longevity as controlled by latitude (photoperiod) and growing season temperature.

B3-6. Ribosomal protein S15a: Dissecting transcriptional regulation in *Arabidopsis thaliana*. J.L. Hulm and P.C. Bonham-Smith. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*
Eukaryotic cytosolic ribosomes are composed of two unequal subunits consisting of four individual ribosomal RNAs and, in *Arabidopsis thaliana*, 81 ribosomal proteins. Functional subunit assembly is dependent on the equimolar production of each ribosomal component. The Arabidopsis cytosolic *RPS15a* gene family consists of four members that, at the amino acid level, share 87-100% identity. Using semi-quantitative RT-PCR we have shown that transcript abundance differs both spatially and temporally among the *RPS15a* genes in non-treated Arabidopsis tissues and in seedlings following a variety of abiotic stresses. The transcription start site of each gene has been mapped using 5′ RACE. *RPS15aA*, *RPS15aD* and *RPS15aF*, the transcriptionally active members of the gene family, all contain a leader intron upstream of the start codon. To determine the minimal region required for gene expression and identify putative *cis*-regulatory elements, a series of consecutive *5′ regulatory region deletion::GUS* fusions have been produced for each *RPS15a* gene and used to generate stable Arabidopsis transformants. *RPS15a* expression patterns in both seedlings and individual mature tissues of independent T_2 lines following histochemical GUS staining will be discussed. Although variation in transcriptional activity of each *RPS15a* gene has been observed, subcellular localization of both *RPS15aA* and *RPS15aD* in the nucleolus has been confirmed *in planta* by confocal microscopy. Our data suggest that *RPS15aA* may be the primary isoform in cytosolic ribosomes of untreated Arabidopsis tissues and, while all three active *RPS15a* genes are transcriptionally regulated, some post-transcriptional and/or translational regulation may also be responsible for final RPS15a levels and function.

B3-7. Characterization of a mitochondrial Arabidopsis glyoxylate/pyruvate-dependent GABA transaminase. S.M. Clark and B.J. Shelp. *Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada.*
Gamma-aminobutyrate (GABA) is a ubiquitous non-protein amino acid that is implicated in stress metabolism and signaling in plants. GABA transaminase (GABA-T) catalyses the catabolic breakdown of GABA to succinic semialdehyde, and both pyruvate- and 2-oxoglutarate-dependent activities are reported in the literature. In this report, we show that a previously-identified *Arabidopsis thaliana* (L.) Heynh. pyruvate-dependent GABA-T also exhibits irreversible glyoxylate-dependent activity. Removal of the mitochondrial targeting domain and co-expression of the truncated cDNA with the GroES/EL molecular chaperone complex in *Escherichia coli* enabled good recovery of soluble recombinant GABA-T. Kinetic parameters for the glyoxylate- and pyruvate-dependent reactions were similar and physiologically relevant, and of the twenty four amino acids tested, only GABA served as an amino donor. Real-time PCR revealed that the transcript was present throughout the plant, and transcript levels in leaves were developmentally regulated. The catalytic lysine residue, lysine 327, was identified via site-directed mutations that prevented Schiff base formation and removed all detectable enzymatic activity, with no impact on protein folding as determined by equilibrium denaturation analysis. Assays of GABA-T activity in cell-free leaf extracts from wild-type *Arabidopsis* and two loss-of-function mutants in different genetic backgrounds confirmed that the enzyme possesses pyruvate- and glyoxylate-dependent, but not 2-oxoglutarate-dependent, activities. The existence of a GABA-T with dual functions suggests the potential for interaction between pathways responsible for GABA and glycolate metabolism.

SESSION C

C1. Pest management 1

C1-1. Variability of *Leptosphaeria maculans* in western Canada based on avirulence genes. H.R. Kutcher, H. Brun, S.R. Rimmer, M. Balesdent, and T. Rouxel. *Agriculture and Agri-Food Canada (AAFC), P.O. Box 1240, Melfort, SK S0E 1A0, Canada; (H.B.) UMR 1099, BiOP3, Institut National de la Recherche Agronomique (INRA), 35653 Le Rheu, Cedex, France; and (M.B. & T.R.) INRA – BIOGER, 78026 Versailles, Cedex, France.*
Variability in pathogenicity among isolates of *Leptosphaeria maculans* (Desmaz.) Ces. & De Not., the cause of blackleg disease of canola (*Brassica napus* L.), has been described in western Canada using the pathogenicity group classification system, which is based on the reactions of cvs. 'Westar', 'Quinta' and 'Glacier'. The objective of this study was to determine the avirulence (Avr) genes present in the pathogen population, which correspond to specific R-genes in the host. Of the 100 isolates of *Leptosphaeria* spp. collected between 1998 and 2005, 93 were determined to be *L. maculans* and 7, *L. biglobosa* R.A. Shoemaker & H. Brun. The *L. maculans* isolates were characterized under controlled conditions on a differential host set of 11 Brassica genotypes for Avr-genes that correspond to R-genes *Rlm1* to *Rlm7*, *Rlm9*, *Rlm10* and *LepR3*. Although further analysis must be conducted, it appears that *AvrLm1* could be present in as many as 78.5% of the isolates. The proportion carrying *AvrLm2* is also high (95.7%), and all isolates carry *AvrLm6* and *AvrLm10*, which correspond to *Rlm6* and *Rlm10*, genes introgressed into *B. napus* from *B. juncea* and *B. nigra*, respectively. All isolates except one were avirulent on 'Surpass 400', which carries *LepR3*, derived from *B. rapa* ssp. *sylvestris*. The *AvrLm9* gene, which corresponds to *Rlm9* in *B. napus*, was carried by 53.8% of the isolates tested. The proportion of *L. maculans* isolates carrying *AvrLm3*, *AvrLm4*, *AvrLm5*, and *AvrLm7* was much lower (8.6 to 28.0%). The corresponding R-genes for these isolates are found in *B. napus*, except for *Rlm5*, which is present in *B. juncea*. This study provides preliminary information on the existence of R-genes effective against current races of the pathogen found in western Canada.

C1-2. Identification of *Penicillium* isolates associated with blue mould on apples in southern Ontario, using PCR-RFLP. V. Popovic, K.W. Ellens, and D. Errampalli. *Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, 4902 Victoria Ave. N., Vineland Station, ON L0R 2E0, Canada.*
Blue mold caused by *Penicillium* spp. is an important postharvest disease of apples and *Penicillium expansum* Link was reported to be the most common and aggressive species. The objective of this study was to identify species of *Penicillium* present in three packinghouses in southern Ontario. Genotypic species identification was performed by analysis of the internal transcribed spacer (ITS) region of rDNA using restriction fragment length polymorphism (RFLP) on fifty six isolates of *Penicillium* spp. collected from the packing houses and six reference isolates of *Penicillium*. The ITS region was amplified using polymerase chain reaction (PCR) with primers ITS4 and ITS5. Digestion of the ~600 bp DNA fragment, amplified from the ITS region, using restriction enzymes *Hinf*I and *Taq*I revealed distinctive banding patterns for *P. expansum* and *P. solitum*. Based on PCR-RFLP analysis, 53 isolates were identified as *P. expansum*, and 3 as *P. solitum*. Of the 56 isolates, 100%, 88%, and 94% of isolates were identified as *P. expansum* in locations 1, 2 and 3, respectively. Isolates of *P. expansum* were more aggressive than *P. solitum* on 'McIntosh' apples. The effect of reduced risk products and biological control agents on the isolates of *Penicillium in vitro* and *in vivo* is being investigated.

C1-3. Induction of hydroxycinnamic acids in canola cultivars leads to differential responses to various pathogenicity groups of *Leptosphaeria maculans*. A. El Hadrami, W.G.D. Fernando, and F. Daayf. *Department of Plant Science, 222 Agriculture Building, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*
Canola (*Brassica napus* L.) is the second largest oilseed worldwide. Large surfaces of this crop are grown in Canada, Australia, China and several countries in Europe. Phoma stem canker (Blackleg) caused by the ascomycete *Leptosphaeria maculans* (Desmaz.) Ces. & De Not. (anamorph: *Phoma lingam* (Tode: Fr.) Desmaz.) is the most threatening disease to Brassicaceae including canola. Controlling this disease often relies on the use of resistant cultivars along with fungicides' application and crop rotations. Populations of *L. maculans* are composed of five known pathogenicity groups (PG1, 2, 3, 4 and T). PG2 is composed of highly-aggressive isolates and has been the most prevalent group in Western Canada in the last two decades. In contrast, PG1 group is represented by hypo-aggressive isolates and emerges only late in the season while plants are senescent. Our investigation intends to explore the use of hypo-aggressive isolates from the PG1 group as a means to control subsequent infections of canola by strains from other pathogenicity groups. The present study examined the constitutive and/or induced phenolics pool of canola leaves interacting with either or both groups of isolates. Both qualitative and quantitative differences were observed among treatments in terms of induced phenolics in response to either PG1 or other PGs. Hydroxycinnamic acids were the main detected compounds. Evidence gathered up-to-date leads to believe that these compounds regenerate lignin around the infection site. The speed by which the accumulation occurs as well as the accumulated amounts may be related to the observed differential responses.

C1-4. The Soybean Rust Sentinel Plot Program: Molecular identification, screening and tracking of *Phakopsora pachyrhizi*. S. Hambleton, R. Tropiano, and A. Tenuta. *Biodiversity (Mycology and Botany), Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; and (A.T.) Ridgetown College, Ontario Ministry of Agriculture, Food and Rural Affairs, P.O. Box 400, Main Street, Ridgetown, ON N0P 2C0, Canada.*

Asian soybean rust (*Phakopsora pachyrhizi* Sydow) is a new and invasive fungal disease in North America. Early detection is critical to managing the disease given the current lack of commercially available resistant cultivars. The Ontario sentinel plot program was started in 2005, in conjunction with a comprehensive monitoring program put in place in the United States. It is designed to provide an "early warning system" and decision support tool for producers and advisors regarding pesticide applications, in the event the disease spreads into Canada in an aggressive pattern. The program involves intensive scouting for symptoms in a series of sentinel plots and molecular testing of suspect samples. In 2005, leaves from 44 sentinel plots were tested weekly for the presence of *P. pachyrhizi* using a real-time PCR assay developed in the US. In 2006, additional technology was implemented to track spore dispersal. Testing switched to screening DNA extracted from rainfall filtrate samples collected using passive rainfall collectors equipped with millipore filters. Real-time PCR assays of all DNA extracts were negative for *P. pachyrhizi*. Some rainfall filtrate samples were positive for the DNA of other rust species providing valuable confirmation that the PCR amplifications were reliable.

C1-5. Marker based identification of *Lr34* in Canadian wheat cultivars. B.D. McCallum and D. Somers. *Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada.*

Leaf rust, caused by *Puccinia triticina* Eriks., is an important disease of wheat in Canada and world-wide. While genetic resistance has been used effectively to control this disease it has often been temporary as many leaf rust resistance genes have been overcome in time due to changes in the *P. triticina* population. The resistance gene *Lr34* has provided effective resistance in Canadian wheat cultivars since it was incorporated in the 1970s. The *Lr34* locus synergistically increases the effect of other leaf rust resistance genes and conditions resistance to other wheat diseases. The wheat stripe rust resistance gene *Yr18* is also completely linked to *Lr34.* Identification of *Lr34* in a broad selection of current and historic Canadian wheat cultivars was done based on the diagnostic marker csLV34 which is tightly linked to *Lr34*. Results from the marker analysis were compared to phenotypic data on the presence or absence of *Lr34* in these cultivars. This information will help in selecting cultivars with *Lr34* for use as parents in breeding programs and identifies the original donors of *Lr34* in the Canadian wheat breeding programs.

C1-6. Fruit breeding at the University of Saskatchewan. R.H. Bors. *Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*

Of primary importance in our fruit program is selection and breeding of dwarf sour cherries and blue honeysuckles for mechanical harvesting and apples for organic production. For these three crops we do value-added research, work closely with grower groups, and have written a cherry manual and numerous articles. On a rotating basis each year we breed a few of the following: hazelnuts, strawberries, plums, choke cherries, raspberries, pears, Missouri currents, and saskatoons. Inspired by the lack of core funding and sporadic funding, we combine extension and breeding activities into workshops and events that assist with making crosses, planting seeds, clonal propagation, selection, and testing of advanced selections. A network of over 150 growers is testing our advanced selections or growing seedlings for us in six provinces, the Yukon and Alaska. Also, we maintain 30 acres of which half is our genebank collection of Zone 2 hardy fruit cultivars and species. In particular, we have world class collections of saskatoons, blue honeysuckles, dwarf sour cherries, and interspecific tetraploid strawberries.

C2. Plant development and improvement 1

C2-1. Inter simple sequence repeat (ISSR) markers to assess genetic diversity and relatedness within strawberry cultivars and breeding lines. S.C. Debnath, S. Khanizadeh, A.R. Jamieson, and C. Kempler. *Atlantic Cool Climate Crop Research Centre, Agriculture and Agri-Food Canada (AAFC), P.O. Box 39088, 308 Brookfield Road, St. John's, NL A1E 5Y7, Canada; (S.K.) Horticultural Research and Development Centre, AAFC, 430 Blvd. Gouin, St-Jean-sur-Richelieu, QC J3B 3E6, Canada; (A.R.J.) Atlantic Food and Horticulture Research Centre, AAFC, 32 Main Street, Kentville, NS B4N 1J5, Canada; and (C.K.) Pacific Agri-Food Research Centre, Agassiz Site, AAFC, 6947 Highway 7, P.O. Box 1000, Agassiz, BC V0M 1A0, Canada.*

Lack of variation among strawberry (*Fragaria* × *ananassa* Duch.) cultivars has been cited as a limiting factor in breeding for strawberry improvement. The goal of this study was to determine the level of genetic diversity and relatedness among 15 strawberry cultivars and 12 breeding lines developed in Canada, using inter simple sequence repeat (ISSR) markers. Seventeen primers generated 225 polymorphic ISSR-PCR bands. Cluster analysis by the unweighted pair-group method with arithmetic averages (UPGMA) revealed a substantial degree of genetic

similarity among the genotypes ranging from 64% to 88% that were in agreement with the principal coordinate (PCO) analysis. Geographical distribution for the place of cultivar and line development explained only 3% of total variation as revealed by analysis of molecular variance (AMOVA). The ISSR markers detected a sufficient degree of polymorphism to differentiate among strawberry genotypes, making this technology valuable for cultivar identification and for the more efficient choice of parents in current strawberry breeding programs.

C2-2. How the antimalarial artemisinin is made in plants. P.S. Covello, K.T. Teoh, D.R. Polichuk, D.W. Reed, and G. Nowak. *Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada.*
Artemisinin, a sesquiterpene lactone endoperoxide derived from the plant *Artemisia annua* L., forms the basis of the most important treatments of malaria in use today. In an effort to elucidate the biosynthesis of artemisinin, an expressed sequence tag approach to identifying the relevant biosynthetic genes was undertaken using isolated glandular trichomes as a source of mRNA. Progress in the elucidation of genes involved in artemisinin biosynthesis will be discussed, especially those encoding enzymes involved in the oxidation and reduction of amorpha-4,11-diene to dihydroartemisinic acid.

C2-3. Cellular localization and its molecular regulation of Arabidopsis cyclin-dependent kinase inhibitors. D.A. Bird, Y. Zhou, M.M. Buruiana, L.C. Fowke, and H. Wang. *Department of Biology, University of Saskatchewan, Saskatoon, SK S7N 5E2, Canada; and (H.W.) Department of Biochemistry, University of Saskatchewan, Saskatoon, SK S7N 5E5, Canada.*
The cyclin-dependent kinase (CDK) inhibitors are important cell cycle regulators. The Arabidopsis has a family of seven CDK inhibitors referred to as ICKs or KRPs. Overexpressing one of the ICK/KRPs inhibits cell division, and profoundly affects plant growth and development. Localization to cellular compartments is an important aspect of regulation for cell cycle regulators. ICK1 is exclusively localized in the nucleus and three independent sequences in ICK1 can all confer nuclear localization of fusion proteins with green fluorescent protein (GFP). Interestingly, the N-terminal sequence of ICK1 specifies a punctate pattern of subnuclear localization while the C-terminal sequence suppresses it. We observed that all ICK/KRPs were localized to the nucleus, suggesting that the Arabidopsis CDK inhibitors function in the nucleus. While three ICK/KRPs were localized to the nucleoplasm homogeneously, four ICK/KRPs showed a punctate pattern of localization. A small motif conserved among the latter group of ICK/KRPs is required to confer this subcellular pattern since deletion of this motif from ICK7/KRP4 changed the punctate pattern to a homogeneous pattern. Results from deletion mutants further indicate that while a single nuclear localization signal is responsible for the nuclear localization of ICK2/KRP2, multiple mechanisms may regulate the nuclear localization of other six ICK/KRPs.

C2-4. Development of the soybean seed coat cuticle. K. Ranathunge, S. Shao, C.A. Peterson, and M.A. Bernards. *Department of Biology, University of Waterloo, 200 University Ave., Waterloo, ON N2L 3G1, Canada; and (S.S. & M.A.B.) Department of Biology, the University of Western Ontario, London, ON N6A 5B8, Canada.*
The outermost cuticle of a soybean seed controls its water uptake during imbibition. Seeds with an intact cuticle take up water extremely slowly and are known as "stone seeds". The more typical "permeable" seeds that imbibe water readily do so initially through small cracks in the outermost cuticle. Both types of seeds are normally produced but their proportions vary with cultivar and water availability during the growing season. In the present study, seed coat cutin deposition had begun by 14 days after pollination (dap) and continued until 42 dap, its rate lagging behind the increasing seed surface area. Despite this, the permeability of the cuticle to water declined until 45 dap. During the next four days, corresponding to the ultimate and most rapid phase of seed expansion, the permeability of stone seeds continued to decline, but the permeability of typical seeds increased abruptly. This increase correlated with cuticular crack formation as seen with SEM. Cessation of cuticle deposition was not due to death of the palisade cells, as this occurred later (during seed drying, 49–65 dap). The timing of crack formation provides an explanation for the increased number of stone seeds during dry years when seeds ripen early and are smaller than usual.

C2-5. Do members of the Lycopodiaceae possess endodermal Casparian bands? D.E. Enstone and C.A. Peterson. *Department of Biology, University of Waterloo, 200 University Ave., Waterloo, ON N2L 3G1, Canada.*
Roots of virtually all vascular plants possess an endodermis with a Casparian band. This structure typically contains lignin and suberin. As a result, along with the endodermal plasmalemma, it has an important function in regulating solute movement into the transpiration stream and maintaining root pressure. In a recent survey of seedless vascular plants, all roots except those of members of the Lycopodiaceae possessed an endodermal Casparian band. In the current study, we examined roots of representatives from the genera *Huperzia*, *Lycopodium* and *Diphasiastrum* using histochemical and apoplastic tracer methods. In each case, several layers of inner cortical cells possessed wall modifications with lignin and/or suberin, including suberin lamellae in some species. For example, *Huperzia lucidula* (Mich.) Trevisan displayed a Casparian band-like structure that extends through the inner tangential walls of one inner cortical layer. On the other hand, roots of *Lycopodium annotinum* L. and *Diphasiastrum complanatum* (L.) Holub do not possess a

similar structure, but have unusual deposits at the cell junctions in the inner cortex. Apoplastic tracer results suggest that there is a strong resistance to inward apoplastic diffusion in the cortex, although a fully effective barrier is lacking. Results to date support the concept that a classic Casparian band is lacking in the Lycopodiaceae.

C2-6. Proteomic analysis of mature tomato (*Lycopersicon esculentum*) and *Arabidopsis thaliana* pollen. I.S. Sheoran, K.A. Sproule, A.R.S. Ross, D.J.H. Olson, and V.K. Sawhney. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; and (A.R.S.R. & D.J.H.O.) National Research Council of Canada, Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada.*
Pollen grains are free and metabolically independent structures which, after release from the anther, germinate on the stigma of the carpel and deliver sperm cells to the ovule via pollen tube. The objective of this study was to conduct a proteomic analysis of tomato and *Arabidopsis* pollen to identify proteins related to various pollen functions. Proteins were extracted from mature pollen, separated using two-dimensional gel electrophoresis and selected spots were analyzed by matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS) or liquid chromatography-tandem mass spectrometry (LC-MS/MS). Proteins were identified using the MASCOT search engine. A total of 133 and 110 distinct proteins were identified in tomato and *Arabidopsis* pollen, respectively. The majority of identified proteins in the pollen of both species were similar, i.e., proteins related to defense mechanisms, energy-related pathways, protein processing, cytoskeleton, Ca^{2+}-binding and signaling, and pollen allergens. Some of the proteins identified in tomato pollen were Tomato Mosaic Virus coat protein, LAT52, phragmoplastin, ACC-oxidase, IAA transcription factor and a G-protein. In *Arabidopsis* pollen a large number of late embryogenesis abundant (LEA) proteins were present. The presence of large number of defense-related proteins in the pollen of both species reflects the survival strategy of free independent pollen, and the energy-related, cytoskelatal, and Ca^{2+}-binding and signaling proteins are potentially required for pollen germination and tube growth.

SESSION D

D1. Plant responses to the environment 1

D1-1. Nitrogen fertilization of butternut squash (*Cucurbita moschata* [Duchesne ex Lam.] Duchesne ex Poir.): Yield, N uptake, and N use efficiency. L.L. Van Eerd. *University of Guelph, Ridgetown Campus, Ridgetown, ON N0P 2C0, Canada.*
With rising input costs and environmental concerns, growers are seeking methods to optimize N use efficiency (NUE) while maintaining crop yields and minimizing off-field N losses. Under the same production system but in three different fields, a processing butternut squash N management study was conducted to 1) determine the optimal economic rate of N, 2) estimate a total N budget and 3) calculate NUEs. Preplant ammonium nitrate was broadcast applied at five rates between 0 and 220 kg N ha^{-1}. In three contrasting years (i.e. cool/wet vs. warm/dry vs. average), marketable yield response to N application was either no response or a quadratic response, with optimal economic yields of 108 and 128 kg N ha^{-1}. Based on total N budgets in all years, there was 51 and 108 kg N ha^{-1} more N remaining in the field as plant residue and soil (0-30 cm depth) mineral N (ammonium plus nitrate) in the 110 and 220 kg N ha^{-1} treatments, respectively, compared to the 0 kg N ha^{-1} control. As expected, NUEs were lower at 220 vs. 110 kg N ha^{-1}, however there were no differences in plant partitioning of N between fruit and shoots. Under this management system, the provincial recommended rate of 110 kg N ha^{-1} provided near optimal economic yields and reasonable NUE.

D1-2. *Botrytis cinerea* manipulates the antagonistic effects between plant immune pathways to restore its disease. M. El Oirdi and K. Bouarab. *Centre de Recherche en Amélioration Végétale, Département de Biologie, Faculté des Sciences, Université de Sherbrooke, 2500 Boulevard de l'Université, Sherbrooke, QC J1K 2R1, Canada.*
Plants are able to defend themselves against attack by a variety of potential pathogens through the deployment of both constitutive and induced defenses. Several of these induced-defense responses are dependent on salicylic acid, ethylene and/or jasmonates. To cause disease, a successful pathogen must counter these induced defences. Suppression of plant immune responses represent a sophisticated strategy used by several pathogens to invade theirs hosts. *Botrytis cinerea* is a necrotrophic pathogen that attacks different plant tissues and has a broad host range which causes important economic losses. The resistance to necrotrophic pathogens as *B. cinerea* is jasmonic acid dependent. We show here that *B. cinerea* manipulates the antagonistic effects between salicylic acid and jasmonic acid pathways to restore its disease. Indeed the fungus secretes an exopolysaccharide β-(1,3)(1,6)-D-glucan that suppresses the expression of *proteinase inhibtors I and II* genes which are dependent on jasmonic acid signalling. Thus, *B. cinerea* β-(1,3)(1,6)-D- glucan seems to be important for the virulence of its producing pathogen.

D1-3. Ferric and cupric reductase activities by iron-limited cells of the green alga *Chlorella kessleri*: Quantification via oxygen electrode. H.G. Weger, C.N. Walker, and M.B. Fink. *Department of Biology, University of Regina, Regina, SK S4S 0A2, Canada.*

The colorimetric Fe^{2+} indicators BPDS (bathophenanthroline disulfonic acid) and FZ (3-(2-pyridyl)-5,6-bis(4-phenylsulfonic acid)-1,2,4-triazine) are routinely used to assay for plasma membrane ferric reductase activity in iron-limited algal and plant cells. Ferric reductase assays using these colorimetric indicators must take into account the fact that Fe^{3+} chelators can also in general bind Fe^{2+} and may therefore compete with the colorimetric Fe^{2+} indicators, leading to the potential for underestimation of the ferric reduction rate. Conversely, the presence of BPDS or FZ may also facilitate the reduction of Fe^{3+}-chelates, potentially leading to overestimation of ferric reduction rates. Lastly, both BPDS and FZ have non-negligible affinities for Fe^{3+} in addition to their well-known affinities for Fe^{2+}; this leads to potential difficulties in ascertaining whether free and/or chelated Fe^{3+} are potential substrates for the ferric reductase. In this work we describe an oxygen electrode-based assay for both ferric and cupric reductase activities that does not use colorimetric indicators. Using this assay system, we demonstrate that the plasma membrane metal ion reductase activity of iron limited cells of the green alga *Chlorella kessleri* reduced complexed Fe^{3+} (i.e. Fe^{3+}-chelates) but did not reduce free (non-chelated) Fe^{3+}, and also reduced free Cu^{2+} to Cu^{+}, but did not reduce Cu^{2+} that is part of Cu^{2+}-chelates. These results suggest that an O_2 electrode-based metal reductase assay system has some specific advantages compared to the traditional colorimetric assay system.

D1-4. Functional analysis of poplar herbivore defense proteins and their effects on insect pests. C.P. Constabel and I.T. Major. *Centre for Forest Biology and Department of Biology, University of Victoria, P.O. Box 3020, Station CSC, Victoria, BC V8W 3N5, Canada.*
Genomics and molecular approaches applied the defense response of hybrid poplar have identified a large family of Kunitz-type trypsin inhibitor genes (KTIs). In order to test the function of these genes, we optimised methods for producing a set of representative recombinant KTI proteins for in vitro and in vivo analyses. Tests with commercially available digestive enzymes confirmed the inhibitory activities of all KTIs tested against serine proteases. As suggested by the high degree of sequence diversity, the recombinant KTIs exhibited distinct specificities to different proteases. Our data thus provide a functional rationale for the observed multiplicity of these genes in poplar. Interestingly, rapid evolution of the poplar Kunitz TI family has been independently demonstrated in native *Populus* populations. When tested against lepidopteran pest midgut extracts, several of the recombinant poplar KTIs showed inhibition of insect digestive enzymes, clearly demonstrating the anti-nutritive potential of these defense proteins. The most active in vitro inhibitor of the insect proteases was produced in large quantity for in vivo insect bioassays, which demonstrated its negative effects on forest tent caterpillar (FTC) performance. FTC larvae that had fed on KTI-containing diets did not switch to KTI-resistant proteases, as has been observed for some other KTIs. However, FTC larvae responded to the KTI diet by overproducing total protease activity, demonstrating a strong effect of the KTI on pest digestive physiology.

D1-5. Mitochondrial anaerobic ATP synthesis using nitrite as an electron acceptor. A.U. Igamberdiev, M. Stoimenova, and R.D. Hill. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*
Mitochondria were Percoll-purified from the roots of barley (*Hordeum vulgare* L.) and rice (*Oryza sativa* L.) seedlings. They oxidized NADH and NADPH anaerobically in the presence of nitrite and nitric oxide (NO) production was detected. The rates of NADH and NADPH oxidation were in the range of 12-16 nmol min^{-1} mg^{-1} mitochondrial protein for both species. The reaction was linked to ATP synthesis at rate of ~8 nmol ATP min^{-1} mg^{-1} mitochondrial protein for barley and ~16 nmol ATP min^{-1} mg^{-1} mitochondrial protein for rice. The rates were of the same order of magnitude as glycolytic ATP production during anoxia and about 3-5% of the aerobic mitochondrial ATP synthesis rate. NADH/NADPH oxidation and ATP synthesis were sensitive to the mitochondrial inhibitors myxothiazol, oligomycin, diphenyleneiodonium and insensitive to rotenone and antimycin A. The uncoupler FCCP completely eliminated ATP production. Succinate was also capable of driving ATP synthesis but at a lower rate. Mitochondrial functionality under anaerobic conditions may contribute to the oxidation of reduced pyridine nucleotides formed in the cytosol during glycolysis and in lipid breakdown. It may also contribute to the oxidation of the intramitochondrial substrates generated due to a limited tricaboxylic acid cycle activity, particularly in rice. NO is one of the products of nitrite reduction. We conclude that plant mitochondria, under anaerobic conditions, have a capacity to use nitrite as an electron acceptor to oxidize cytosolic NADH/NADPH, produce NO and generate ATP.

D2. Plant development and improvement 2

D2-1. Development of smut resistant hulless barley using molecular markers. T.S. Grewal, B.G. Rossnagel, and G.J. Scoles. *Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*
CDC McGwire (a barley variety from the Crop Development Centre, University of Saskatchewan, Saskatoon barley breeding program) is a high yielding hulless barley variety susceptible to true loose and covered smut. Screening for resistance to these diseases is time, labour and space consuming with frequent escapes making it necessary to screen putative resistant lines several times to confirm resistance. As both the diseases are floral

infecting, simultaneous screening is not possible. Molecular Marker Assisted Selection (MAS) is a good alternative to effectively and efficiently combine the resistance to both the diseases in the same genotype. Two strategies, doubled haploidy (DH) and marker-assisted backcrossing (MAB), were used to simultaneously introgress covered (*Ruhq*) and loose smut resistance (*Run8*) into CDC McGwire. Thirty-five DH lines were developed from a cross of the hulless loose smut resistant line SH00752 (CDC McGwire/TR251) with the hulless covered smut resistant line SH01470 (CDC McGwire/ Q21861). By screening the 35 DH lines for each of the markers, 14 were identified as positive for both. Following three rounds of screening by artificial inoculation, 12 were identified as resistant to both diseases. In the MAB program, "blind" selection based solely on markers was conducted through the BC_3F_2 generation and lines resistant to both diseases were obtained. One line, designated HB390, has been advanced to 2nd and final year of the Western Canadian Hulless Barley Co-operative yield trials for potential release as a new variety in 2008. These results confirm that molecular markers can be used in either DH or MAB programs to assist in the rapid introgression of simply inherited disease resistance genes into elite lines, with considerable time and cost savings.

D2-2. Field performance of double haploid dill (*Anethum graveolens* L.). D. Waterer and A. Ferrie. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; and (A.F.) Plant Biotechnology Institute, National Research Council, Saskatoon, SK S7N 0W9, Canada.*

Anther culture techniqes were used to generate a population of double haploid (DH) dill. The parental line cv. 'Mammoth' is tall, with an indeterminent growth habit and produces moderate yields of large seeds containing relatively low concentrations of essential oils. The DH lines were grown out using standard production practices in small plot trials conducted from 2004-2006. As expected, the DH lines were phenotypically distinct from the parental line. In most cases the variations from the parental line were undesirable. However, DH lines with superior earliness, uniformity of stature, biomass and seed yield and seed essential oil content have been identified. Field trials of double haploid caraway, fennel, anise and coriander are ongoing.

D2-3. Mapping quantitative trait loci controlling common bunt resistance in the spring wheat cross 'RL4452 × AC Domain'. D.G. Humphreys, B. Fofana, S. Cloutier, C.A. McCartney, and D.J. Somers. *Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada; and (C.A.M.) Department of Plant Sciences, College of Agriculture and Bioresources, Agriculture Building, 51 Campus Dr., Saskatoon, SK S7N 5A8, Canada.*

Genetic resistance to common bunt in spring wheat is a highly desirable trait because it provides environmentally friendly crop grade protection. Although valuable breeding achievements have been made to develop wheat varieties with enhanced resistance to common bunt, less is known about the chromosomal locations of the trait. In this study, we have determined the common bunt reaction of a segregating population of 185 spring wheat doubled haploid lines derived from the cross 'RL4452 × AC Domain'. Reactions to a mixture of common bunt races were assessed indoors at two locations over two years. A total 369 polymorphic marker loci including 356 microsatellite loci, five expressed sequences tags, and eight genes were used to develop a linkage map. Quantitative trait loci (QTL) analysis using composite interval mapping detected three QTLs associated with common bunt resistance. Two QTLs were located on chromosome 1B and a minor QTL was mapped to chromosome 7A. Additive effect of allele substitution indicates that AC Domain contributed the common bunt resistance at all three QTLs. Potential usefulness of the identified QTLs in marker-assisted breeding for common bunt resistance will be discussed.

D2-4. Age-related resistance studies with the potential to improve biofuel production. R.K. Cameron, J. Carviel, F. Al-Daoud, and A. Mohammad. *McMaster University, Department of Biology, 1280 Main St. W., Hamilton, ON L8S 4K1, Canada.*

Age-related resistance (ARR) occurs in numerous plant species including *Brassica*. ARR develops in mature *Arabidopsis thaliana* plants in response to *Pseudomonas syringae* or *Peronospora parasitica* infection. Studies in our lab indicate that intercellular washing fluids collected from plants expressing ARR exhibit anti-bacterial activity to *Pseudomonas* and intercellular SA accumulation is required for ARR. Taken together, this suggests that SA may accumulate in intercellular spaces and act as an anti-microbial agent. ARR in Arabidopsis is associated with the onset of flowering. A number of ARR mutants isolated in our lab are not only affected in the ARR response, but also in the onset of flowering. Thus it may be possible to manipulate these ARR genes to delay flowering and increase biomass in Arabidopsis and its close relative canola and at the same time increase disease resistance. There is interest in improving Canada's ability to produce biofuels as one way to reduce CO_2 emissions. Biodiesel can be produced from vegetable oils such as canola and can be used in today's diesel engines with similar efficiency to regular diesel while producing less particulate pollution. Further study of these ARR developmental genes and their role in ARR will allow us to manipulate the ARR response with the dual affect of increasing biomass production and disease resistance and ultimately biofuel production.

D2-5. Mapping QTLs for pre-harvest sprouting tolerance in spring wheat: Implication in hard white wheat breeding. B. Fofana, D.G. Humphreys, G. Rasul, S. Cloutier, S.M. Woods, A. Brûlé-Babel, O.M. Lukow, and D.J. Somers. *Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada; and (A.B.-B.) Department of Plant Science, 222 Agriculture Building, 66 Dafoe Road, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*

Hard white wheat (*Triticum aestivum* L.) is a value-added product that is of great interest to the milling industry because of its processing advantages over red wheat. It is also preferred over red wheat in certain Asian and Middle Eastern markets, offering new market opportunities. However, white wheat is recognized as being more susceptible to pre-harvest sprouting (PHS) than red wheat and as a consequence is more prone to yield losses and low grades for the producers and losses in baking and noodle quality. To identify quantitative trait loci (QTLs) associated with PHS tolerance for marker assisted selection in white wheat, we have developed a doubled haploid (DH) mapping population from a cross involving the CWRS variety 'AC Domain' and the white wheat line 'RL4137'. A partial genetic map was constructed using microsatellite markers selected from wheat chromosome groups 3, 4, 5, and 6. A population of 174 DH lines were characterized for important aspects of PHS including sprouting score, germination index, falling number and seed coat colour. QTL analyses were performed using composite interval mapping. A total of 11 QTLs were identified on group 3 chromosomes and chromosome 5D. Four QTLs associated with PHS traits were found to be co-incident with seed coat colour on chromosomes 3A and 3B. The importance of these findings in white wheat breeding for PHS tolerance will be discussed.

SESSION E

E1. Plant responses to the environment 2

E1-1. Overexpression of damaged DNA binding protein 1A (DDB1A) enhances *Arabidopsis* DNA repair. W.M. Al Khateeb and D.F. Schroeder. *Department of Botany, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*

The conserved Damaged DNA binding protein (DDB) complex consists of two subunits: DDB1 and DDB2. DDB1 is involved in genome stability, cell cycle progression, histone modification and DNA repair. *Arabidopsis* has two homologs of DDB1: DDB1A and DDB1B. In this study we examined the role of DDB1A in *Arabidopsis* DNA repair using a DDB1A null mutant (*ddb1a*) and overexpression lines generated using a 35S promoter, resulting in 9-fold overexpression of *DDB1A* relative to wildtype. When a root bending assay was used to test the effect of different levels of UV light on root growth, no significant difference was observed between wildtype plants and *ddb1a* mutants. On the other hand, overexpression lines showed higher levels of UV-resistance than wildtype. Furthermore, when 3-week-old seedlings were treated with different doses of UV light, the overexpression lines showed healthier plants than wildtype and *ddb1a*. To study the effect of UV on *DDB1A* expression levels, seedlings were treated with UV and samples taken after different time intervals. RT-PCR showed that *DDB1A* expression levels increased after UV treatment and reached the maximum 1-3 hrs after exposure. By using DDB1A-3HA tagged protein lines we were able to study the abundance of DDB1A in response to UV. Similar trends were observed as detected in RT-PCR analysis. In conclusion, these results indicate a crucial role of DDB1A in *Arabidopsis* damaged DNA repair.

E1-2. Non-targeted FT-ICR MS analysis of AM fungi growth stimulating carrot root exudates. Y. Ferhatoglu, D.D. Douds, and G. Nagahashi. *Phenomenome Discoveries, Saskatoon, SK S7N 4L8, Canada; and (D.D.D. & G.N.) USDA Agriculture Research Service, Eastern Regional Research Center, Wyndmoor, PA 19038, USA.*

Previously, carrot exudates collected from carrot root grown in liquid culture either in the presence (+P) or absence (–P) of phosphorus had been examined and the exudates from –P grown carrot had stimulated arbuscular mycorrhizal (AM) fungi growth. Crude exudates and purified active root exudates were analyzed by non-targeted FT-ICR MS. As a result of this analysis, metabolites related to membrane phospholipids, fatty acids, lactones, terpenes, flavonoids, lignins were found at higher levels in –P root exudates compared to +P root exudates. A putative retinoic acid / kaurenic acid, OH-ABA, and OH-methyl-strigol (strigol analog) that are synthesized from the common precursor b-carotene, were also among the –P accumulated metabolites. This clearly shows –P stimulates the synthesis of secondary products from isoprene, changing the architecture of membrane lipids that may be crucial during the colonization of host roots and AM fungi-host root interaction.

E1-3. Transcriptional regulation of PR-5 proteins during fungal infection in *Prunus* spp. A. El-Kereamy, A. Taheri, D. Errampalli, K.P. Pauls, and S. Jayasankar. *Department of Plant Agriculture, University of Guelph, 4890 Victoria Ave. N., Vineland Station, ON L0R 2E0, Canada; (D.E.) Agriculture and Agri-Food Canada, 4902 Victoria Ave. N., P.O. Box 6000, Vineland Station, ON L0R 2E0, Canada; and (A.T. & K.P.P.) Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Pathogenesis related (PR) proteins are induced by different factors such as pathogen infection in the host plant. Timely expression of these proteins is often associated with

resistance to fungal diseases. Brown rot, caused by the *Monilinia fructicola* is the most serious fungal disease of *Prunus* spp. This fungus attacks flowers causing blossom blight and also ripe fruits leading to serious economic loss. Very little is known about the resistance to this pathogen at the cellular and molecular level. Hence, we studied the molecular mechanism of resistance to brown rot in *Prunus domestica* L. SDS-PAGE of total proteins extracted from the infected fruits show a tremendous increase in PR-5 proteins. We cloned the PR-5 gene and its promoter from for further analysis. Cis-elements for different transcription factors including GCC box, W box, *Myb* binding site and ABRE were found in the promoter region. Based on this information, we cloned the *Myb* and *ERF* transcription factors and studied their expression during ripening and fungal infection using Real-Time PCR. Preliminary studies show that these transcription factors are likely to be involved in the regulation of PR-5 expression and further confirmatory work is in progress. From these studies, we expect to identify useful molecular markers to complement conventional breeding.

E1-4. Functional analyses of *Alpha-dioxygenase* in salt-stressed *Arabidopsis*. T.S.T. Aung, A. Plant, and M. Hamberg. *Department of Biological Sciences, Simon Fraser University, Burnaby, BC V5A 1S6, Canada; and (M.H.) Department of Medical Biochemistry and Biophysics, Karolinska Institutet, Stockholm, S-17177, Sweden.*

Alpha-dioxygenases (α-DOX) are involved in the oxygenation of fatty acids to produce reactive hydroperoxides that are further converted into 2-hydroxy fatty acids or fatty aldehydes. The physiological role of *α*-DOX has remained elusive, but evidence suggests that they protect plant tissues from oxidative damage associated with pathogen attack. The objective of this study was to assess the function of the two *α-DOX* genes (*Atα-DOX1* and *Atα-DOX2*) in salt stressed *Arabidopsis*. *Atα-DOX1* was constitutively expressed in the root but not in shoot tissues whereas *Atα-DOX2* was expressed in shoot tissues but at a much lower level than *Atα-DOX1*. Abscisic acid, salicylic acid and, to a lesser extent, ethylene are major hormone signals that regulate *Atα-DOX* expression in *Arabidopsis*. The expression of both *Atα-DOX* genes in root and shoot tissues was enhanced by salt stress. Enzyme assays have revealed increased *α-DOX* products (2-hydroxy fatty acids and fatty aldehydes) in salt stressed root and shoot tissues. *Atα-DOX1* was responsible for forming all *α-DOX* products in roots and the majority of products in salt-stressed shoot tissues. *Alpha-DOX* T-DNA insertion lines, over-expressing lines, and promoter-GUS fusion lines are being assessed to elucidate a role for α-DOX in salt stressed plants. Thus far, *α*-DOX have a limited role in salt tolerance, as gauged by root growth experiments, but they may affect the formation of lateral roots and thereby could influence root system architecture.

E1-5. Detection of algal metabolic phenotypes by ^{1}H-NMR. H.D. Bestman, J. Zee, and C. Preuss. *Department of Biology and the King's Centre for Molecular Structure, The King's University College, 9125 – 50 Street, Edmonton, AB T6B 2H3, Canada.*

As part of a systems biology approach to studying metabolism ^{1}H-NMR spectroscopy can be used as a rapid screen to characterize differences in metabolite fingerprints prior to obtaining more detailed metabolic profiles by 2-D NMR or GC-MS. We are measuring the effect of growing conditions on the polar metabolite fingerprint of the alga *Chlamydomonas reinhardtii*. The algae (wild type strain CC-125 mt^{+}) are grown autrophically under light (300 $\mu mol/m^2/sec$ PAR) in continuous culture systems (160 mL) with a 2-L/min airflow (1500 ppm CO_2). Heterotrophic conditions are created by adding sodium acetate to the medium (25 mM final concentration) and placing the culture system in the dark. This induced the glyoxylate shunt enabling the algae to synthesize carbohydrates from acetate. Following treatment the algal cells are collected, frozen in liquid nitrogen, and freeze dried. Algal metabolites are extracted in NMR solvent (8:2 D_2O:CD_3OD; *Phytochemistry*, 2003, 62:949-957). The NMR spectra are processed unsupervised and reduced to integrated regions of equal width (0.01 ppm). Treatment effects are determined by Principal Component Analysis (MatLab with PLS Toolbox). When *Chlamydomonas* is grown heterotrophically for 6 hrs with acetate as its carbon source the metabolite fingerprints differ significantly from those of algae growing under autotrophic conditions. PCA-generated biplots show that changing the growing conditions from autotrophic to heterotrophic is accompanied by significant changes in intensity at the 1.3, 1.89-1.91, 3.60, 3.73, 3.89, and 3.94 ppm chemical shift regions of the spectrum.

E1-6. Stomatal conductance and heat stress genetic mechanism. N. Murtaza. *Department of Plant Breeding and Genetics, University College of Agriculture, Bahauddin Zakaryia University, Multan, Pakistan.*

Stomatal conductance is an important heat avoidance mechanism and its association with higher yield and heat resistance has been established in Pima cotton. Experiments were carried out on upland cotton under heat-stressed and non-stressed greenhouse as well as field regimes, to understand the impact heat-stressed and non-stressed environments on the genetic and combining ability variations for stomatal conductance. The experimental material comprised 8 upland cotton cultivars and their 15 F_1 cross combinations obtained in a line x tester mating arrangement. Results showed high genetic variability for stomatal conductance under single environment, but low genetic variability across environments, due to higher magnitude of environmental interaction especially that cause by temperature regimes. Interaction effect of temperature regimes also substantially modified general and specific combining ability variations for stomatal

conductance. Relative contributions of general and specific combining abilities to total phenotypic variation for stomatal conductance also under went great change across field temperature regimes. Non-stressed regime favored the expression of genes causing additive type of genetic variability. Heat-stressed field regime however, favored the expression of both additive and non-additive types of genetic variations for stomatal conductance in upland cotton. Recurrent selection for accumulating favorable genes for general combining ability under non-stressed conditions was suggested for improving enhanced stomatal conductance in applied cotton breeding programs.

E2. Plant development and improvement 3

E2-1. Genotypic variation in traits contributing to early seedling vigour in field grown barley. A.O. Anyia, J.J. Slaski, P.R. Watson, and J.M. Nyachiro. *Alberta Research Council, P.O. Box 4000, Vegreville, AB T9C 1T4, Canada; and (J.M.N.) Alberta Agriculture and Food, 5030 - 50 Street, Lacombe, AB T4L 1W8, Canada.*

Early seedling vigor is a desirable trait that allows plants to form a canopy more quickly, reducing soil evaporation, increasing canopy transpiration and inhibiting the growth of weeds. Field experiments were conducted in 2006 at Vegreville, Lacombe and Castor, Alberta to evaluate early seedling vigour in barley. One hundred and twenty six genotypes, comprising germplasms and commercial varieties used in western Canada, were evaluated using non-replicated 4-row × 4 m plots with 6 replicated checks. Sixteen genotypes, representing the range of seedling performance observed in the field, were tested for consistency of performance in a greenhouse trial using three replicate soil beds seeded with four 0.65 m-long rows. To assess early seedling vigour, presence of a coleoptile tiller, leaf area and specific leaf area (SLA) of the second leaf at BBCH 13 and leaf area index (LAI) at BBCH 30 were determined. Seed weight, embryo size and seed vigour were determined on harvested seeds. When field data were averaged across all 3 locations, large genotypic differences in all traits measured was observed. For leaf area, extreme genotypes differed by 8.5 cm^2 and 5.6 cm^2 for two-row and six-row genotypes, respectively. Similarly, LAI differed by 1.9 and 1.7 while SLA differed by 203 cm^2/g and 351 cm^2/g for two-row and six-row genotypes, respectively. Except for SLA, genotypic performance was consistent for traits measured under field or greenhouse conditions, which may suggest high heritability and the possibility of greenhouse screening of breeding lines for these traits.

E2-2. Floral symmetry and nectary structure: Investigation of spurless, single-spurred and peloric, multi-spurred flowers of toadflax (*Linaria genistifolia* (L.) P. Mill.). A.R. Davis and S. Vogel. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; and (S.V.) Department of Morphology and Reproductive Ecology, Institute of Botany, University of Vienna, Rennweg 14, Vienna, Austria*.

Floral symmetry is known to have a major impact on recognition and associative learning behaviour of flower visitors, and undoubtedly has played an integral role in coevolution between angiosperms and their pollinators. Fundamentally, flowers exist as one of two types: radially-symmetric (actinomorphic), or with bilateral symmetry (zygomorphic). A species typically produces one or the other. However, the possession of starkly-contrasting actinomorphic and zygomorphic flowers - within the same plant - has afforded an opportunity to relate floral symmetry with nectary structure and nectar production, a topic rarely investigated before. Certain plants of toadflax (*Linaria genistifolia* (L.) P. Mill.) growing in the Botanic Garden at the University of Vienna, produce an abundance of single-spurred flowers (zygomorphic), yet also yield small numbers of spurless (zygomorphic) and 3- to 5-spurred, peloric flowers (actinomorphic). When they occur, the latter usually occupy the terminus of an inflorescence. The floral nectary was largest, and itself radially symmetrical, within these peloric flowers. However, a smaller, bilaterally-symmetrical nectary occurred within each of the two zygomorphic forms (spurless and single-spurred). All floral morphs possessed modified stomata on their nectary surfaces, but interestingly, their number and location varied greatly with nectary symmetry. The potential underlying mechanisms for these important differences among floral morphs are also being investigated.

E2-3. Vegetable research at the University of Saskatchewan. D. Waterer. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.*

The Vegetable Research Program (VRP) at the University of Saskatchewan is one of the last university-based programs of its type in Canada. The VRP focuses on research and extension issues of specific interest to Saskatchewan, but also addresses issues of wider interest. The VRP conducts one of the largest vegetable cultivar evaluation programs in Canada. Vegetable agronomy projects include trials on plasticulture and high tunnel production, integrated pest management, crop fertility and post-harvest management. Over 50% of the research conducted by the VRP deals with potatoes. Variety development and then determining agronomic practices suited to the new varieties is the primary focus of the potato research program. Integrated management strategies for potato diseases such as scab, silver scurf, late blight and black dot are also research priorities. The VRP website (http://www.usask.ca/agriculture/plantsci/vegetable) has proven to be an invaluable extension and outreach tool.

E2-4. The *Arabidopsis autobahn* mutation causes defects to auxin transport and alters leaf vein pattern and phyllotaxis. J. Garrett, J. Meservy, L. Tavernini, M. Blackshaw, and E.A. Schultz. *Department of Biological Sciences, University of Lethbridge, Lethbridge, AB T1K 3M4, Canada.*

Current models for phyllotaxis suggest that developing leaf primordia act as sinks for auxin through directed and asymmetrical localization of auxin efflux (PIN1) and auxin influx (AUX1) proteins. Since auxin is required for primordial outgrowth, withdrawl of auxin establishes a zone around each primordium in which new primordia cannot be initiated. As leaf primordia develop, the formation of vein pattern also depends upon directed localization of PIN1 and possibly AUX1 in procambial cells; thus the generation of vein pattern bears many similarities to the generation of phyllotactic pattern. We have identified a novel *Arabidopsis* mutant, *autobahn* (*abn*) that shows defects to both phyllotactic and vein patterns. Leaves of the *abn* mutant form an almost parallel array of multiple midveins that join late in development to form loops of random shape and size. Expression of the auxin responsive reporter gene *DR5::GUS* and expression of procambial marker *AthB9::GUS* in *abn* leaves is consistent with defects to auxin transport. Treatment of wild type with the auxin influx inhibitor NOA partially phenocopies the *abn* phenotype and the *abn* phenotype is partially suppressed by *aux1*; both results are consistent with *abn* being defective in auxin influx as a result of AUX1 mislocalization. Whereas the wild type phyllotactic pattern shows a progression from decussate to spiral, in *abn* the pattern remains decussate. A similar pattern can be induced in wild type by treatment with NOA. We suggest that defects to phyllotaxis and vein pattern in *abn* most likely result from defective auxin influx through AUX1 mislocalization.

E2-5. Functional characterization of four Arabidopsis *UEV1* genes and the involvement of *AtUEV1D* in DNA damage response. R. Wen, J.A. Torres-Acosta, X. Lai, L. Pastushok, L. Newton, W. Xiao, and H. Wang. *Department of Microbiology and Immunology, University of Saskatchewan, Saskatoon, SK S7N 5E5, Canada; and (J.A.T.-A. & H.W.) Department of Biochemistry, University of Saskatchewan, Saskatoon, SK S7N 5E5, Canada.*

DNA damage tolerance (DDT) is a newly defined pathway in eukaryotes. In budding yeast, this is achieved by covalent modifications of the proliferating cell nuclear antigen (PCNA). A ubiquitin-conjugating enzyme Ubc13 and a Ubc enzyme variant (Uev) are required for a unique Lys63-linked polyubiquitination of PCNA. We isolated two UBC13 and four UEV genes from Arabidopsis thaliana. All four AtUev1 proteins are able to form a stable complex with AtUbc13 as well as Ubc13 from yeast and human. These genes are able to functionally replace the corresponding yeast UBC13 or MMS2 genes for the DDT functions in vivo. Although all two AtUBC13 and four AtUEV1 genes are ubiquitously expressed in most tissues, AtUEV1D is expressed at a much higher level in germinating seeds and in pollen. We obtained a null *Atuev1d* T-DNA insertion line. Compared with wild type plants, seeds from the *Atuev1d* null plant germinated poorly when treated with a DNA damaging agent, and the germinated seedlings grew slower and majority ceased growth within two weeks. To our knowledge, this is the first report of Ubc13-Uev functions in tolerating DNA damage in a multicellular organism.

E2-6. Hormonal interactions in fruit development. J.A. Ozga, B.T. Ayele, and D.M. Reinecke. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.*

Fruit development involves a complex interplay of cell division, differentiation and expansion of sporophytic and gametophytic tissues that is carefully coordinated over time. Plant hormones are signals that regulate many processes of plant development including fruit development leading to mature fruit and viable mature seed. Auxins and gibberellins (GAs) have been implicated at various stages of fruit development. In this study, the role of endogenous auxins on GA deactivation during pea fruit development was investigated using physiological, biochemical, and molecular approaches. Using quantitative RT-PCR, we found that the growth-active auxin, 4-Cl-IAA, represses *PsGA2ox1* (mainly responsible for conversion of GA_{20} to biologically inactive GA_{29}) and stimulates *PsGA2ox2* (mainly responsible for conversion of growth-active GA_1 to inactive GA_8) mRNA levels. The observed 4-Cl-IAA-induced expression pattern for *PsGA2ox* genes, along with the previously reported 4-Cl-IAA stimulation of *PsGA20ox* and *PsGA3ox* gene expression (Ozga and Reinecke, J Plant Growth Regul 22: 73-81, 2003), is accompanied by production of GA_1 as demonstrated by $[^{14}C]GA_1$ synthesis from $[^{14}C]GA_{12}$ by 4-Cl-IAA-treated pericarps. These data suggest that a pulse of bioactive GA is produced by the pollinated ovary in response to auxin, which leads to fruit set and development. This research was supported by a grant from NSERC to JAO.

E3. Pest management 2

E3-1. Comparative genomics to assess horizontal gene transfer between mycorrhizal fungi and plants. T. Hsiang. *Department of Environmental Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*

During millions of years of evolution, mycorrhizal fungi have developed intimate associations with plants. These mutualistic adaptations may conceivably have involved an exchange of genes, or an evolution of proteins toward greater sequence similarity between the partners. With the

advent of high throughput genomic sequencing and the availability of complete genomes, we can examine relationships between organisms by comparing many thousands of sequences. There are currently over 50 fungal genomes that have been sequenced, but only a few are mycorrhizal (e.g. *Laccaria bicolor* and *Glomus intraradices*). Relatively few plant genomes have been sequenced or almost completely sequenced, but these few plant genomes allow us the opportunity to compare the similarity of gene sets of mycorrhizal fungi and closely related non-mycorrhizal fungi to plants, to test the hypothesis of horizontal gene transfer between mycorrhizal fungi and plants. In this study, predicted protein sequences of a mycorrhizal fungus (*Laccaria bicolor*) were compared to the predicted proteins of three plant species, *Oryza sativa*, *Arabidopsis thaliana* and *Populus trichocarpa* using BLAST. *Coprinus cinereus*, which is non-mycorrhizal but in the same order (Agaricales) as *Laccaria* was subjected to the same tests to see whether particular sequences are shared only between the mycorrhizal fungi and plants, and not found in related fungi. The results of this study on potential horizontal gene transfer between mycorrhizal fungi and plants are discussed.

E3-2. An extract from dwarf mistletoe (genus *Arceuthobium*) demonstrates antimicrobial activity against Gram-positive bacteria, including Methicillin Resistant *Staphylococcus aureus* (MRSA). K.Y. Pernitsky and C.M. Ross. *Department of Biological Sciences, Thompson Rivers University, P.O. Box 3010, 900 McGill Road, Kamloops, BC V2C 5N3, Canada.*

Dwarf mistletoes (*Arceuthobium* M. Bieb.) are evergreen, dioecious angiosperms that parasitize Pinaceae Lind. and Cupressaceae Rich. ex Bartl. As the dwarf mistletoe shoots are exposed to potential aggressors year-round, we hypothesized that the plant produces antimicrobials. We prepared a methanolic extract from *A. americanum* Nutt. ex Englm. growing on *Pinus contorta* var. *latifolia* (Engelm.) Critch. Using standard disc diffusion and optical density trials, we tested the extract for activity against Gram-positive bacteria, including Methicillin Resistant *Staphylococcus aureus* (MRSA), as well as Gram-negative bacteria. The extract demonstrated substantial antimicrobial activity against the Gram-positive bacteria, including MRSA, producing considerable zones of inhibition (14 ± 2 mm for MRSA), and being effective at a remarkably low concentration. The lack of inhibition of Gram-negative bacteria suggests the *Arceuthobium* extract has a specific mode of action, critical for the feasible development of a therapeutic agent. A provisional United States patent application has been filed.

E3-3. Detection of *Pantoea stewartii* by Taqman real-time PCR. J.T. Tambong, N. Mwange, M. Bergeron, T. Ding, and F. Mandy. *Agriculture and Agri-Food Canada, Eastern Cereal and Oilseed Research Centre, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; and (M.B., T.D. & F.M.) Immunology Laboratory, Centre for Infectious Disease Prevention and Control, Tunney's Pasture, Ottawa, ON K1A 0L2, Canada.*

Pantoea stewartii causes Stewart's vascular wilt and leaf blight of sweet corn and maize. Detection techniques currently used are time-consuming and relatively insensitive. Increasingly, real-time PCR is being used for accurate detection of plant pathogens. This study reports the development of a real-time PCR assay for detection of *P. stewartii* based on the capsular polysaccharide stewartan gene. A set of specific primers and Taqman probe were designed and evaluated for specificity and sensitivity. Optimized real-time PCR conducted on serial-dilutions of genomic DNA purified from *P. stewartii* exhibited consistent amplification of the *cpsD* target fragment at the 1 pg level. Corn leaf lesions from artificially inoculated plants were processed and assayed by real-time PCR for the presence of *P. stewartii*. *P. stewartii* was detected in all inoculated plants by direct processing of 40 mg of leaf lesions. The detection limit for bacterial cell suspension is about 10^4 CFU/ml in repeated experiments. Simultaneous staining of the same bacterial cell suspension with propidium iodide and SYTO 9 followed by flow cytometric analysis provided clear discrimination between intact ("live") cells (92.2%) and dead cells (7.8%). This suggests that the fluorescence recorded by the real-time PCR assay was mostly due to the presence of "live" bacterial cells. The real time PCR assay developed here could be useful for rapid and accurate detection and identification of *P. stewartii*.

E3-4. Direct real-time PCR (DRT-PCR): Rapid and cost effective detection and its applications on different pathogen diagnosis. W.-S. Kim, A.M. Svircev, and L.W. Stobbs. *Agriculture and Agri-Food Canada, Southern Crop Protection and Food Research Centre, 4902 Victoria Ave. N., P.O. Box 6000, Vineland Station, ON L0R 2E0, Canada.*

Direct real-time PCR (DRT-PCR) was initially developed for field detection of Plum Pox Virus (PPV) without the requirement for RNA purification. Supernatants of leaves macerated with direct pathogen extract buffer (DiPEB) were used as a template for real-time PCR. The DRT-PCR was shown to be a rapid, sensitive and cost effective procedure comparable to conventional real-time PCR which requires purified RNA as a template. In comparative studies with ELISA the DRT-PCR was able to detect over 30% more positives than ELISA. The DRT-PCR system was also easily adapted for the detections of other plant pathogens (including *Erwinia amylovora*, *Xanthomonas axonopodis* pv. *citri*, *Clavibacter michiganens*, Tobacco rattle virus, *Phytophthora*, Pepino mosaic virus) using extract from different sample tissues (leaves, cambiums, seeds, pollen, flowers and insects vectors). SYBR Green and TaqMan probe system were adaptable to both single and multiplex DRT-PCR reactions. The DRT-PCR protocol has been applied to understanding dynamics of

pathogen populations in the field, general epidemiology and vector transmission efficiency and early disease warning systems. Results of our studies will be discussed.

E3-5. Responses of lodgepole pine to infection by western gall rust. J.M. Wolken and P.V. Blenis. *University of Alberta, Department of Renewable Resources, 751 General Services Bldg., Edmonton, AB T6G 2H1, Canada.*
The effects of western gall rust [WGR; *Endocronartium harknessii* (J.P. Moore) Y. Hiratsuka] on water conduction, growth patterns and foliar nitrogen concentration [N] of lodgepole pine [*Pinus contorta* Dougl. ex Loud.] (P_l) were examined. Twelve P_l trees, approximately 12 years old, with stem gall encirclements of 0-100 percent were harvested. Hydraulic conductivity (K_ψ) was measured through the galls, and the leaf area (A_L), sapwood area (A_S), and foliar [N] were measured above the galls. K_ψ, foliar [N], A_L and A_S decreased with increasing gall size, resulting in the A_L/A_S ratio remaining constant. These results confirm that galls reduce water flow, and that trees respond by reducing their A_L to accommodate the reduced capacity of the stem to deliver water. In a second study, one-year-old P_l trees were either inoculated with WGR or left as controls. After three growing seasons A_L, A_S, foliar [N], root and shoot dry weights (DW), and total non-structural carbohydrates (TNC) for each DW component were determined. Galled trees allocated proportionally more resources to stem growth, while control trees invested more resources in foliage. The TNC were greater above galls than below galls, suggesting that galls also disrupt phloem transport to the roots.

E3-6. Enzymatic browning in selected apple genotypes. A.P.K. Joshi, S. Cheng, S. Khanizadeh, N.L. Pitts, and H.P.V. Rupasinghe. *Department of Environmental Sciences, Nova Scotia Agricultural College, P.O. Box 550, Truro, NS B2N 5E3, Canada; and (S.K.) Horticultural Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin, St-Jean-sur-Richelieu, QC J3B 3E6, Canada.*
Enzymatic browning in apples, a result of the action of polyphenol oxidases (PPO), is the major factor for the deterioration of quality in many processed apple products such as juice, fresh-cut slices, and chips. Apple genotypes with low post-cut enzymatic browning can be used not only to study the biochemical mechanisms leading to the post-cut enzymatic browning but also to develop value-added fruit products. Post-cut enzymatic browning, polyphenolic profiles using LC-MS/MS, PPO activity, and antioxidant capacity using FRAP and ORAC were determined in three new apple genotypes, 'Eden', 'SuperMac', and 'SJCA16R5A15' and compared these in 'Empire' and 'Cortland'. Among the five apple genotypes, 'Eden' exhibited the least post-cut enzymatic browning as estimated by Whiteness Index. 'SuperMac' possessed characteristic yellowish flesh color with low enzymatic browning. A negative correlation was observed between cholorogenic acid, catechin and epicatechin contents in the flesh and enzymatic browning while flavonols were independent from post-cut enzymatic browning. The biochemical mechanisms associated with the PPO activity of these apple genotypes and the substrate specificity to PPO and other possible factors determining the intensity of enzymatic browning will be discussed.

SESSION F

F1. Plant development and improvement 4

F1-1. Selection for straw fibre in oilseed flax. N.A. Coetzee and G.G. Rowland. *Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*
In Canada flax (*Linum usitatissimum* L.) is grown primarily for its seed oil, and the straw is a waste product. The traditional use of flax fibre in the linen industry requires long fibres, which necessitates a different plant type from that needed for a high seed yield. Recently new markets have become available for flax fibre, which are far less stringent in the type of fibre required. However, the fibre content in oilseed flax straw is highly variable, and more information is required on the heritability of fibre in flax, and on the effect of selection for both oil and fibre traits. For these reasons, this study was initiated, with F_2 populations of 43 crosses planted in one location in 2005, a two-location $F_{2:3}$ lines of six selected crosses planted in 2006, and $F_{2:4}$ lines planted in three locations in 2007. This study was also made possible with the development of an NIR analysis for the fibre content of flax straw samples. Preliminary results indicate that year and location have an effect on fibre content, as is known from previous studies. There may also be a slight negative correlation between fibre content and seed yield. Most interesting is that it may be possible to predict from the F_2 generation, which crosses will have higher fibre content.

F1-2. Identification of factors affecting isoflavonoid biosynthesis in soybean seeds. S. Dhaubhadel. *Southern Crop Protection and Food Research Center, Agriculture and Agri-Food Canada, 1391 Sandford Street, London, ON N5V 4T3, Canada.*
Isoflavonoids are a diverse group of secondary metabolites that accumulate in soybean seeds during development. They serve important roles in symbiotic nitrogen fixation, as well as defence against various biotic and abiotic stresses. Several clinical studies have suggested a role for isoflavonoids in human health and nutrition. The amount of isoflavonoids present in soybean seeds is influenced by both genetic and environmental factors that are not fully

understood. We have conducted a detailed gene expression analysis of developing soybean seeds in two cultivars that differ in the level of isoflavonoid accumulation. Our results indicated that the differential expression of Chalcone Synthase (CHS) 7 and CHS8 may be a responsible factor for the difference in the level of isoflavonoid accumulation. The search for factor(s) that regulate the expression of key isoflavonoid biosynthetic genes is underway and the results will be discussed.

F1-3. Differential regulation of ethylene perception elements during fruit ripening in plum (*Prunus salicina* L.). I. El-Sharkawy, W.S. Kim, A. El-Kereamy, A.M. Svircev, D.C.W. Brown, and S. Jayasankar. *(I.E.-S., A.E.-K. & S.J.) Department of Plant Agriculture, University of Guelph, 4890 Victoria Ave. N., Vineland Station, ON L0R 2E0, Canada; (I.E.-S., W.S.K. & A.M.S.) Agriculture and Agri-Food Canada, 4902 Victoria Ave. N., P.O. Box 6000, Vineland Station, ON L0R 2E0, Canada; and (D.C.W.B.) Agriculture and Agri-Food Canada, Southern Crop Protection and Food Research Centre, 1391 Sandford St., London, ON N5V 4T3, Canada.*

All stone fruits including Japanese plums (*Prunus salicina* L.) exhibit a double sigmoid growth pattern, typical of climacteric fruits. However, this is not a general trend, since some plum cultivars show a suppressed climacteric pattern. In order understand the developmental control of ethylene perception during their unique growth pattern, four Ethylene Perception and Signal Transduction Component (EPSTC) elements were isolated and characterized. This includes two ETR1-like proteins, one CTR1-like protein, and an ERF. Their regulation was studied throughout fruit development and ripening two plum cultivars, early ('Early Golden') and late ('Shiro'), based on their ripening dates and behavior. Analysis of transcript levels for the four cDNAs revealed that only *Ps-ERF1* and *Ps-ERS1* accumulated at and after flower pollination, respectively. Increases in *Ps-ETR1* and *Ps-CTR1* transcript levels were observed only at S3 of fruit development. 'Early Golden' showed ripening patterns typical of climacteric fruits accompanied by sharp increases in the transcript levels of these four genes in an ethylene-dependent manner. 'Shiro' exhibited a suppressed-climacteric pattern, with only a slight increase in ethylene production associated with ripening. The accumulation of *Ps-ETR1* transcripts in 'Shiro' was in an ethylene-independent manner, while that of *Ps-CTR1* was not. *Ps-ERS1* mRNA was expressed in low, constant levels and *Ps-ERF1* remained undetectable in 'Shiro'. The differences between the two plum cultivars in the date and rate of ripening in relation to the expression level and pattern of *Ps-ERS1* and *Ps-ERF1* mRNA will be discussed.

F1-4. Developing a scale-up system for the micropropagation of thidiazuron-induced strawberry shoots using a bioreactor. S.C. Debnath. *Atlantic Cool Climate Crop Research Centre, Agriculture and Agri-Food Canada, P.O. Box 39088, 308 Brookfield Road, St. John's, NL A1E 5Y7, Canada.*

The use of large-scale liquid cultures and automation in a bioreactor system has the potential to resolve the manual handling of the various stages of micropropagation and decreases production cost significantly. In an attempt to improve the micropropagation protocol for strawberry (Fragaria × ananassa Duch.) developed at the Centre, a procedure for the mass propagation of adventitious shoots regenerated from leaf, sepal and petiole explants of cv. 'Bounty' using a bioreactor system is described. Sepals, leaf disks and petiole halves produced multiple buds and shoots without an intermediary callus phase on 2-4 μM thidiazuron (TDZ)-containing gelled shoot induction medium within 5-6 weeks of culture initiation. TDZ supported rapid shoot proliferation at low concentration (1.1 μM) but induced 20 to 30% hyperhydricity in a bioreactor system containing liquid medium. Subculturing improved the number of shoots per responding explant, shoot height, and shoot vigor but increased hyperhydricity. Bioreactor-multiplied hyperhydric shoots were transferred to gelled medium containing 2-4 μM zeatin and produced normal shoots and roots within 4 weeks of culture. In vitro-derived plantlets were acclimatized and eventually established in the greenhouse. Present results suggested the possibility of large-scale multiplication of strawberry shoots in bioreactors.

F1-5. NSERC News / Nouvelles du CRSNG. M.V. Lamarca. *Life Sciences and Special Research Opportunities / Sciences de la vie et Occasions spéciales de recherche, Research Grants and Scholarships / Subventions de recherche et Bourses, 350 Albert St. / 350, rue Albert, Ottawa, ON K1A 1H5, Canada.*

Grant Selection Committees (GSC) Structure Review: The current structure of NSERC's discipline-based GSCs has been in place for more than 30 years. NSERC has recently undertaken a review of such structure and would like to update the community on the review's status as well as gather input on the process so far, and on future directions.

International Review of Discovery Grants Program: NSERC is commissioning an International Review to assess the merit of its approach to supporting research in the natural sciences and engineering, and the extent to which its Discovery Grants Program fosters and supports research excellence. NSERC will present the context of this study as well as gather feedback from the research community on the initial steps of the study.

Discovery Grants Competitions Results 2007: NSERC will present a brief report on the most recent Discovery Grants competition.

Revue de la structure des Comités de sélection (CSS) : La structure actuelle de nos CSS est en place depuis plus de 30 ans. Le CRSNG a récemment entrepris une revue de cette structure et aimerait donner une mise à jour à la communauté sur cette revue, ainsi que recueillir les

commentaires de celle-ci sur le processus en place, et sur ses orientations futures.
Revue internationale du Programme de subventions à la découverte : Le CRSNG a entrepris une revue internationale pour évaluer le mérite de son approche au soutien à la recherche en sciences naturelles et en génie, ainsi que le degré auquel le Programme de subventions à la découverte favorise et soutient l'excellence en recherche. Le CRSNG vous décrira le contexte de cette étude et recueillera les commentaires de la communauté de recherche sur les étapes initiales de celle-ci.
Résultats des concours 2007 des subventions à la découverte : Le CRSNG vous présentera un bref rapport sur le plus récent concours de subventions à la découverte.

F2. Plant development and improvement 5

F2-1. Overview of research towards optimizing *Brassica* sp. as biodiesel feedstocks - A research theme in the "Green Crop Network". J.K. Vessey, W. Keller, L. Kunst, P. McVetty, and H. Fei. *Department of Biology, Saint Mary's University, Halifax, NS B3H 3C3, Canada; (W.K.) National Research Council of Canada, Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada; (L.K.) Department of Botany, University of British Columbia, Vancouver, BC V6T 1Z4, Canada; and (P.McV.) Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*
The "Green Crop Network" (GNC) is an NSERC Strategic Research Network initiated in early 2006 with the goals of optimizing agricultural crop production, while mitigating greenhouse gas emissions, and providing specific new feedstocks for biofuels. The GCN involves 55 researchers, 18 universities, three federal government departments and three industry partners. One of the four Research Themes within the GCN is Theme 4 – Biofuel Crops. The goal of this Theme is to optimize Brassicas (edible rapeseed, canola and mustards) as biodiesel feedstocks. Optimization for this purpose involves maximizing oil seed production while minimizing greenhouse gas production and involves three integrated research projects: Project 4a – Identification of *Brassica* genotypes and molecular markers for increased seed oil content; Project 4b – Investigation of the contribution of oil biosynthetic enzymes to seed oil content in *Brassica napus* and *Arabidopsis thaliana*; and Project 4c – The bilateral influence of plant and rhizosphere characteristics in *Brassica* sp. varying in seed oil productivity. Project 4a involves genotype screening, classical breeding techniques, double-haploid germplasm development, and identification of genetic markers for marker-assisted selection of improved genotypes. Project 4b investigates the genetic manipulation of specific genes coding for enzymes involved in fatty acid and tri-acyl glycerol synthesis pathways in *A. thaliana* and *Brassica* sp. Finally, Project 4c assesses the effects of genetically manipulating seed-oil productivity on C partitioning within the plant and between the root and rhizosphere, and on nitrogen use efficiency. Project 4c will also determine if the microfloral composition of the rhizosphere can be manipulated to increase *Brassica* productivity and decrease greenhouse gas emissions from the rhizosphere.

F2-2. Phylogenomic evidence for pterin-dependent enzymes in plants. A.D. Hanson, A. Noiriel, and V. de Crécy-Lagard. *Horticultural Sciences Department, University of Florida, Gainesville, FL 32611, USA; and (V. de C.-L.) Microbiology and Cell Science Department, University of Florida, Gainesville, FL 32611, USA.*
Genome sequences have enormous potential utility in plant improvement but this potential will remain underexploited until functions can be assigned to all genes. About 50% of the genes in plant and prokaryote genomes currently have no known function, or merely vague ones such as 'oxidoreductase'. Comparative genomics ('phylo-genomics') is a powerful tool for discovering the function of such genes, and pterin metabolism provides examples of this. Pterins are known to be vital to plants as folate precursors but – until now – not as anything else. Yet animals, fungi and bacteria require pterins as cofactors for aromatic hydroxylases (AHs) and other enzymes, and have a unique pterin cofactor recycling system. The first clue that plants have pterin-dependent enzymes is that all plant genomes encode the unique pterin cofactor recycling enzyme pterin carbinolamine dehydratase (PCD). The next clue is that gymnosperm, moss, and algal genomes specify novel AH proteins. Representative AH and PCD genes were shown to have the expected activities by functional complementation in *Escherichia coli* and by assays of recombinant proteins. As these plant AHs mediate conversion of phenylalanine to tyrosine they may impact the synthesis both of phenylalanine-derived products (lignin, phenylpropanoids) and of tyrosine-derived ones (e.g., tocopherols). Phylogenomics shows that angiosperms lack AH-like genes, as do many bacteria with PCD in their genomes. These groups therefore probably have unknown pterin-dependent enzymes. Two candidates for these unknown enzymes in bacteria have been found by analyzing genes that cluster on the chromosome with known pterin-related genes and show similar phylogenetic distributions.

F2-3. Microarray analysis of phenylpropanoid gene expression. V.S. Bhinu, U.A. Schäfer, R. Li, J. Huang, and A. Hannoufa. *Agriculture and Agri-Food Canada, Saskatoon Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*
Plants produce numerous phytochemicals including isoflavones, lignans and phenolics. Many of these compounds, synthesized by phenylpropanoid pathway have diverse roles in plant defense, UV protection, seed coat colour and nodulation. The phenylpropanoid pathway

occurs in most land plants. However, in the seeds of canola and related species, one of the metabolic branches is extended to produce sinapine. Sinapine is a major anti-nutritional in canola. Since the phenylpropanoid pathway genes *per se* have been well-characterised, we were interested in their pleiotropic effects related to plant metabolism including primary metabolism. Knowledge of multiple effects from single genes helps us better understand metabolic networks and therefore design prudent metabolic engineering strategies which can be extended to canola. We therefore, undertook a systematic study of three genes in *Arabidopsis thaliana* namely the *fah* (ferulic acid hydroxylase), *omt* (*O*-methyltransferase), and *sct* (sinapoylglucose:choline sinapoyltransferase) that are involved in the phenylpropanoid pathway. Arabidopsis lines with disruption in these genes had significantly altered levels of metabolites (total phenolics and sinapine) in comparison to wild type Columbia plants, confirming their respective roles. Three mutant Arabidopsis lines, namely *fah*-KO, *omt*-KO and *sct*-KO were selected for microarray studies and some interesting roles of these genes will be discussed.

F2-4. Characterisation of *Ascochyta rabiei* - *Cicer arietinum* interaction for resolving the genetic basis of resistance. H.M. Booker, G.K. Kishore, A. Sharpe, B. Tar'an, and L. Buchwaldt. *Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; and (B.T.) Crop Development Centre, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.*

Ascochyta rabiei (Pass.) Lab. is a serious constraint to chickpea (*Cicer arietinum* L.) production world wide mainly because the pathogen is genetically diverse in contrast to low variation in the host. Our objectives are 1) to demonstrate a gene-for-gene interaction; 2) to determine allelism of resistance genes and their epistatic interaction; and 3) to select chickpea lines for characterization of pathogen populations globally. A detached leaf assay was developed in which a fixed number of leaflets are inoculated with single spore isolates (2×10^5 conidia per ml) in replicated tests, followed by an unbiased rating of infected versus uninfected leaflets over time (3 to 10 days after inoculation). A high correlation between this assay and whole plant inoculation was established. A total of 225 line-isolate interactions were examined by inoculation of 16 lines with 19 isolates. Statistical significant line-isolate interactions were identified indicating a gene-for-gene interaction in lines ILC 72 and ICC 4475. To address objectives 2 and 3, six ascochyta resistant lines, ILC 72, ICC 4475, ILC 2956, ILC 3279, ICC 4200 and Amit, are being inter-crossed to determine the number of different R-genes present in each line.

F2-5. A flavone-specific *O*-methyltranferase gene family in grain plants. R.K. Ibrahim and J.M. Zhou. *Biology Department, Concordia University, Montréal, QC H4B 1R6, Canada.*

O-Methylation of natural products plays important roles in plant growth and development and its interactions with the surrounding environment. It is catalyzed by enzymes encoded by members of the *O*-methyltransferase (OMT) gene superfamily. One of these, TaOMT2 (from *Triticum aestivum* L.) catalyzes the sequential methylation of tricetin (5,7,3′,4′,5′-pentahydroxy-flavone) to its 3′,5′-dimethyl ether derivative, tricin (Zhou et al., Biochim. Biophys. Acta 1260: 1115, 2006). A number of homologous genes occur in several cereal species such as barley, maize, rice and sorghum as well as two other monocot species, ryegrass and sugar cane. Most of the latter genes were erroneously annotated in GenBank as caffeic acid OMTs based on sequence homology and/or incomplete biochemical identification of their gene products. The objectives of the present study were to conduct a phylogenetic study of these genes and determine the substrate preferences of their gene products. Our results show that several homologs of TaOMT2 encode OMTs that utilize tricetin as the preferred substrate and produce tricin as the major enzyme reaction product. In view of the potential health benefits of tricin as an anticancer agent, among others, we are currently pursuing the genetic modification of wheat using *TaOMT2* with the aim of increasing the endogenous level of tricin in endosperm tissue.

F2-6. Evaluation of environmental effects and stability of isoflavone content in soybean (*Glycine max* L. Merr.). S.E. Murphy, L. Woodrow, and G.R. Ablett. *Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada; (L.W.) Agriculture and Agri-Food Canada, Harrow, ON N0R 1G0, Canada; and (G.R.A.) Ridgetown Campus, University of Guelph, Ridgetown, ON N0P 1C0, Canada.*

Isoflavones are naturally occurring, biologically active compounds found in soybeans (*Glycine max* L. Merr.). Research has shown that the consumption of soy-foods, a dietary source of isoflavones, has a positive impact on human health. Conversely, the isoflavones contained in soy-based infant formula have been suggested to be detrimental to infant health. Development of soybean cultivars with desired levels of total isoflavone would be beneficial to all levels of the soyfood industry. A strong genotype by environment interaction (GEI) however may present a challenge in breeding for isoflavone content. The objectives of this research were 1) to investigate the environmental causes of the underlying GEI effect on isoflavone content in soybean and 2) to evaluate the stability of soybean lines derived from two different populations and identify genotypes which have relatively stable isoflavone content. The results of the study, conducted over 10 environments, indicate that high daily maximum temperatures experienced during the seed filling period result in decreased levels of total isoflavone. GGE biplot analysis revealed several stable genotypes with either high or low isoflavone content. Despite the strong

effect of the environment, specifically temperature, cultivars with stable isoflavone content, both high and low, can be developed through conventional breeding.

F3. Plant responses to the environment 3

F3-1. Determination of dry matter and stability of carotenoids in kale and spinach during drying. M.G. Lefsrud, D.A. Kopsell, C.E. Sams, R.M. Augé, J.B. Wills Jr., and A.J. Both. *McGill University, Bioresource Engineering, 21, 111 Lakeshore, St-Anne-de-Bellevue, QC H9X 3V9, Canada; (D.A.K., C.E.S. & R.M.A.) University of Tennessee, Plant Sciences, 2431 Joe Johnson Drive, Knoxville, TN 37996, USA; (J.B.W.) University of Tennessee, Biosystems Engineering and Soil Science, 2506 E.J. Chapman Drive, Knoxville, TN 37996, USA; and (A.J.B.) Rutgers University, Bioresource Engineering, 20 Agriculture Extension Way, New Brunswick, NJ 08901, USA.*

Drying of spinach (*Spinacia oleracea* L.) and kale (*Brassica oleracea*) is required to determine the percentage of dry matter (%DM) and the pigment content of fresh leaves. 'Melody' spinach and 'Winterbor' kale were greenhouse grown in hydroponic nutrient solutions containing 13 or 105 mg L^{-1} nitrogen (N). Utilizing vacuum freeze dryers and convection ovens, plant tissues were dried for 120 hr at five different temperature treatments: (1) freeze drying at –25°C, (2) freeze drying at 0°C, (3) vacuum drying at +25°C, (4) oven drying at +50°C and (5) oven drying at +75°C. Spinach leaf tissue %DM was affected, but kale %DM was not affected by drying temperature. Spinach and kale leaf tissue %DM were both affected by N treatment. The high N spinach decreased from 7.3 to 6.4 %DM and low N spinach decreased from 12.7 to 9.6 %DM as the drying temperature increased. Kale ranged from 13.2 to 15.0 %DM for the high N treatment and from 21.4 to 22.5 %DM for the low N treatment. Lutein, β-carotene and chlorophyll levels for both spinach and kale leaf tissue were affected by drying temperature. Measured concentrations of all pigments decreased over 70% as the drying temperature increased. The spinach and kale samples dried between –25 and +25°C were not significantly different from each other in %DM or pigment concentration. Drying leaf tissue for accurate pigment analysis required temperatures below +25°C, using vacuum or freeze drying technology.

F3-2. Ecology of feral alfalfa (*Medicago sativa* L.) populations along the road verges of southern Manitoba. M.V. Bagavathiannan, R.C. Van Acker, M.H. Entz, S. McLachlan, and L. Friesen. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; (R.C.V.-A.) Chair, Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada; and (S.M.) Faculty of Environment, Earth and Resources, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*

Alfalfa is the most common managed forage crop in North America. It is a robust legume perennial and apart from cultivated fields, feral populations of this species can also be found in road verges, which have both agronomic and ecological consequences. Alfalfa is being considered as a platform for the production of novel traits, some of which will require confinement. Feral alfalfa populations could act as a genetic bridge for the transfer of novel traits from fields of genetically altered alfalfa to conventional and organic fields. The presence of feral alfalfa populations could also affect the balance of natural habitats and result in a reduction in the quantity and quality of such habitats. Despite the agronomic and ecological significance of feral alfalfa populations, there is limited information available on the ecology of feral alfalfa. In this context, a survey of feral alfalfa was done in three rural municipalities in southern Manitoba. The survey results revealed the widespread existence of feral alfalfa populations along road verges. These feral populations were most commonly found in areas bordering alfalfa production fields. Detailed study of these populations showed that feral alfalfa populations have active seed banks and can establish a self-perpetuating population. Possible origins of feral alfalfa populations are discussed as well as their implications for novel trait confinement.

F3-3. Density fluctuations in *Pinus banksiana* Lamb. and *Picea mariana* [Mill.] BSP trees, in Nopiming Provincial Park, Manitoba. M. Hoffer and J. Tardif. *Centre for Forest Interdisciplinary Research (C-FIR) and Department of Biology, University of Winnipeg, 515 Portage Ave., Winnipeg, MB R2B 2E9, Canada.*

In dendrochronology, little research exists on density fluctuations (DFs) in tree rings. This tree-ring anomaly can be used to understand tree growth and to potentially help reconstruct past climatic events. The main objective of this study was to explore the association between DFs and variations in climate. Sampling was conducted in Nopiming Provincial Park, Southeast Manitoba. Five jack pine (*Pinus banksiana*, Lamb.) stands were sampled. In each stand, wood cores were extracted from both jack pine and black spruce (*Picea mariana*, [Mill.] BSP), when present. After crossdating, all cores were measured for earlywood, latewood, and total ring width. All DFs were identified and their position within a tree ring determined. Both tree species showed similar radial growth and density fluctuation patterns. In jack pine trees, DFs were more abundant in the juvenile period. Results indicated that cool/snowy springs and dry summers were both conductive to a higher frequency of DFs. These anomalies could be formed partly in response to the timing of the start of the growing season as well as to conditions during that growing season that lead to interruption and subsequent resumption of normal growth. It was also observed that

radial growth in jack pine was more sensitive to precipitation, compared to black spruce which was more sensitive to temperature.

F3-4. Influence of mycorrhizal fungi on growth and water relations in *Populus*. J.A. Siemens and J.J. Zwiazek. *4-42 Earth Sciences Bldg., Department of Renewable Resources, University of Alberta, Edmonton, AB T6G 2E3, Canada.*
Mycorrhizal fungi are known to be of some benefit to tree species exposed to environmental stresses under certain conditions, although little research has been conducted regarding the nature of mycorrhizal associations with *Populus* species, and the effects of mycorrhizae on water relations in *Populus*. *Hebeloma crustuliniforme* (Bull.) Quél and *Wilcoxina mikolae* v. *mikolae* (Yang & Wilcox) Yang & Korf, were used to inoculate trembling aspen (*Populus tremuloides* Michx.) seedlings and balsam poplar (*Populus balsamifera* L.) cuttings. Roots of mycorrhizal and non-mycorrhizal aspen seedlings were exposed to short-term pH changes. All mycorrhizal and non-mycorrhizal seedlings were measured for changes in growth and root water relations parameters. Microscopic examination of colonized roots indicated that *W. mikolae* v. *mikolae* formed an ectendomycorrhizal association in balsam poplar, compared to the ectomycorrhizal association with *H. crustuliniforme*. Results indicate that mycorrhizal fungi resulted in improvements to some, but not all, growth parameters, with *W. mikolae* v. *mikolae* being more beneficial than *H. crustuliniforme*. Mycorrhizal fungi also resulted in higher root hydraulic conductivity and changes in activation energy of water transport, but differences were species-dependent. Differences in the type of mycorrhizal association may influence the extent of mycorrhizal benefits to trees with respect to growth and water relations.

F3-5. Effects of summer CO_2 enrichment on leaf photosynthesis and fruit yield of greenhouse tomatoes. Q. Wang, X. Hao, S. Khosla, and S. Borhan. *Greenhouse and Processing Crops Research Centre, Agriculture and Agri-Food Canada, 2585 County Road 20, Harrow, ON N0R 1G0, Canada; and (S.K.) Ontario Ministry of Agriculture, Food and Rural Affairs, 2585 County Road 20, Harrow, ON N0R 1G0, Canada.*
Although CO_2 enrichment is generally practiced in winter for improving plant growth and fruit yield of greenhouse tomatoes (*Lycopersicon esculentum* Mill.), its effects in summer greenhouse tomato production in Ontario are still unclear. The objective of this study was to investigate the effects of CO_2 enrichment on leaf photosynthesis, plant growth and fruit yield under summer conditions. Two beefsteak cultivars, 'Big-Dina' and 'Macarena', and one cluster cultivar, 'Clarance', were used in the study. The response curves of leaf photosynthesis to CO_2 concentrations in the morning, noon and afternoon were similar. This indicated leaf photosynthesis was not limited by the feed-back control from the accumulation of carbohydrates during the day and thus CO_2 enrichment in the afternoon could be as effective as in the morning. The leaf photosynthesis increased much faster with increasing CO_2 concentration under strong light conditions than under low light conditions. However, despite the higher leaf photosynthesis, the fruit yield was not increased by the summer CO_2 enrichment. Further study is needed to determine the factors limiting the benefit of summer CO_2 enrichment on fruit production.

F3-6. Neural networks to predict weekly yields of sweet peppers in a commercial greenhouse. B.D. Hill and W.C. Lin. *Lethbridge Research Centre, Agriculture and Agri-Food Canada, P.O. Box 3000, Lethbridge, AB T1J 4B1, Canada; and (W.C.L.) Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1000, Agassiz, BC V0M 1A0, Canada.*
The production of greenhouse-grown sweet pepper (*Capsicum annuum* L.) is highly irregular with a peak-and-valley pattern of weekly yields. We monitored the yields and environment in a commercial greenhouse in BC over six (2000-2005) growing seasons. Light was defined as cumulative light over the current week with L_1, L_2, L_3, L_4, L_5, L_6 representing light over previous weeks. Temperature was defined as the current weekly average of 24-h air temperatures with T_1, T_2, T_3 representing temperatures over previous weeks. Inputs were also created for the current weekly yield (Yield) and previous weekly yields (Y_1, Y_2, Y_3, Y_4). Neural network (NN) modelling was used to predict yield 1 wk in advance of the actual fruit harvest. Data records consisted of up to 22 inputs (different week, light, temperature and yield variables) paired with the known output (Yield+1) on a week-by-week basis. Data for five different years were combined for model training with the year to be predicted held separate as a validation set. The best models used 16 inputs with R^2 of 0.62, 0.65, 0.68, 0.43, 0.81 and 0.85 for 2000-2005, respectively. Y_4, (Yield-Y_1), T_1, Y_2, (Yield-Y_4), L_5 and week of the year were important inputs. NN have good potential for predicting pepper yields.

SESSION G

G1. Pest management 3

G1-1. Implications of foliar diseases and possible control strategies in wild blueberry production. D.C. Percival, L.I. Stewart, and P.D. Hildebrand. *Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, NS B2N 5E3, Canada; and (P.D.H.) Agriculture and Agri-Food Canada, 32 Main St., Kentville, NS B4N 1J5, Canada.*

Foliar diseases including *Septoria* leaf spot and blueberry rust (*Naohidemyces vaccinii*) have recently been attributed to causing significant yield reductions in wild blueberry (*Vaccinium angustifolium* Ait.) production. Field trials were initiated near Debert (Nova Scotia) and Tracadie (New Brunswick) to evaluate the impact of four fungicides on the occurrence of these foliar diseases and impact on leaf photochemistry, yield components and harvestable yield. Five treatments consisting of chlorothalonil (Bravo®), boscalid and pyraclostrobin (Pristine®), pyraclostrobin (Cabrio®), propiconazole (Topas®) and an untreated control were used with three application dates (early August 2005, early August 2005 and early June 2006, and early June 2006), and five replications. Results from this study indicated (i) disease incidence and severity was reduced with the use of chlorothalonil, (ii) the chlorophyll efficiency and photosynthetic rates of the chlorothalonil treatment were higher than the control, and (iii) an increase in floral bud number occurred with the use of chlorothalonil occurred at the Debert site. Significant differences in berry yield were also present with the chlorothalonil and boscalid and pyraclostrobin treatments having 101 and 83.1% greater harvestable yields at the Gavreau site, and boscalid and pyraclostrobin having a 13.3% greater harvestable yield than the control at the Debert site.

G1-2. Virulence of stem rust race TTKS on Canadian wheat cultivars. T. Fetch Jr. *Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada.*
Stem rust of wheat (*Triticum aestivum*), caused by *Puccinia graminis* f. sp. *tritici*, is a major disease that has been under control in Canada since the mid-1950's through the use of resistant cultivars. Stem rust race TTKS, originally found in east Africa in 1999, has broad virulence to most *Sr* genes and poses a threat to Canadian wheat production. Evaluation of the virulence of this race on Canadian wheat cultivars and on single-gene differential lines was conducted at Njoro, Kenya in 2005 and 2006. A few Canadian cultivars were found to possess high to intermediate levels of resistance (5R to 20MRMS) to TTKS based on their field reaction, but the majority were susceptible. The most resistant spring bread wheat cultivars observed were 'Peace' and 'AC Cadillac' (5R), while several durum cultivars expressed resistance (10RMR to 30 MRMS). It also was noted that lines with *Lr34* had enhanced resistance to TTKS compared to lines without this gene. Furthermore, based on reactions observed on single-gene differential lines and several wheat cultivars, it appears that a new variant of TTKS with additional virulence to the widely-effective gene *Sr24* evolved in 2006. Additionally, it has been confirmed that race TTKS has migrated across the Red Sea into Yemen, which increases the likelihood of continued migration of this dangerous pathogen. Continued research to monitor the spread and the evolution of this pathogen is critical for the protection of Canadian wheat production.

G1-3. Detached leaf approach for disease resistance or pathogenicity test requires reevaluation: A lesson from *Arabidopsis-Colletotrichum* interaction. G. Liu, R. Kennedy, D.L. Greenshields, G. Peng, L. Forseille, and Y. Wei. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; and (G.P. & L.F.) Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*
Detached leaf assays are widely adopted for examination of plant disease resistance and pathogen virulence, and these results are subsequently applied to intact plants. During the process of screening for a novel pathogenic fungus *Colletotrichum* in *Arabidopsis thaliana* (L.) Heynh., we found significant differences in defense responses between detached and attached leaf assays. A near-adapted isolate *C. linicola A1* Schimp. & Spenn. could only launch a typical infection on detached, but not attached *Arabidopsis* leaves. The differences between the detached leaf and intact plant assays were further confirmed on defense-defective mutants following inoculation with the virulent reference isolate *C. higginsianum* Sacc., where the greatest inconsistency occurred on ethylene-insensitive mutants. In intact *Arabidopsis* plants, both the salicylic acid- and ethylene-dependent pathways were required for resistance to *C. higginsianum*. In contrast, disease symptom development in detached leaves appeared to be uncoupled from these defense pathways, and more closely associated with senescence. In addition, both chemically-mimicked and genetically-stimulated senescence supported an association between senescence and anthracnose symptom development in detached leaves. Remarkably, *R*-gene mediated resistance also requires intact plants, since leaf detachment abolished the hypersensitive response of the *RCH* locus to *C. higginsianum*.

G1-4. Antibody microarray for the detection of grapevine and tree fruit viruses. I. Abdullahi, M. Rott, C. Masters, and R. Johnson. *Centre for Plant Health, Canadian Food Inspection Agency, 8801 East Saanich Road, Sidney, BC V8L 1H3, Canada.*
Antibody or protein microarray, the state-of-the-art technology developed for protein expression analysis, has found its way into the field of disease diagnostics and has the potential to revolutionize plant disease detection. To the best of our knowledge, very limited work has been done on the application of microarray technology to plant disease diagnostics. Our work represents the first attempt to develop a standard protocol for antibody arrays in plant virus detection. Using the conventional monoplex immunoassay as a benchmark, we developed antibody microarrays for the detection of grapevine and tree fruit viruses including; *Arabis mosaic virus*, *Grapevine fanleaf*

virus, and *Little cherry virus*. Two microarray experimental formats were considered; (1) direct labelling, and (2) dual antibody sandwich assays. In the direct labelling approach, we covalently labelled clarified viral concentrates (CVC) and detected bound viruses after incubation on an antibody microarray. In the sandwich assay, as in a standard immunoassay using microtitre plates, viruses captured on an antibody microarray were detected by a secondary antibody conjugated to alkaline phosphatase. The pros and cons of each design are discussed. Our antibody microarray system shows the sensitivity and specificity of ELISA methods, but uses much less amounts of reagents compared to the 96-well plate ELISA format.

G1-5. Agriculture and Agri-Food Canada develops carrot foliage trimmer for control of Sclerotinia rot in carrots. K.R. Sanderson and R.D. Peters. *Crops and Livestock Research Centre, Agriculture and Agri-Food Canada, 440 University Ave., Charlottetown, PE C1A 4N6, Canada.*

Mowing the carrot canopy can alleviate conditions that are conducive to the development of Sclerotinia rot of carrots (SRC) caused by *Sclerotinia sclerotiorum*. Canadian carrot growers commonly grow on a hilled system. Currently, there is no commercial equipment available to trim the carrot canopy. To further develop this concept as a tool for plant disease management, a prototype carrot foliage trimmer (CFT) was designed and manufactured in 2006 at the Harrington Research Farm in Prince Edward Island. The CFT was designed to trim four adjacent carrot rows using rotary saw blades that could be adjusted for width to define the severity of cut. The unit also has a series of lifter bars which lift older foliage lying on the soil surface prior to cutting with the blades. This opening of the carrot canopy allows sunlight to penetrate, foliage to dry and remove older senescing foliage. Initial field evaluation indicates that trimming has no effect on carrot yield or quality. Trimming at row closure significantly (P=0.05) reduced the incidence of SRC on foliage by about 82%. After one month in storage, SRC was reduced by 75%. The CFT provides an environment-friendly option to manage a disease for which there are currently no adequate control measures.

G1-6. Microscopic study of germ tube fusion in wheat leaf rust (*Puccinia triticina* Eriks). X. Wang and B.D. McCallum. *Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada.*

The population of *Puccinia triticina* in North America is highly variable and its pathogenic variability is thought be originated from sexual recombination, mutation and somatic hybridization. Since the susceptible host for sexual recombination of *P. triticina* is not found in North America, the possibility of somatic hybridization as a mechanism of for the emergence of new races is of special interest. In this study, urediospores from 40 *P. triticina* isolates were used to study germ tube fusions in *P. triticina*. There was considerable variability in the formation of fusion bodies among different isolates. Isolates WR-03-97-2 and WR-03-120-1 only produced 2-5 fusion bodies while other isolates formed 30-70 fusion bodies per 1000 of urediospores 24 hours after inoculations. Two types of fusion bodies were formed when urediospores were germinated on media containing different concentrations of sucrose or glucose. Large transparent fusion bodies were formed when urediospores were germinated on agar in absence of sugar while only small yellowish fusion bodies were formed on agar with 8% sucrose or glucose. The formation of fusion bodies was found to be essential for consequent germ tube fusions since germ tube fusion was no longer visible when fusion bodies were not present or suppressed by the addition of free water.

G1-7. Identity of tar spot of maple in Canada. T. Hsiang and L. Tian. *Department of Environmental Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Tar spot of maple has a worldwide distribution. In the late 2006, this disease became particularly abundant in the Great Lakes region of North America, with leaves of Norway maple (*Acer platanoides* L.) bearing multiple black round splotches. Tar spot disease was not as common on silver (*A. saccharinum* L.), sugar (*A. saccharum* Marsh.), red (*A. rubrum* L.) or other maples in this region. Numerous attempts to isolate the causal agent in pure culture from infected leaf tissue or ascospores were unsuccessful. However, we were able to obtain DNA from tar spots on Norway maple and silver maple in Ontario, as well as from big-leaf maple (*A. macrophyllum* Pursh.) in British Columbia and from sycamore maple (*A. pseudoplatanus* L.) in Germany and England. Based on analyses of DNA sequences of ribosomal DNA, we determined that the Norway maple tar spot fungus is the same species (*Rhytisma acerinum* Fr.) as that which occurs in Europe on sycamore maple, whereas our native large tar spot which occurs on silver maple and probably red and sugar maples is a separate species (*R. americanum* Hudler & Banik). A third species, *R. punctatum* Pursh., was observed only on big-leaf maple. Although *R. americanum* was delineated from *R. acerinum* by Hudler & associates of Cornell University based on morphology and DNA-RFLP, this is the first proof based on full DNA sequence analysis.

G1-8. Revisiting the classification of crown rust fungus: An insight from rDNA sequences. M. Liu, R. Tropiano, E. McCabe, J. Bergeron, and S. Hambleton. *Biodiversity (Mycology and Botany), Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada.*

Crown rust of oats has caused severe damage and economic losses historically. Classification of the causal

agent, *P. coronata* Corda, has attracted much attention because of the economic importance of oat production but also because of the wide host range of the pathogen. Based on minute morphological variations and host ranges, various approaches about the classification have been proposed, which fall into three major categories: 1. A two-species system, namely *P. coronifera* and *P. coronata*; 2. A one-species system, *P. coronata*, subdivided into many formae speciales (f. spp.), in which the host range of each f. sp. is restricted to host grass species within one genus; 3. A one-species system, *P. coronata*, subdivided into a few varieties with host ranges that may overlap. In order to examine whether the fungi causing crown rust on oats can be differentiated from those on other hosts, we extracted DNA from infected leaf samples, using herbarium specimens and recently collected samples, representing a wide range of hosts and wide geographic range. Analyses of internal transcribed spacer (ITS) sequences revealed eight clades, which may represent eight morphologically cryptic species. Crown rust fungi infecting oats have wide host ranges, while those on *Bromus* spp., *Agrostis* spp., and *Calamagrostis* spp. are restricted to one host genus.

G2. Plant responses to the environment 4

G2-1. Enhancing the economic viability of home gardens. H. Elsadr and D. Waterer. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.*

Hobby gardeners striving to produce fruits, vegetables and herbs within the confines of a typical urban garden rarely generate sufficient yields of quality produce adequate to offset the direct and indirect costs of the garden. This three year undergraduate student project looked at the potential to improve the yield potential and cost efficiency of a typical urban garden by utilizing various methods of site development and crop management. Extensive modification of the soil on site proved expensive but represented a major step towards enhancing the long term productivity of the garden. Selection of crops and cultivars best suited to the garden site represented a much less costly means of enhancing productivity. This selection process had to be balanced against the need to maintain sufficient variety of crops and cultivars in the garden to insure against losses to biotic and abiotic stresses and to meet the dietary needs and taste preferences of the gardener. Losses to insects and diseases were relatively minor over the three years of the study, but represent a potential threat within an intensively cropped hobby garden. The retail value of produce generated within the garden exceeded the cost of materials and labor in all three years of the study. "Profitability" (retail value – costs) of the garden increased as production techniques were refined to better suit the selected crops and the characteristics of the production site.

G2-2. Cover crops, nitrogen cycling and weed dynamics in subsequent cucumber (*Cucumis sativus* L.) crop. L.L. Van Eerd, D.E. Robinson, and A. Verhallen. *University of Guelph, Ridgetown Campus, Ridgetown, ON N0P 2C0, Canada; and (A.V.) Ontario Ministry of Agriculture, Food and Rural Affairs, Ridgetown, ON N0P 2C0, Canada.*

Ontario vegetable growers are concerned that changes in N dynamics and weed pressure due to cover crops may not be beneficial to the subsequent vegetable crop. A cover crop trial was established to assess N partitioning and weed establishment through to the subsequent cucumber crop. After the August 2005 cucumber harvest, six cover crops were planted. In late October, there were no differences between cover crops in biomass accumulation (ca. 2000 kg ha^{-1}) but there were differences in plant N uptake between vetch (*Vicia villosa* L.) and oilseed radish (*Raphanus sativus* L. cv. Némex) at 94 and 28 kg N ha^{-1}, respectively. In May, there were differences in plant N between vetch and oilseed radish, with 169 and 16 kg N ha^{-1}, respectively. Over sampling times (2005: August, October and 2006: May, June, July), the only difference in soil nitrate-N (0-60 cm depth) was between vetch and sweet corn (*Zea mays* L.) with 71 and 42 kg N ha^{-1}, respectively. Although vetch had the largest impact on N dynamics, it may not be appropriate in cucumber because of high redroot pigweed (*Amaranthus retroflexus* L.) pressure. In contrast, oilseed radish had the greatest suppressive effect on weeds and a moderate influence on N dynamics. Even with differences in N and weed dynamics, cucumber yield was not influenced by cover crop type; likely due to high Downey mildew (*Pseudoperonospora cubensis* (Berk. & Curtis) Rost) pressure.

G2-3. Enhancement of salinity tolerance by engineering chloride volatilization into plants. P. Koonjul, S. Kaur, S. Babayeva, and H.S. Saini. *Institut de recherche en biologie végétale, Université de Montréal, 4101 rue Sherbrooke est, Montreal, QC H1X 2B2, Canada; and (H.S.S.) Faculty of Environmental Studies, University of Waterloo, Waterloo, ON N2T 3G1, Canada.*

Several organisms possess enzymes that can convert chloride ions to chloromethane gas through one-step enzymatic methylation of the former. Presence of this enzyme activity in certain organisms that live in saline habitats has been interpreted as a possible mechanism for chloride detoxification via its volatilization. However, this possibility has never been experimentally tested. Our research group has cloned a cabbage gene encoding a thiol methyltransferase (TMT) enzyme that can methylate a variety of substrates, including chloride ions. Although chloride methylation is not the natural function of TMT in cabbage, we engineered this gene into tobacco, which normally lacks the enzyme as well as its usual metabolic context. Transgenic plants carrying the *TMT* gene acquired

an ability to efficiently transform chloride ions to chloromethane. Parallel with this, *TMT*-containing plants developed a high degree of tolerance to NaCl salinity, which was toxic to the untransformed counterparts. In contrast, over-expression of the *TMT* gene in *Arabidopsis* — which naturally contains the TMT enzyme and the associated thiol metabolism — had no effect on the salinity tolerance of this species. The results demonstrate that volatilization of chloride is a detoxification event that can contribute to plant's ability to withstand salinity stress. This ability, therefore, may be useful to engineer crop species with enhanced salt tolerance.

G2-4. The characterization of two green algal isolates from a northern Saskatchewan uranium mine site. A.M. Macdonald and K.E. Wilson. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*
Because of their haploid genomes and rapid growth rates, unicellular green algae can adapt to their growth environments quickly. Thus, it is expected that green algal strains isolated from extreme environments will have evolved specific physiological traits to aid their survival under difficult conditions. Areas of Northern Saskatchewan contain very rich uranium deposits which are mined by excavation of surface pits. However, this leaves large open areas that need to be remediated upon mine decommissioning to meet federal and provincial environmental standards. Often these pit mines flood due to ground water seepage or flooding from the surrounding areas. A previous study determined that a former mine site contained green algae. Our hypothesis was that these algal strains will have developed specific adaptations to survive the heavy metal contamination and low temperatures of the pit water. We identified two Chlamydomonas species growing in the mine water, using rDNA and ITS sequence analysis. We also compared the ability of the mine isolates and similar species obtained from algal culture collections to grow both in the mine-pit water, and at low temperatures.

G2-5. Hay yields are declining on Canadian farms: A Saskatchewan perspective. P.G. Jefferson and F. Selles. *Western Beef Development Centre, P.O. Box 1150, Humboldt, SK S0K 2A0, Canada; and (F.S.) Agriculture and Agri-Food Canada, Brandon Research Centre, P.O. Box 1000A, R.R.#3, Brandon, MB R7A 5Y3, Canada.*
Hay yield data collected by Statistics Canada show that annual "on farm" yields have been declining in most Canadian provinces for the last 40 years. Statistics on forage acres seeded, hay acres harvested, and the number of beef cows were used to examine the relationships between hay yield in Saskatchewan and the beef industry. Weather from 16 sites across Saskatchewan's agricultural region for the April, May, and June (AMJ) period was also examined from 1967 to 2003. As the Saskatchewan beef cow herd has grown larger and the area harvested for hay increased, hay yields per acre have declined. Precipitation during AMJ was positively correlated to hay yield but the difference between maximum and minimum temperatures was negatively correlated. Hay yield expressed as water use efficiency (WUE) exhibited a negative correlation to year. Examination of census data on tame forage and tame pasture acres by district did not support the hypothesis that more hay has been seeded in lower yield regions of the province. Our analysis cannot exclude the possibility that climate change is negatively affecting the province's ability to produce hay, particularly since low inputs of fertilizer and infrequent stand rejuvenation are practiced on forage crops. This problem needs more in-depth analysis to confirm the cause of this decline and avoid a future scenario where low hay yields make beef production economically unsustainable in Canada.

G2-6. Flower-visitor constancy in tall-grass prairie ecosystems. D.B. Robson. *The Manitoba Museum, 190 Rupert Avenue, Winnipeg, MB R3B 0N2, Canada.*
The tall-grass prairie ecosystem in Canada is fragmented and endangered. There is only limited information about the key flower visitors of this ecosystem. This study examines flower-visiting insect activity on two tall-grass prairie preserves in Manitoba to determine year-to-year and site-to-site constancy. Flower-visiting insect richness and visitation rates were monitored in 2004 and 2005 every two weeks from June to September. Plant-flower visitor matrices for both sites and years were calculated and compared. Connectance and the number of species interactions at each site were similar between years. The insect richness and visitation rates were not significantly different at each site between 2004 and 2005 but the composition varied. The majority of insect visitor taxa were Dipterans, followed closely by Hymenopterans. Hymenopteran family visitations were more common at the drier site while Dipteran family visitations were more common at the moister site. Only 17 taxa (18% of all taxa observed) were seen at both sites and in both years. However, those 17 taxa were responsible for 72% of all observed visitations. These 17 taxa each visited seven more plant species on average than the taxa observed in only one year. Thus these taxa are among the key floral visitors in the tall-grass prairie ecosystem in Manitoba and should be assessed for their effectiveness as pollinators.

G2-7. Leaf life span and plant height as adaptive traits along gradients of productivity and disturbance. P. Ryser and J. O'Hara. *Laurentian University, Department of Biology, Ramsey Lake Road, Sudbury, ON P3E 2C6, Canada.*
Long-lived leaves are generally considered to be adaptive in unproductive habitats as they minimize resource losses. Based on previous experiments, however, we hypothesize that in the absence of disturbance, long-lived leaves pose an advantage for a species also in productive environments. We also hypothesize that plant height is an

important trait for competitive ability in productive environments. Using 12 herbaceous perennial wetland species we conducted a garden experiment to investigate the association between interspecific variations in leaf longevity, plant height and competitive ability at high and low nutrients (10-fold difference) along a short successional gradient (2 years). Tillers were planted in 18-liter pots in 2004. Species abundances in mixtures and monocultures were assessed monthly during the growing seasons of 2005 and 2006. Competitive ability of the species (ratio of mixture to monoculture abundances assessed using a pin-frame) was related to plant height at both nutrient levels, but more clearly at high nutrients. Leaf longevity was associated with increase in the species' competitive ability along the successional gradient, regardless of nutrient supply. We conclude that interspecific variation in leaf longevity has primarily to be seen as an adaptation to variation in habitat disturbance, not productivity. These findings suggest that the adaptive nature of interspecific variation in height should be emphasized more than is currently the case in ecological theory.

ABSTRACTS

Contributed Posters

POSTERS

P1. Pest management

P1-1. Characterization of bioactive secondary metabolites from a race 3 isolate of *Pyrenophora tritici-repentis*. N. Bouras and S.E. Strelkov. *Department of Agricultural, Food and Nutritional Science, University of Alberta, 410 Agriculture/Forestry Centre, Edmonton, AB T6G 2P5, Canada.*

Tan spot, caused by the fungus *Pyrenophora tritici-repentis*, is an economically important foliar disease of wheat. Race 3 isolates of the pathogen differentially induce chlorosis and necrosis on hexaploid and tetraploid wheat genotypes, respectively. The production of bioactive secondary metabolites in mycelial extracts and culture filtrates from a race 3 isolate was examined by high performance liquid chromatography with diode array detection. Many of the compounds detected were identified as triticones and anthraquinones based on their UV spectra. One compound (designated F10) appeared to induce chlorosis in a semi-specific manner, causing extensive chlorosis on wheat line 6B365, weak symptoms on 4B160, and no symptoms on the tan spot-resistant cv. Erik. The chemical properties of F10 and its role in disease development are being characterized further. An orange pigment was also isolated and identified as an anthraquinone antibiotic, suggesting that it may potentially modify the microbial community accompanying *P. tritici-repentis* on the phylloplane and during its saprophytic phase. Additional secondary metabolites from race 3 of the fungus are being investigated for bioactivity on wheat and other microorganisms.

P1-2. Cross pathogenicity of *Verticillium dahliae* isolates on potato and sunflower cultivars. H.A. Alkher, A. El Hadrami, L.R. Adam, K.Y. Rashid, and F. Daayf. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; and (K.Y.R.) Agriculture and Agri-Food Canada, Morden Research Station, 101 Route 100, Unit 100, Morden, MB R6M 1Y5, Canada.*

Potato and sunflower are important crops worldwide and greatly contribute to the economy of Manitoba. Verticillium wilt is a soilborne disease that affects both the yield and the quality of both crops. To date, it is not clear whether the same isolates affecting potato can affect sunflower, to what extent, and *vice-versa*. Studying such a cross pathogencity of *V. dahliae* on these crops may help understand how *V. dahliae* gains/looses pathogenic ability to different hosts, and ultimately might provide better strategies to manage Verticillium wilt. Twenty-two *V. dahliae* isolates (10 from sunflower, 12 from potato) were tested for their pathogenicity under greenhouse conditions on 4-week-old seedlings of moderately tolerant and susceptible sunflower accessions and potato cultivars ('6946', 'IS8048' 'Runger Russet' and 'Kennebec', respectively). Variation was observed among isolates based on the type of symptoms that they induced and the amount of diseased leaf areas. Disease severity was based on the over time progress (2-8 weeks post inoculation) of percent leaf infection and the degree of vascular discoloration. Isolates were more aggressive on their original host. However, potato isolates were more aggressive than sunflower isolates on both potato and sunflower, whereas sunflower isolates were less aggressive than potato isolates on potato cultivars.

P1-3. Proteomic changes in the roots of *Brassica napus* in response to infection by *Plasmodiophora brassicae*. T. Cao, S. Srivastava, N.N.V. Kav, N. Hotte, M. Deyholos, and S.E. Strelkov. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; and (N.H. & M.D.) Department of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9, Canada.*

Clubroot, caused by the obligate parasite *Plasmodiophora brassicae* Wor., has emerged as an important new disease of canola (*Brassica napus* L.) in Alberta, Canada. Changes in the canola (*Brassica napus*) root protein profile induced by *P. brassicae* (SACAN03-1) infection were examined at 12, 24, 48 and 72 h after inoculation, using two-dimensional gel electrophoresis. A total of 20 spots were identified as either up- (13 spots) or down-regulated (7 spots) relative to water-treated controls. The identities of these proteins were established by tandem mass spectrometry, and included proteins involved in the detoxification of reactive oxygen species (ROS), lignin biosynthesis, programmed cell death, glycolysis, and intracellular calcium homeostasis and signal transduction. The significant down-regulation of adenosine kinase 1, which is involved in cytokinin homeostasis, supported previous reports indicating a key role for cytokinin in the early phases of clubroot infection. The down-regulation of caffeoyl-CoA *O*-methyltransferase, by approximately six-fold, suggested a reduction in host lignin biosynthesis after pathogen challenge, and is consistent with the compatible nature of the interaction examined. Levels of enzymes involved in ROS metabolism declined sharply at 12 h after inoculation, but increased at 24 to 72 h. Collectively, these data suggest major changes in canola metabolism shortly after challenge by the pathogen, which may result in the susceptibility of the host. Validation of the roles of these proteins in the *P. brassicae*-canola interaction is underway.

P1-4. Disease severity assessment of fungal foliar diseases with a public domain computer image analysis program. C.P. Wijekoon, T. Hsiang, and P.H. Goodwin. *Department of Environmental Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Digital image analysis combined with computer software can be used to evaluate leaf color. A method was previously reported using a flat bed scanner with the public domain software, Scion Image (www.scioncorp.com), to measure changes in leaf color due to nutritional changes.

As foliar diseases can also cause changes in leaf color, we modified the method of leaf color analysis to quantify several fungal foliar diseases. Leaves of *Nicotiana benthamiana* L. were inoculated with different concentrations of *Colletotrichum destructivum* O'Gara, which causes anthracnose. A strong correlation (r=0.83) was found between the percentage diseased tissue measured by Scion Image and the number of leaf spots. The method was tested on a range of foliar diseases: anthracnose of lily of the valley, apple scab, phlox powdery mildew and goldenrod rust, and was successful in measuring disease severities ranging from 1 to 90%. For some diseases, such as powdery mildew, the brightness and contrast of the images had to be adjusted, and modifications were also made in processing images. However, each set of modifications was applied consistently for each disease. As the method required using detached leaves with a flat bed scanner, an alternative method was developed using attached leaves with a digital camera. This allowed us to quantify the disease development of anthracnose on *N. benthamiana*.

P1-5. Investigations on *Fusarium* wilt of lentil. C.A. Rauf and S. Banniza. *Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*
Vascular wilt of lentil (*Lens culinaris* Medikus), incited by the fungus *Fusarium oxysporum* Schlect. ex Fr. f. sp. *lentis* Vasudeva and Srinivasan, is one of the most significant and severe soil-borne threats to lentil cultivation worldwide. The disease may cause complete failure of the crop under favourable conditions. In Canada, *F. oxysporum* f. sp. *lentis* has not been reported to date, but low levels of wilt-like symptoms caused by other pathogens are common under certain conditions. Lentil plants with wilt-like symptoms were noticed at a significant level during the 2003 crop season at the Goodale Research Farm of the University of Saskatchewan near Saskatoon. Studies were initiated with the objective to identify the causal pathogens among fungi isolated from infected lentil plants, and to characterize the isolates. Fungi recovered from diseased samples comprised *F. oxysporum* (20 isolates), *F. acuminatum* (3 isolates), *F. equiseti* (1 isolate) and *F. sporotrichioides* (1 isolate). A screening protocol was developed to assess virulence of the isolates on lentil cultivars with different levels of resistance to fusarium wilt. Pathogenicity determination of 25 isolates on the lentil cultivar CDC Blaze (resistant) and line 1743T-22 (susceptible) showed considerable variation in wilt suggesting various levels of virulence among isolates. Likewise, morphological characterization of isolates revealed differences among them.

P1-6. Are fungal siderophores pathogen-associated molecular patterns? D.L. Greenshields, G. Liu, G. Selvaraj, and Y. Wei. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; and (G.S.) Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada.*
Iron is an essential element for both plants and fungal pathogens. Plant iron is generally bound to proteins and small molecules during transport and storage, which prevents the generation of toxic free radicals via iron-mediated redox reactions. In order to scavenge plant host iron, fungal pathogens have evolved at least two distinct iron acquisition strategies. One iron uptake strategy involves the secretion and subsequent uptake of small iron chelators called siderophores and the other system uses cell surface reductases which reduce plant bound ferric iron to ferrous iron for uptake. While investigating the role of iron in plant defence, we found that various fungal and bacterial siderophores were able to induce the expression of pathogenesis-related genes in both *Triticum monococcum* L. and *Arabidopsis thaliana* (L.) Heynh. We also found that the siderophore system of iron uptake was essential for the full virulence of *Fusarium graminearum* Schwabe, while the reductive iron uptake pathway was dispensible. To date, all of the fungal pathogens shown to require siderophores exhibit a necrotrophic lifestyle. In contrast, investigations into biotrophic fungal pathogens have shown that biotrophs instead use the reductive iron uptake pathway during infection, suggesting that siderophores may alert plants to the presence of pathogens.

P1-7. Biological control of post-harvest fungal decay of pome fruit. D.L.M. Hirkala, L.M. Nelson, S. Stokes, and P. Sholberg. *University of British Columbia Okanagan, 3333 University Way, Kelowna, BC V1V 1V7, Canada; and (S.S. & P.S.) Pacific and Agri-Food Research Centre, Summerland, BC V0H 1Z0, Canada.*
Post-harvest losses as a result of fungal decay are a significant problem for the apple industry accounting for a 5-10% loss of profits annually. Fifteen bacteria isolated from the rhizosphere of legumes grown in Saskatchewan soils were tested as potential biological control agents for use on pome fruit against blue mold (*Penicillium expansum* Link), grey mold (*Botrytis cinerea* Pers.:Fr) and Mucor rot (*Mucor piriformis* E. Fisch), important post-harvest diseases of pome fruit. Seven of the 15 bacterial isolates were able to inhibit the growth of all three fungal pathogens on plate assays. Four of the strains significantly reduced lesion diameter by 60-80% in apples infected with *P. expansum* or *B. cinerea* at 1°C and one of these was also effective at 20°C. The same experiments conducted on apples with the simultaneous application of the biocontrol and the pathogen, *M. piriformis*, resulted in a 36% decrease in lesion diameter compared to the pathogen control when isolate 6-25 was applied. Inhibition of the pathogen was more affected by the biocontrol isolate than by the timing of pathogen challenge. The effectiveness of the biocontrol treatments were not significantly affected by the application of the ethylene inhibitor, 1-methylcyclopropene, to the fruit. The four

most effective bacteria have been identified as three *Pseudomonas* spp. and one *Serratia* sp.

P1-8. Effect of pasmo (*Septoria linicola*) on six different flax cultivars. L. Grant, K.Y. Rashid, and L. Lamari. *Department of Plant Science, University of Manitoba, 220 Agriculture Building, Winnipeg, MB R3T 2N2, Canada; and (K.Y.R.) Agriculture and Agri-Food Canada, Morden Research Centre, Morden, MB R6M 1Y5, Canada.*

Septoria linicola (Speg) Garassini (teleomorph *Mycosphaerella linorum* Naumov) is the causal agent of Pasmo disease of flax (*Linum usitatissimum* L.). Pasmo has been reported to cause yield losses and affect oil and protein content of the seed. Six flax cultivars ('AC Emerson', 'AC Linora', 'AC Macbeth', 'McGregor', 'Norlin' and 'Vimy') were studied to determine their response to the disease under field conditions both in resisting infection and in maintaining favourable agronomic characteristics such as yield, oil and protein content of the seed under disease pressure with and without the aid of a fungicide. Artificial inoculation was used along with two to five applications of the fungicide Pyraclostrobin (Headline). Fungicide application was found to increase yield, oil content, and seed weight and to decrease disease symptoms. Protein content tended to be higher when the fungicide was applied. Use of the fungicide Pyraclostrobin has been seen to reduce the negative effects of pasmo.

P1-9. First report of *Puccinia lagenophorae* on common groundsel (*Senecio vulgaris*) in Canada. W.L. Bruckart, A.S. McClay, S. Hambleton, R. Tropiano, and G. Hill-Rackette. *USDA-ARS-FDWSRU, 1301 Ditto Ave., Ft. Detrick, MD 21702, USA; (A.S.M.) McClay Ecoscience, 15 Greenbriar Crescent, Sherwood Park, AB T8H 1H8, Canada; (S.H. & R.T.) Biodiversity (Mycology and Botany), Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada; and (G.H.-R.) 1302 Falconer Road, Edmonton, AB T6R 2V7, Canada.*

Samples of a rust disease were collected on common groundsel at two sites in Alberta, Canada. Identification of the pathogen as *Puccinia lagenophorae* Cooke was based on host plant, macroscopic symptoms and fungal morphology, and on molecular characters. Infected plants with twisted stems and deformed leaves had aecia present (clusters of orange, cup-shaped pustules bordered by a recurved peridium), but not telia. ITS sequences determined from PCR products were identical for representative specimens from each location but had two areas of ambiguity in the ITS1 spacer region. Our data from cloned PCR products confirmed the presence of two ITS genotypes in each sample, one identical to a sequence published for the species from the United Kingdom and the other identical to a sequence from the United States. As far as we are aware, this is the first report of groundsel rust caused by *P. lagenophorae* in Canada. Groundsel rust occurs at several locations in the U.S. and was reported on more than 60 species in several genera. Questions remain about the amount of damage *P. lagenophorae* will cause to groundsel in North America and whether it might affect other related hosts.

P1-10. Development of *in vitro* inoculation protocols for turfgrass diseases. A.M. Cortes and T. Hsiang. *Department of Environmental Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Turfgrasses are affected by numerous fungal diseases, and because of low aesthetic tolerance for symptomatic plants in amenity turfgrasses, extensive efforts are made to manage diseases. In vitro disease assessments could facilitate observations of the interaction between host and pathogen, and allow for more precise control over specific conditions required to produce disease than in the field. In this study, in vitro inoculation protocols were developed for the turfgrass diseases caused by *Rhizoctonia solani* (Kühn), *Sclerotinia homoeocarpa* (Bennett), *Microdochium nivale* (Fr.) Samuels & Hallett, *Magnaporthe grisea* (Hebert) Barr, *Colletotrichum graminicola* (Ces) Wilson and *Pythium aphanidermatum* (Edson) Fitzp. Different inoculum growth media and concentrations, and incubation conditions were tested. Two grass species, *Agrostis stolonifera* L. and *Lolium perenne* L., were grown for 2 to 3 wk in 6-well plates (3.5 cm wide by 1.8 cm deep) containing 1 cm of sand. The grass was inoculated with conidia from *C. graminicola* grown on NaCl-sucrose-yeast extract agar media or mycelium of *M. nivale* grown in malt broth or plugs of *R. solani* or *S. homoeocarpa* grown on oatflakes agar, or *P. aphanidermatum* grown on V8 agar. All inoculated plants were incubated at room temperature (23°C) except for *M. nivale* which was incubated at 15°C. These conditions were found to produce the highest disease severity among conditions tested.

P1-11. Germination of ascospores of *Gibberella zeae* after exposure to various levels of relative humidity and temperature. J. Gilbert, S.M. Woods, and U. Kromer. *Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada.*

Fusarium head blight (FHB) is the most important cereal disease in Canada, and has caused major losses to the grain industry. The principal pathogen causing FHB in North America is *Fusarium graminearum* Schwabe (teleomorph *Gibberella zeae* [Schwein.] Petch). Disease forecasting systems are being developed that enable more effective use of fungicides. How long ascospores survive and the conditions under which they remain viable once released from perithecia are poorly understood. This study sought to determine the germination of ascospores after exposure to different relative humidities (RH) and temperatures. Ascospores were recovered from lids of Petri dishes, where they adhered in condensation droplets, within 24 hours of being released from perithecia. Humidity

chambers were created using the salts $MgCl_2 \cdot 6H_2O$, $NaBr \cdot 2H_2O$[5], and KNO_3[11] to provide RH levels of 33%, 59% and 93.5%, respectively at 15, 20, and 30°C for 24 and 48 hour periods. Viability was tested by germination on water agar. Germination rates fell with increasing temperatures at both times and at all humidity levels. After 48 hours, germination at 15°C and 20°C ranged from 74% to 85%, and 52% to 72% respectively. At 30°C germination ranged from 36% to 59% after 24 hours and from 13% to 47% after 48 hours. Germination was highest at 93.5% RH and lowest at 59% RH. Successful germination, even under these extreme conditions, suggests that ascospores are sufficiently robust to constitute potential sources of inoculum under most environmental conditions encountered during the growing season.

P1-12. Comparison of *ToxA* and *ToxB* genes of *Pyrenophora tritici-repentis* isolates among different races from different geographic regions of the world. M. Miyamoto, G.M. Ballance, and L. Lamari. *Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB R3T 2N2, Canada.*

Pyrenophora tritici-repentis (Died.) Drechs is the causal agent of the foliar leaf spot disease of wheat (*Triticum aestivum* L.) known as tan spot and isolates of this pathogen are found in all areas where wheat is grown. The principal disease symptoms of this disease, tan necrosis, chlorosis and extensive chlorosis, are the result of three independent genetic loci of which genes for *ToxA* (responsible for tan necrosis) and *ToxB* (responsible for extensive chlorosis) have been extensively characterized. Currently eight distinct races of the pathogen have been identified. Expression of *ToxA* occurs in races 1, 2, 7 and 8 while expression of *ToxB* occurs in races 5, 6, 7 and 8. The occurrence of the *ToxA* and *ToxB* genes and the similarity within each gene were examined by PCR, Southern blotting and sequencing using 133 isolates from around the world. The *ToxA* gene was found to be highly conserved in gene copy number and in sequence across all races and regions tested. The *ToxB* gene was variable in copy number within and across races but data suggests the sequences are largely conserved.

P1-13. Seeding date influences the incidence and severity of clubroot on Shanghai pak choy and flowering edible rape in Ontario. M.R. McDonald, S.M. Westerveld, B. Kornatowska, and A.W. McKeown. *Crop Science Building, Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada; and (S.M.W. & A.W.M.) Simcoe Research Station, Department of Plant Agriculture, University of Guelph, P.O. Box 583, 1283 Blueline Road, Simcoe, ON N3Y 4N5, Canada.*

Shanghai pak choy (*Brassica rapa* L. subsp. *chinensis* (Rupr.) var. *communis* Tsen and Lee) and flowering edible rape (*B. rapa* L. subsp. *chinensis* (Rupr.) var. *utilis* Tsen and Lee) were seeded into organic soil naturally infested with the clubroot pathogen (*Plasmodiophora brassicae* Woronin) at the University of Guelph Muck Crops Research Station in May, June, July, and August of 2000 and 2001. At harvest, the incidence and disease severity index (DSI) of clubroot were assessed. Data from 18 trial years at the research station were used to compare disease incidence and DSI with weather conditions during crop development. Clubroot incidence and DSI were highest for crops seeded in June and July and lowest for the August seeding. Mean air temperatures during crop development ranged from 15 to 22°C and were positively correlated with disease incidence and DSI for both Shanghai pak choy (r=0.68) and flowering edible rape (r=0.73). Clubroot damage can be avoided by early spring and late summer seeding of these crops.

P1-14. Epidemiological value of Ptr ToxA and Ptr ToxB in tan spot of wheat. M. Rezaey and L. Lamari. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*

The epidemiological value of Ptr ToxA and Ptr ToxB, the host-selective toxin(s) of *Pyrenophora tritici-repentis*, was studied on seven Canadian cultivars. Six susceptible and one resistant wheat cultivars (five hexaploid and two tetraploid wheats) were inoculated with a pathogen population consisting of a mixture of isolates from the eight known races of the pathogen (one isolate/race). New pathogen generations were constructed by mixing 80-150 single-spore isolates obtained from individual lesions. These populations were inoculated to produce the next generation. In this study, four consecutive generations were constructed, and the population structure at second and fourth generations was determined by PCR (TOXA and TOXB primers), using 30 single-spore cultures. Ptr ToxA-producing isolates were dominant on all the hexaploid and one tetraploid (4B160) wheat cultivars, followed by isolates that produce both Ptr ToxA and Ptr ToxB. Ptr ToxB-producing isolates, which are not part of the Canadian pathogen population, survived on all the major wheat cultivars grown in western Canada over the past century and included in this study. This suggests that Ptr ToxB-producing isolates would have been a threat to wheat production if they were part of pathogen population. The production of Ptr ToxA and/or Ptr ToxB appears to confer a competitive advantage to the producing isolates, as determined by population shifts over four generations.

P1-15. Reduction of potato scab with acidified liquid swine manure soil amendment. K.L. Conn and G. Lazarovits. *Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, 1391 Sandford Street, London, ON N5V 4T3, Canada.*

Common scab [*Streptomyces scabies* (Thaxter) Lambert & Loria] severity can be reduced by the volatile fatty acids present in liquid swine manure (LSM) when added to soils at pH <6. In order to increase the efficacy of LSM in pH 6-8 soils we added LSM plus sulfuric acid (H_2SO_4) to

temporarily lower soil pH. In a micro-plot study started in 2004, treatments included 98% H_2SO_4 (950-4800 L/ha), LSM (55 hL/ha), and LSM plus H_2SO_4 added to soils (pH 5.2-6.9) collected from eight commercial potato fields. The aim was to lower the pH to 4.4. Potatoes were planted in 2004, 2005, and 2006 without further addition of amendments. In 2004, identical treatments were applied to soil (pH 6.9) in a commercial potato field where potatoes were grown for 2 years without any further amendment. In 2005, an experiment was set up in the same potato field with H_2SO_4 treatments that reduced soil pH to 5.8 and 4.6 and LSM plus H_2SO_4 treatments reducing soil pH to 6.2 and 5.5. Soils where treatments reduced the pH to below 5 did not rebound to control levels until the second or third year, depending upon the soil. In such instances the H_2SO_4 and the LSM plus H_2SO_4 treatments both reduced scab severity to near zero levels in the year of application in all soils tested. By the third year, scab severity had returned to 40-100% of the levels found in control treatments for all acid and LSM plus acid treatments. For treatments in the field where soil pH was reduced to 5.5-5.8, only the LSM plus acid treatment, not the acid alone treatment, reduced scab severity. Thus, reducing soil pH to below 6 when combined with LSM can reduce scab severity in a broader range of soils. However, this may not be practical for soils where the pH is high and the soil is well buffered. Lowering soil pH to below 5 reduces yields and it takes longer for the soil to return to pretreatment pH levels. A pH range of 5 to 6 is a better target as it reduces disease but does not lower yield and requires less acid.

P1-16. Infection process of *Stenocarpella macrospora* on leaves of maize (*Zea mays* L.). I.I. Idikwu, S.R. Gowen, and A.N. Jama. *School of Agriculture, Policy and Development, University of Reading, Earley Gate, P.O. Box 236, Reading, RG6 6AR, UK.*

Stenocarpella leaf spot is one of the major constraints to maize production in Nigeria, resulting in considerable yield losses and contamination of grains with mycotoxins which may affect man and livestock. Light microscopy was used to study germination, penetration and infection of the fungus on the host. Plants were cultivated in a glasshouse at the University of Reading. Leaves were removed at the four to five leaf stage, cut into discs and inoculated with conidial suspensions of the pathogen (10^5 conidia ml^{-1}). Conidia began to germinate 3-6 h after inoculation, germ tubes emerged from apical and/or lateral parts of the conidium. Maximum germination (85-90%) occurred by 24-48 h at 20-25°C, and minimum (20-25%) by 12-18 h at 35°C. Penetration occurred directly through the cuticle, epidermal cell wall and through the stomata, causing infections on both upper and lower surfaces of leaves. Infection of the upper surface was significantly higher than on the lower surface. Formation of pycnidia bearing spores 12 days after inoculations suggested completion of the infection process.

P1-17. Evaluation of resistance of elite wheat germplasm from the northern Great Plains of North America to septoria diseases of wheat. P.K. Singh, M. Mergoum, S. Ali, and T.B. Adhikari. *Department of Plant Sciences, North Dakota State University, Fargo, ND 58105, USA; and (S.A. & T.B.A.) Department of Plant Pathology, North Dakota State University, Fargo, ND 58105, USA.*

Stagonospora nodorum blotch (SNB) caused by *Phaeosphaeria nodorum* (E. Müller) Hedjarroud and Septoria tritici blotch (STB) caused by *Mycosphaerella graminicola* (Fückl) J. Schröt. in Cohn form the major components of Septoria disease complex of wheat in North America. This study was conducted to determine the disease reaction of 126 elite hard red spring, white, and durum wheat cultivars and advanced breeding lines collected from the northern Great Plains of USA and Canada to SNB and STB. Seedling evaluation of the 126 genotypes was done under controlled environmental conditions with *P. nodorum* isolate Sn2000 and *M. graminicola* isolate Ma04-9-4. Additionally, the 126 genotypes were also infiltrated with culture filtrate of *P. nodorum* isolate Sn2000. Based on disease reactions, three cultivars and twelve advanced breeding lines adapted to the northern Great Plains were found to be resistant to both the pathogens and insensitive to the culture filtrate tested. Additionally, eight genetically diverse lines/ cultivars, including two tetraploid wheats, were identified to be resistant to Septoria diseases. These results suggest that the wheat germplasm contains a broad genetic base for resistance to the Septoria diseases in the northern Great Plains of the USA and Canada and the resistant sources identified in this study may be utilized in wheat breeding programs to develop resistant cultivars to the Septoria diseases.

P1-18. Development of simple sequence repeat markers for the genetic analysis of wheat leaf rust (*Puccinia triticina* Eriks.). X. Wang, G. Bakkeren, and B.D. McCallum. *Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada; and (G.B.) Pacific Agri-Food Research Centre, 4200 Highway 97, Summerland, BC V0H 1Z0, Canada.*

Leaf rust (*Puccinia triticina* Eriks.) is an important foliar pathogen on wheat worldwide, causing significant grain yield loss in the Canadian prairies. Various molecular marker such as random amplified polymorphic DNA (RAPD) and amplified fragment length polymorphic DNA (AFLP) have been used to characterize the molecular diversity in populations of *P. triticina*. But these are dominant markers. Codominant sequence-specific microsatellite markers are more powerful and can be very useful in population biology and the genetic study of *P. triticina*. 152 sequences containing simple sequence repeats (repeat number larger than six) were identified from 4484 *P. triticina* EST sequences. PCR primers were designed to amplify the flanking regions. 75 EST

sequences successfully amplified fragments of appropriate size. The polymorphism of these potential SSR loci was then evaluated on 40 *P. triticina* isolates and 19 loci were found to be polymorphic among the isolates tested. The majority of the isolates were heterozygous at polymorphic loci suggesting a high degree of heterozygosity.

P1-19. Agronomic and economic implications of the wheat stem sawfly resurgence for wheat production on the southern prairies of Canada. B.L. Beres, H.A. Cárcamo, and J.R. Byers. *Agriculture and Agri-Food Canada, Lethbridge Research Centre, P.O. Box 3000, Lethbridge, AB T1J 4B1, Canada.*

The wheat stem sawfly *Cephus cinctus* Norton (Hymenoptera:Cephidae) has reached outbreak status at most locations in the southern Canadian prairies. Solid-stemmed cultivars, which are less susceptible to damage, remain the primary management option. This paper quantifies the effect of wheat stem sawfly damage on grain yield and quality at harvest, and determines how cultivar selection affects harvest losses. Solid-stemmed cultivars were compared to hollow-stemmed cultivars and to blends of a 1:1 ratio of each. The hollow-stemmed cultivars with the exception of 'McKenzie', which had intermediate levels of stem cutting, were all significantly more susceptible to stem cutting than solid-stemmed cultivars. Cultivar blends had lower damage but were still significantly higher than the solid-stemmed cultivars. The solid-stemmed cultivars 'AC Eatonia' and 'AC Abbey' had the lowest levels of stem cutting and ranked second and third overall for yield in 2001 and 2002. 'McKenzie' ranked first, which reflects its yield potential in combination with its partial resistance to stem cutting. Lower cutting in 'AC Eatonia', 'AC Abbey', 'McKenzie', and the blend of 'AC Abbey' / 'McKenzie' was significantly correlated with lower grain losses. Grain lost at harvest has major economic implications if sawfly pressure is moderate to high, and susceptible cultivars predominate.

P1-20. A new stem rust resistance gene in barley derived from *Hordeum bulbosum*. T. Fetch Jr. and R. Pickering. *Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada; and (R.P.) Crop and Food Research, Lincoln, New Zealand.*

Stem rust of barley (*Hordeum vulgare*), caused by *Puccinia graminis* f. sp. *tritici*, has been controlled since the mid-1950's through the use of resistance gene *Rpg1* in resistant cultivars. In 1988, a race (QCC) with virulence to *Rpg1* was described. The only known resistance gene in barley with resistance to QCC is *rpg4*, thus research to find new resistance was undertaken. Barley lines with introgressions of *Hordeum bulbosum* chromatin were developed at the Crop and Food Research Institute in Lincoln, New Zealand and evaluated for resistance to races QCC and MCC. Line 212Y1 was found to express seedling resistance to both races. Allelism tests to the source line of *rpg4* found that the genes segregated independently. Crosses were made to the cultivar 'Morex' that has *Rpg1*, and progeny evaluted with both races QCC and MCC. Results indicated a single recessive gene conferred resistance to QCC, and two genes (*Rpg1* and the recessive gene) conferred resistance to MCC. It is proposed to designate this new recessive gene from Hordeum bulbosum as *rpg6*, which may be useful as a different source of resistance to stem rust race QCC.

P1-21. Cultivar response and seed treatments of seedling blight and root rot of faba bean in Alberta. K.F. Chang, S.F. Hwang, G.D. Turnbull, R. Bowness, D.J. Bing, and S.E. Strelkov. *Field Crop Development Centre, Alberta Agriculture and Food (AAF), 6000 C&E Trail, Lacombe, AB T4L 1W1, Canada; (S.F.H. & G.D.T.) Crop Diversification Centre North, AAF, 17507 Fort Road, Edmonton, AB T5Y 6H3, Canada; (D.J.B.) Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C&E Trail, Lacombe, AB T4L 1W1, Canada; and (S.E.S.) Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.*

Root rot of faba bean (*Vicia faba* L.) caused by *Fusarium* spp. is common in Alberta. Forty-nine isolates were collected from diseased roots at four locations. A third of the isolates showed strong virulence to faba bean, causing pre-emergence damping-off. Field trials to assess the impact of three fungicide seed treatments [Thiram; metalaxyl-M + fludioxonil (Apron Maxx); carbathiin + thiram (Vitaflo 280)] on seedling blight were established at Lacombe and Vegreville, AB in 2004 and 2005. Inoculation with *Fusarium avenaceum* (Corda ex Fries) Sacc. reduced seedling emergence and seed yield, compared to the noninoculated control. Both Vitaflo 280 and Apron Maxx improved seedling establishment relative to the nontreated control in treatments inoculated with *F. avenaceum*. In inoculated treatments at Lacombe and Vegreville, seed emergence rate and yield for Apron Maxx and Vitaflo 280 was higher than the nontreated control in both years. To screen cultivars or lines for resistance to fusarium root rot, 12 genotypes were tested under field conditions at Lacombe in 2006. Inoculation significantly reduced seed emergence rate and yield in all genotypes except the cvs Ben and Scirocco, as compared to the control treatment. The cultivar Ben showed highest emergence rate and yield in both the inoculated and control treatments, while the line Faba 214 showed the highest susceptibility to the pathogen. Application of fungicide seed treatments and planting of resistant cultivars or lines can effectively increase stand establishment of faba bean.

P1-22. Differences in cavity spot severity among carrots with different pigments. M.R. McDonald, K. Vander Kooi, and P.W. Simon. *University of Guelph, Department of Plant Agriculture, Guelph, ON N1G 2W1, Canada; and*

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Cavity spot of carrot, caused by *Pythium sulcatum* (Pratt and Mitchell), *P. violae* (Chesters & C.J. Hickman) and other *Pythium* spp., results in dark lesions on the surface of the carrot root. Field trials were conducted in the Holland/Bradford Marsh region of Ontario, from 2002–2006, to determine if pigmentation in carrots was related to susceptibility to cavity spot. White, yellow, dark orange, red and purple carrot breeding lines from the USDA breeding program at the University of Wisconsin were seeded in muck soil (pH 6.4–7.2, 39–60% organic matter) in late May, harvested in late October and assessed for disease in early December each year. In 2005 and 2006 commercial cultivars of coloured carrots were included in the trial. Disease severity was moderate in 2002, 2003 and 2005 (21, 22, 24%), high in 2004 (44%) and highest in 2006 (58%). Cavity spot severity was lowest in the purple carrot line, higher but similar in the yellow and white lines, and highest in the red line. Cultivar 'Atomic Red' was very susceptible to cavity spot, while purple cultivar 'Purple Haze' was the most resistant. Susceptibility to cavity spot was consistent among the breeding lines, but when breeding lines and cultivars were compared, pigmentation alone did not determine disease reaction.

P1-23. Phytoplasma diseases in Canadian vineyards. C. Olivier, T. Lowery, L. Stobbs, B. Galka, L. Bittner, and T. Vickers. *Saskatoon Research Centre, Agriculture and Agri-Food Canada (AAFC), 107 Science Place, Saskatoon, SK S7N 0X2, Canada; (T.L.) Summerland Research Centre, AAFC, Highway 97, Summerland, BC V0H 1Z0, Canada; and (L.S., L.B. & T.V.) Vineland Research Station, AAFC, 4902 Victoria Ave. N., Vineland, ON L0R 2E0, Canada.*

Grapevine yellows (GY) of *Vitis vinifera* is caused primarily by phytoplasmas. Phytoplasmas multiply in phloem tissue and are transmitted by phloem feeding insects, mainly leafhoppers. They are graft-transmissible, but have never been cultured *in vitro*. Each year, the Canadian grape industry imports a large number of grafted vines from France and Germany, where two devastating phytoplasma diseases of grapes, flavescence dorée (FD) and bois noir (BN), are spreading despite strong compulsory control measures. BN has recently been detected in vineyards in British Columbia and there is concern that FD might already be present in Canada. In response, a survey for GY in vineyards in Ontario and British Columbia was conducted in the summer of 2006. Insects and plants were sampled and tested for the presence of phytoplasma using PCR. FD and BN were not found in the survey. The detection of aster yellows phytoplasma and the distribution of the infected plants and insects in the vineyards are discussed.

P1-24. Managing carrot density helps control Sclerotinia rot in carrots. K.R. Sanderson and R.D. Peters. *Crops and Livestock Research Centre, Agriculture and Agri-Food Canada, 440 University Ave., Charlottetown, PE C1A 4N6, Canada.*

Sclerotinia rot in carrots (SRC) is a devastating disease caused by *Sclerotinia sclerotiorum*. SRC is especially important where fresh pack carrots are grown for winter storage. The disease develops within the carrot canopy when lack of sunlight and airflow fails to keep foliage dry. In 2005 and 2006, we seeded carrots (cv. Neptune) to investigate the impact of seeding rate (46, 59, 82, 95 and 112 seeds m^{-1}) and canopy trimming (not trimmed and trimmed) on SRC development. Marketable yield was not affected by seeding rate, however, trimming reduced yield in 2005. In 2006, both trimming and the reduction in seeding rate resulted in a lower number of diseased petioles recorded in the field. In storage, SRC was significantly less in carrots from both trimmed plots and those with lower seeding rates. Treatments did not affect the number of diseased petioles observed in the field or carrots infected in storage in 2005. Field conditions were more favorable for the development of SRC in 2006 versus 2005. Results indicate that reducing the canopy by managing carrot seeding rate and trimming may reduce SRC both in the field and in winter storage.

P1-25. Pathogenic and genetic diversity of *Didymella rabiei* isolates from southern Alberta, Canada. S.F. Hwang, K.F. Chang, H.U. Ahmed, A.-H. Khadhair, S.E. Strelkov, and G.D. Turnbull. *Crop Diversification Centre North, Alberta Agriculture and Food (AAF), Edmonton, AB T5Y 6H3, Canada; (K.F.C. & H.U.A.) Field Crop Development Centre, AAF, Lacombe, AB T4L 1W8, Canada; and (A.H.K. & S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.*

Sixty-three isolates of *Didymella rabiei* collected from southern Alberta were analyzed for pathogenic variability, using six differential chickpea genotypes. All isolates were pathogenic on all of the differentials, although they varied in virulence. Based on the reaction of the host genotypes, the isolates were grouped into 25 pathotypes, suggesting a very high level of diversity in the pathogen population. Two pathotypes were predominant, with each comprising 14% of the total isolates. Cluster analysis generated two main groups, at an average distance of 1.0 between the clusters. Fourteen sub-groups were identified among the isolates, at an average distance between isolates and within sub-groups of 0.5. No associations were found between geographical origins, pathotypes, cluster groupings, parts of the plants or the host genotype from which the isolates were obtained. Genetic diversity of 58 isolates was determined by RAPD analysis of genomic DNA using six primers. A dendrogram was constructed to establish the genetic relationship and distance between isolates. All of the isolates were found to belong to five genotypes in a phylogenetic tree. The genetic diversity among the polymorphic loci of these isolates was 47%, based on the

pattern of the bands in the binary form matrix. No relationship was found between the pathotype designations and the groupings obtained by RAPD analysis.

P1-26. Challenges in the identification of the causal pathogen of stripe rusts. M. Liu, R. Tropiano, E. McCabe, J. Bergeron, and S. Hambleton. *Biodiversity (Mycology and Botany), Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada*.
Stripe rust of grasses is caused by *Puccinia striiformis* West. The symptoms of the disease are yellow chlorotic streaks composed of elongated uredial pustules in rows, and these symptoms are often used to identify the pathogen. To study the relationships between *P. striiformis* and closely allied species, we located multiple specimens of *P. striiformis* in five herbaria (BP, BR, HMAS, K, & PUR), extracted DNA, then amplified and sequenced rDNA regions. DNA sequence analyses revealed that the specimens identified as *P. striiformis* did not form a monophyletic group. Individual collections grouped with *P. coronata*, *P. hordei*, and *P. recondita*. The results cast doubt about the identification of these specimens. Microscopic examination of six specimens identified as *P. striifomis* but grouping in the *P. coronata* clade revealed telia and teliospores of *P. coronata* in one specimen, indicating possible misidentification. As for the *P. striifomis* specimens in other clades, i.e. *P. hordei* and *P. recondita*, given that morphologically, *P. striiformis* is similar to *P. hordei* and *P. recondita*, it is also likely those *P. striiformis* have been misidentified. The plasticity of morphological characters within species and overlap among species provides challenges for correctly identifying *P. striiformis*. Thus, DNA based techniques for identification would be a useful development.

P1-27. Development and epidemiology of tar spot of maple in southern Ontario. X.L. Tian and T. Hsiang. *Department of Environmental Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*
Tar spot of maple is caused by *Rhytisma acerinum* (Pers.) Fr. This disease was particularly abundant in 2006 across eastern North America with leaves of Norway maple (*Acer platanoides* L.) bearing multiple black spots. In southern Ontario, the early symptoms appeared in late June as small, round, light green, chlorotic spots, 2 mm across. Spots enlarged to 15 mm by mid-August, and developed black tar-like raised structures on the adaxial surface with a yellow margin. Conidia, which are considered non-infective and possibly spermatizing, appeared as a shiny layer on the black stroma. To examine the epidemiology of this disease, overwintered maple leaves were gathered weekly from multiple locations in southern Ontario from March through August 2006. These leaves were inspected for the presence of filiform ascospores, which initiate infections. After snowmelt in early spring, asci and paraphyses were visible in cross sections of the hysterothecia. Ascospores were first observed in early May. In early June, only 10% of the asci had fully discharged their spores. By the end of June, nearly all the asci were empty. The practical implication is that fungicide protection against tar spot, if necessary, needs only to be applied during a very short period, which begins at the end of full leaf expansion in Norway maple.

P1-28. Effect of mulch and bio-solid applications on the populations of both beneficial and pathogenic *Pythium* species in the root zone of apple. D.T. O'Gorman, G.H. Neilsen, J. Braumberger, and C.A. Lévesque. *Pacific Agriculture Research Centre, Agriculture and Agri-Food Canada (AAFC), Highway 97, Summerland, BC V0H 1Z0, Canada; and (C.A.L.) AAFC Eastern Cereal and Oilseed Research Centre, K.W. Neatby Bldg., 960 Carling Ave., Ottawa, ON K1A 0C6, Canada.*
Previously, a long term study had been conducted to examine the effects of five different mulches and bio-solid treatments on soil property, tree growth and fruit yield within apple orchards (Can. J. Soil Sci. 83:131-137). The plots containing randomized, replicated herbicide check, paper mulch, geotextile, Greater Vancouver Regional District (GVRD) bio-solids and GVRD bio-solids + paper mulch soil management treatments were maintained since tree planting in 1994. These plots were utilized in our present study initiated in 2005, to assess the population dynamics of *Pythium* species inhabiting the soil within the different treatments. A macro-array, developed to identify all known *Pythium* ex-type species (AEM 72:2691-2706) was used to test DNA extracted and amplified from soil taken at 0-15 cm depth from the different treatments. Diversity of *Pythium* spp. found within the different treatments showed the GVRD + paper mulch to have the highest number of individual species (33), while the geotextile soils had the lowest diversity with a moderate suppression of overall numbers (22). While the paper mulch and herbicide check possessed intermediate number species (28 and 29 respectively). *Pythium ultimum* Trow, a major pathogen of apple, was found to be present in soil in all the treatments, but its frequency was observed to be greatly reduced in soils under any treatment containing paper mulch. The treatments containing paper mulch also correlated with a general increase in plant health as well as an increased frequency of *P. oligandrum* Dreschler, a species reported to be a potential growth promoter and native bio-control organism.

P1-29. Persistence of recombinant plant DNA in the soil environment in corn/soybean rotations. R.H. Gulden, S. Lerat, M. Hart, J. Powell, R. Campbell, D. Levy-Booth, J.T. Trevors, K.P. Pauls, J.P. Klironomos, and C.J. Swanton. *Department of Plant Agriculture; (S.L. & J.T.T.) Department of Environmental Biology; (M.H., J.P. & J.P.K.) Department of Integrative Biology; and (D.L.-B.) Land Resource Science, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Genetically-modified (GM) corn and soybean currently comprise a large portion of the annual planted acreage of these crops. There are concerns regarding the possible uptake of plant recombinant DNA (rDNA) by soil microbes, yet little is known of the temporal and spatial distribution of plant rDNA in the soil environment. The objectives of this study were to determine the short-term temporal distribution and persistence of plant DNA in the soil environment in corn/soybean rotations with differing use intensity of herbicide-resistant GM technology. In three separate field experiments, soil was sampled four times each year (before seeding, after herbicide application, at maximum crop biomass, and after harvest). Total DNA was extracted from the soil samples using a modified commercial kit and the amount of corn or soybean rDNA was quantified using real-time polymerase chain reaction with specific primers and a molecular beacon. Corn and soybean rDNA can readily be detected in soil while plants are actively growing, however, our results indicate that persistence of plant rDNA after harvest is low. Nonetheless, small quantities of corn or soybean plant rDNA were still detected in some samples in the spring of the year following the respective crop. Even under continuous use of this technology, there is no indication of plant rDNA accumulation in the soil environment to date. The experiments are ongoing.

P1-30. Weed communities in glyphosate-resistant cropping systems in Ontario. R.H. Gulden, P.H. Sikkema, A. Hamill, F. Tardif, and C.J. Swanton. *Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada; and (A.H.) Agriculture and Agri-Food Canada, 2585 County Road 20, Harrow, ON N0R 1G0, Canada.*

Herbicide resistant crops are popular among producers and the availability of glyphosate-resistant genotypes in a number of crops allows for these to be grown in rotation. This can result in the reliance on a single herbicide for weed management. The long-term effects of high use intensities of this technology remain unknown. Corn and soybean, treated with glyphosate or conventional soil-residual herbicides, were grown in rotation with and without winter wheat for six years at five locations in Ontario in a fully-phased experiment. Of the five experiments, two were no-till, while the remaining three experiments were under conventional tillage management. Mid-season weed ground cover was rated and densities of each weed species were determined at this time. Treatment with glyphosate improved weed control in corn and soybean compared to conventional herbicide programs, but mid-season weed densities did not always agree with weed control ratings and may have been influenced by different recruitment patterns in the two tillage systems. Canonical discriminant analysis revealed different mid-season weed communities in the glyphosate-based systems compared to the conventional herbicide programs in corn and soybean. Weed communities in glyphosate treated corn and soybean tended to be more similar to each other than weed communities in corn and soybean treated with conventional herbicides. In comparison, the mid-season weed communities associated with winter wheat in the three year rotation tended to be distinctly different from those found in corn and soybean using either herbicide program.

P1-31. Sources of resistance against blackleg of canola caused by *Leptosphaeria maculans* PG3. M. Dusabenyagasani and W.G.D. Fernando. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*

Blackleg disease of canola (*Brassica napus* L.) caused by *Leptosphaeria maculans* (Desm.) Ces. & de Not, is an important disease in the Canadian prairies. *L. maculans* PG3 is one of the strains recently discovered in the Prairies but there is no resistance in the commercially available cultivars. The objectives of this work are to identify sources of resistance and develop marker-assisted-selection (MAS) tools. Sources of resistance were screened from the University of Manitoba *Brassica* germplasm and mapping populations produced by crossing Westar, a susceptible variety, with resistant parents. These populations were used to develop sequence related amplified polymorphic (SRAP) and sequence characterized amplified region (SCAR) markers. *Brassica napus* varieties Dunkeld and Quinta were resistant against PG3. F2 populations were obtained from Westar x Dunkeld and Westar x Quinta crosses. Resistance segregation ratio within the progeny was 3:1. Bulk segregant analysis and SRAP approaches were used to screen 180 primer combinations. A SRAP marker closely-linked to the resistance against PG3 strains was found in the variety Dunkeld. A SCAR marker was developed from that SRAP fragment using DNA sequencing and PCR. Segregation ratios of the SRAP and the SCAR markers were 3:1. This SCAR marker will be used for MAS of canola resistance against blackleg caused by *L. maculans* PG3.

P1-32. Chemotype shifting and gene flow of *Fusarium graminearum* in wheat fields in Manitoba. X.W. Guo, W.G.D. Fernando, and M. Seow. *Department of Plant Science*, *University of Manitoba, Winnipeg, MB R3T 2N2*, *Canada; and (M.S.) Department of Microbiology, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*

Fusarium graminearum Schwabe (*Gibberella zeae* Schwein.) Petch causes fusariun head blight disease in wheat worldwide. Two strain-specific profiles of trichothecene, 15-acetyl-deoxynivalenol (15ADON) and 3ADON chemotypes, were observed in *F. graminearum* in North America. 3ADON chemotype, the higher-level DON producer, is replacing 15ADON chemotype from eastern to western Canada, causing an increasing concern to food and feed industries. This study was to investigate the chemotype shifting, genetic diversity and gene flow of

F. graminearum. The study was conducted in 14-22 wheat fields across Manitoba from 2004 to 2006. Approximately 400 *F. graminearum* isolates were collected. Chemotype was identified using multiplex PCR markers with four primers targeting *Tri3* gene. Genotype was investigated using sequence-related amplified polymorphism (SRAP) technique. 15ADON chemotype was predominant in the northwest part of Manitoba, and 3ADON chemotype isolates were more prevalent in the southern part, indicating 3ADON chemotype is replacing 15ADON chemotype from southeast to northwest in southern Manitoba. 3ADON chemotype isolates increased in the same locations over years. Studies on genetic diversity and gene flow of *F. graminearum* in Manitoba are underway and will be reported at the conference.

P1-33. Sunflower rust races in Manitoba in 2003–2006. K.Y. Rashid. *Morden Research Station, Agriculture and Agri-Food Canada, Morden, MB R6M 1Y5, Canada.*
Sunflower rust, caused by *Puccinia helianthi* Schwein., is a common disease affecting sunflower (*Helianthus annuus* L.) in North America and worldwide. This pathogen completes its life cycle on sunflower with a high frequency of sexual recombination and the formation of new races. Local inoculum causes early disease development when environmental conditions are favorable for rust infection. The incidence and severity of rust vary across years and regions of sunflower production. Rust epidemics occurred in 1999 and 2003 in the North Central Plains, where up to 25% reductions in yield were estimated in southern Manitoba. Rust isolates were collected from Manitoba and Saskatchewan from 2003 to 2006, and the virulence was assessed on nine host-differential sunflower genotypes under controlled growth room conditions. Race-groups 300 and 700 were the most predominant in the region with several race variations within each group. Race-group 700 includes the races 726, 776, and 777, which are more virulent on sunflower than race-group 300 (326, 334, and 336). Presently, race-group 700 is at lower frequency than race-group 300 in the rust population on the Canadian Prairie. Race-groups 100 and 500 were at very low frequency in the rust population. Most commercial sunflower hybrids express various levels of resistance to race-groups 100 and 500, but are susceptible to race-groups 300 and 700.

P1-34. Effect of indole-acetic acid (IAA) on the development of symptoms caused by *Pythium ultimum* on tomato plants. V. Gravel, H. Antoun, and R.J. Tweddell. *Centre de recherche en horticulture, Université Laval, QC G1K 7P4, Canada.*
The effect of indole-acetic acid (IAA) on the development of symptoms caused by *Pythium ultimum* Trow on tomato plants was investigated using different bioassays. Application of IAA (5 µg ml^{-1}) on tomato seedlings inoculated with *P. ultimum* did not affect their emergence. However, IAA was shown to influence the development of *P. ultimum* symptoms on tomato plantlets. Low concentrations of IAA (0 to 0.1 µg ml^{-1}) within the rhizosphere of plantlets increased the overall negative effect of *P. ultimum* on plant development, while higher concentrations (10 µg ml^{-1}), applied either by drenching to the growing medium or by spraying on the shoot, reduced the damages caused by this pathogen. In addition, the study demonstrated that *P. ultimum* produces IAA in liquid culture amended with L-tryptophan, tryptamine or tryptophol (200 µg ml^{-1}) or in unamended culture.

P1-35. Variations among Canadian isolates of *Fusarium avenaceum* determined by phenotypes and vegetative compatibility, rDNA analyses, heat shock tolerance, and pathogenicity on wheat. P. Daida, L. Abdellatif, M. Fernandez, and V. Vujanovic. *Department of Applied Microbiology and Food Science, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; (M.F.) Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1030, Swift Current, SK S9H 3X2, Canada; and (V.V.) Department of Applied Microbiology and Food Science, and Agri-Food Innovation Fund Chair in Agric Microbiology and BioProducts, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.*
About 91 different isolates of *Fusarium avenaceum* were collected from various Saskatchewan and Canadian fields under wheat-pulses-canola rotation system. The isolates were regrouped into 15 phenotypes, 10 VCGs (vegetative compatibility group) and 8 ITS (internal transcribed spacers) rDNA groups, which ranged from highly pathogenic to non-pathogenic on wheat plants during seed germination. Highly pathogenic and moderately pathogenic Saskatchewan isolates showed more adaptability in colonizing a broad range of hosts and geographical regions compared to non-pathogenic isolates had a relatively restrained distribution. Considerable variability in heat tolerance between isolates was observed and measured by assessing physiological change and colony growth alteration. Clustering analyses confirmed the presence of the cluster-A isolates had low heat tolerance and the cluster-B isolates showed very high temperature (80°C) tolerance for over four hours. Phylogenetic profile obtained from ITS rDNA sequences, PCR-DGGE fingerprinting profile of EF-alfa gene, and vegetative incompatibility analyses using nitrate non-utilizing mutants displayed considerable variation among *F. avenaceum* isolates.

P1-36. New plant growth-promoting fungal endophytes reprogram wheat and provide disease resistance. L. Abdellatif, S. Bouzid, and V. Vujanovic. *Department of Applied Microbiology and Food Science, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; (S.B.) Department of Biology, Faculty of Sciences, University Tunis El Manar, Tunisia; and (V.V.) Agri-Food Innovation Fund Chair in*

Agric Microbiology and BioProducts, and Department of Applied Microbiology and Food Science, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.

The world's environmental and energetic crisis urges microbial biotech science to find solutions to reduce the usage of pesticides, while enhancing plant biomass production for biofuels. The endophytic fungi discovered by our laboratory seem promising solution on this matter and in response to raising demands. In this research study, more than 50 endophytic fungal (EF) candidates were selected from AFIF (Agri-Food Innovation Fund) Chair's Microbial Biotechnology Collection (University of Saskatchewan) and analyzed for their biological activity against *F. graminearum* and *F. avenaceum* pathogens, as well as for their ability to enhance wheat growth. *In-vitro* and greenhouse bioassays revealed 18 EFs exhibiting both inductions of Plant Growth Promoting (PGP) and Systemic Acquired Resistance (SAR) by localized root infections in plants. Molecular, proteomic and microscopic studies are underway to better characterize the EF-plant interactions and mechanism of "endophytism" leading to disease reduction and increasing yield in crop plants.

P1-37. Subcellular localization of the tomato verticillium wilt resistance gene *Ve2* protein. L. Kawchuk, N. Ruthardt, R. Fischer, and N. Emans. *Lethbridge Research Centre, Agriculture and Agri-Food Canada, P.O. Box 3000, Lethbridge, AB T1J 4B1, Canada; and (N.R., R.F. & N.E.) Institute for Molecular Biotechnology (Biology VII), RWTH Aachen, Worringerweg 1, 52074 Aachen, Germany.*

Positional cloning of *Ve* revealed *Ve1* and *Ve2*, two closely linked inverted genes from tomato independently conferring resistance against verticillium wilt, a common fungal disease. The amino acid sequences of the two genes display structural domains reminiscent of cell-surface receptors. The cytosolic domain of *Ve2* displays a YXXϕ motif commonly involved in receptor-mediated endocytosis. In addition, *Ve2* concludes with the residues KKF, similar to the KKX motif that signals endoplasmic reticulum retention in mammalian and plant cells. To define the subcellular localization and study possible endocytic dynamics of the *Ve2* protein, we generated fusions of *Ve2* and a *Ve2* mutant with altered YXXϕ signal sequence to GFP for expression in tobacco BY-2 suspension cells and tobacco plants. Fluorescence microscopical analysis revealed localization of both fusion proteins exclusively within the ER. Additional constructs with removed terminal KKF residues in the GFP fusion also appeared in the golgi after expression in tobacco cells. These results indicate that the *Ve2* protein is predominantly located in the ER.

P1-38. Inheritance of stem rust resistance in 'Ronald' and 'AC Gwen' oat. J.W. Mitchell Fetch, T. Fetch Jr., and J. Gold-Steinberg. *Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada.*

Knowledge of resistance genes in cultivars is invaluable for their effective deployment. In Canadian oat cultivars, oat stem rust (OSR) resistance genes *Pg1*, *Pg2*, *Pg4*, *Pg9*, and *Pg13* have been utilized. Inheritance of resistance in cultivars 'Ronald' and 'AC Gwen' was investigated through crosses to 'Triple Crown' (OSR susceptible). Five randomly chosen F_1 seeds were selfed to produce F_2 seed. Two random F_2 populations from each cross were inoculated with race NA1. Pooled data fit a 13 resistant: 3 susceptible ratio for 'Ronald' (X^2=0.011, p=0.9165) and 'AC Gwen' (X^2=3.82, p=0.0506). Progeny were selfed to produce F_3 families, which were individually inoculated with races NA1, NA8, and NA30. Resulting data fit a ratio of 7 HR:8 Segregating:1 HS when inoculated with NA1, indicating two genes (1 dominant, 1 recessive) are present in both 'Ronald' and 'AC Gwen'. Each population and pooled data fit a ratio of 1HR:2 Segregating:1 HS when inoculated with NA30 or NA8. Segregating families fit a 1R:3S ratio for NA30 and a 3R:1S ratio for NA8. This indicates that genes *Pg13* (recessive, resistant to NA30 and NA1) and *Pg2* (dominant, resistant to NA8 and NA1) are present in both 'Ronald' and 'AC Gwen'. This combination confers resistance to most North American OSR races except NA67, which is currently predominant in the OSR population in western Canada.

P1-39. A PCR-DGGE procedure to assess the biodiversity of *Fusarium* species in semiarid Saskatchewan durum wheat fields following pulses and canola crops. D. Mavragani, C. Hamel, and V. Vujanovic. *Department of Applied Microbiology and Food Science, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; (C.H.) Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1030, Swift Current, SK S9H 3X2, Canada; and (V.V.) Department of Applied Microbiology and Food Science, and Agri-Food Innovation Fund Chair in Agric Microbiology and BioProducts, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.*

Members of the fungal genus *Gibberella* (teleomorph) / *Fusarium* (anamorph) are among the most potent plant pathogens throughout the world, causing FHB (Fusarium Head Blight) and FDK (Fusarium Damaged Kernels) on cereals. Hence, the objective of this study was to evaluate *Fusarium*'s biodiversity in semi-arid Saskatchewan durum wheat fields by using a PCR-DGGE procedure. For this purpose, suitable DGGE markers for fungal species recognition were developed, and PCR-DGGE fingerprinting method was tested. Major findings with regard to *Fusarium* biodiversity in wheat fields revealed the presence of different *Fusarium* taxa: *F. avenaceum*, *F. arthrosporoides*, *F. poae*, *F. graminearum*, *F. equiseti*, *F. flocciferum*, *F. reticulatum*, *F. torulosum*, *F. tricinctum*, and *F. sporotrichioides*. As an overall conclusion, the

PCR-DGGE approach allowed the differentiation between the *Fusarium* species and successful monitoring in fluctuation of *Fusarium* populations in natural samples. Also, this culture-independent DGGE method demonstrates efficiency for the FHB and FDK risks assessment.

P1-40. Development of bioassays for the screening of toxin(s) produced by *Verticillium dahliae*. S. Pu, M. Duchscher, A.F. El-Bebany, H. Alkher, L.R. Adam, A. El Hadrami, and F. Daayf. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*
Verticillium dahliae Kleb. is a soilborne pathogen and the primary cause for Verticillium wilt in many crops. It causes serious economic losses in herbaceous annuals, perennials, and woody plant species under various climates. Plants affected by this disease exhibit symptoms ranging from chlorosis to necrosis of the leaves, wilting as well as a brown discoloration of the vascular system. Former studies suggested that *V. dahliae* releases toxin(s) into the plant host tissues. In the present study, we first investigated whether or not *V. dahliae* produces toxin(s) in artificial media then determined if this/these toxin(s) is/are constitutively or exclusively produced upon induction by components from the host plant. In a second step, we examined the effects of these toxic fractions using a series of bioassays and determined their host-specificity. Filtrates of the fungus grown on two artificial media were produced *in vitro* in presence and in absence of host root extracts, concentrated, purified and applied to either whole seedlings or various plant sections from different host plants. Infiltration of these purified filtrates into a range of host plant seedlings led to typical Verticillium wilt symptoms. Examination of the effect of these filtrates on different sections of the plant tissues showed a characteristic vascular discoloration similar to that produced by the fungus on host plants. A series of analyses will be carried out to investigate the nature of the toxin(s) produced by two isolates exhibiting various levels of pathogenicity and their effect on selected host plants.

P1-41. Development of a SNP based marker system based on variable microsatellite flanking regions for *Phytophthora infestans*. C.T. Lewis, C.L. Abbott, J. Chapados, R.D. Peters, H.W. Platt, M.D. Coffey, and C.A. Lévesque. *Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (C.L.A.) Pacific Biological Station, Fisheries and Oceans Canada, 3190 Hammond Bay Road, Nanaimo, BC V9T 6N7, Canada; (R.D.P. & H.W.P.) Crops and Livestock Research Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PE C1A 4N6, Canada; and (M.D.C.) University of California Riverside, Department of Plant Pathology and Microbiology, 3206 Webber Hall, Riverside, CA 92951, USA.*
Since the introduction of the A2 strain in Europe and North America, population genetics and strain typing of *Phytophthora infestans* (Mont.) de Bary are important components of research on epidemiology and disease management. The ideal genetic marker system for intraspecific analyses provides a high degree of resolution and is applicable to processing a large number of samples. Single nucleotide polymorphisms (SNPs) offer advantages over frequently used microsatellite markers for population- and individual-level analyses and are amenable to high-throughput chip-based approaches, though finding enough markers to characterize populations is often problematic. This study tested a SNP discovery technique involving mining of the public domain genome sequence data of *P. infestans* for SNPs in microsatellite flanking regions (MFRs). MFRs are located immediately adjacent to microsatellite repeat arrays and contain point and length mutations; however, they have rarely been targeted as sources of molecular markers. A bioinformatics pipeline was developed to identify all unique MFRs in the genome sequence and filter out those containing internal duplication. The list of remaining loci was manually refined to provide a set of 95 loci. MFRs around longer repeats were preferentially selected and the number of MFRs around trinucleotide repeats was restricted. The primer pairs were PCR tested using two *P. infestans* strains, and 60 produced strong, single PCR bands of the expected size, from which 35 provided good quality sequences without further optimization. A panel of *P. infestans* strains is currently being screened to fully assess marker variability.

P1-42. *WITHDRAWN*

P1-43. Effects of canola nutrient regimes on the performance of the herbivore diamondback moth and its parasitoid. R.M. Sarfraz, L.M. Dosdall, and B.A. Keddie. *Department of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9, Canada; and (L.M.D.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.*
Soil fertility can have great importance for developing and implementing integrated crop management practices, yet soil nutrients are usually not considered beyond their effects on host plants. In this study, we manipulated soil fertility regime to investigate bottom-up effects on canola plants, *Brassica napus*, and in turn on the important canola herbivore, the diamondback moth, *Plutella xylostella*, and its parasitoid *Diadegma insulare*. Different fertilizer applications significantly affected the nutrient contents of *B. napus* foliage, and this in turn affected host preferences and performance of *P. xylostella* as well as *D. insulare*. Female *P. xylostella* discriminated among host plants subjected to different levels of soil fertility for oviposition, and tended to select plants on which pre-imaginal survival and development of their offspring was optimal, and on which new generation adults had highest longevity when

their food was limited. Plants subjected to herbivory by *P. xylostella* responded by producing elevated levels of some nutrients (e.g., sulfur), but other nutrient levels declined in infested leaves (e.g., nitrogen). Regardless of fertility rate, plants compensated for herbivory by increasing root mass relative to their non-infested counterparts; plants grown under optimum fertility developed the most robust root systems when infested. In addition, host plant fertility levels on which *P. xylostella* host larvae were reared affected some developmental parameters of the parasitoid, *D. insulare*. In integrated crop management systems, selecting optimal fertility levels should consider not only effects on yield in the absence of pests, but also effects on compensatory abilities of plants when under attack, and downstream effects on the developmental biology of herbivores and their parasitoids.

P1-44. Population dynamics, growth and seed transmission of *Fusarium equiseti* in ginseng. Z.K. Punja, A. Wan, M. Rahman, R.S. Goswami, T. Barasubiye, K.A. Seifert, and C.A. Lévesque. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada; and (T.B., K.A.S. & C.A.L.) Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada.*

Fusarium equiseti is prevalent in ginseng soil, straw mulch and ginseng root tissues and is the cause of a root surface discoloration on ginseng grown in British Columbia. Inoculum levels of the fungus in ginseng fields were highest at 0-5 cm soil depth compared to 10-15 cm. Barley or wheat straw added to soil significantly increased population levels under laboratory conditions. Mycelial growth was highest at 28-30°C and at pH 7.2-7.5. Spore monitoring studies revealed the presence of air-borne inoculum of *F. equiseti* during June-August, 2006. Samples of flowers and berries, and harvested seed, contained DNA of *F. equiseti* detected using a *Fusarium*-specific DNA array. A high degree of genetic variation in the EF-1 alpha gene sequence was present among 52 isolates of *F. equiseti* which were from ginseng fields. At least 9 clades were identified. Inoculum dispersal from straw mulch used in ginseng gardens can result in seed contamination by the fungus. In addition, fungal growth near the soil surface under warm summer conditions can result in infection and crown discoloration of ginseng roots.

P1-45. Frequency of isolation of Diaporthe-Phomopsis complex from soybean plants in Ontario. A.G. Xue, M.J. Morrison, E. Cober, T.R. Anderson, S. Rioux, G.R. Ablett, I. Rajcan, R. Hall, Y. Chen, and J.X. Zhang. *Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada (AAFC), 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (T.R.A.) Harrow Research Centre, AAFC, 2585 County Road 20 East, Harrow, ON N0R 1G0, Canada; (S.R.) CEROM, 2700 Einstein, Quebec City, QC G1P 3W8, Canada; (G.R.A.) Ridgetown College, University of Guelph, Ridgetown, ON N0P 2C0, Canada; (I.R.) Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada; and (R.H.) Department of Environmental Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Diaporthe-Phomopsis (D-P) complex, consisting of *Diaporthe phaseolorum* (Cke & Ell.) Sacc. var. *caulivora* Ath. & Cald. (Dpc), *D. phaseolorum* var. *sojae* (Lehman) Wehm. (Dps), and *Phomopsis longicolla* Hobbs (Pl), causes substantial yield loss to soybean in Canada. To determine the predominant species of the D-P complex occurring in Ontario soybean, 2700 stem tissues, 2700 pod tissues, and 9000 seeds from diseased plants collected at nine locations representing the five crop heat unit (CHU, 2400, 2600, 2800, 3100, 3400) areas in Ontario were sampled each year during 2002-2004. The D-P complex was recovered from 17280 of 43200 plant tissues and seeds tested over the three years. Seventy-three % of the isolates were from the stem, 23% were from the pod, and only 3% were from the seed. *Phomopsis longicolla* was the predominant species (41% of isolates), followed by Dpc (37%), and Dps (22%). The correlation between stem and pod infection was highly significant ($P < 0.01$) for each of the three pathogens. The correlation between seed and pod infection or between seed and stem infection, however, was not significant for either pathogen. The low incidence of D-P complex in seed and the lack of significant correlations between seed infection and the pod or stem infection suggest that seed-borne D-P complex in non-epidemic years may not have a significant impact on seed quality and seed decay.

P1-46. Evaluation of winter wheat genotypes for reaction to *Tilletia controversa* in Ontario. A.G. Xue, A. Tenuta, X.L. Tian, E. Sparry, M. Etienne, D.A. Gaudet, J.G. Menzies, R.J. Graf, D.E. Falk, A. Smid, and R.S. Pandeya. *Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada (AAFC), 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (A.T.) Ontario Ministry of Agriculture and Food, P.O. Box 400, Ridgetown, ON N0P 2C0, Canada; (E.S.) C&M Seeds, R.R. #3, Palmerston, ON N0G 2P0, Canada; (M.E.) Hyland Seeds, 11087 Petty Street, Ailsa Craig, ON N0M 1A0, Canada; (D.A.G. & R.J.G.) Lethbridge Research Centre, AAFC, P.O. Box 3000, Lethbridge, AB T1J 4B1, Canada; (J.G.M.) Cereal Research Centre, AAFC, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada; (D.E.F.) Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada; and (A.S.) Ridgetown College, University of Guelph, Main Street East, Ridgetown, ON N0P 2C0, Canada.*

Dwarf bunt, caused by *Tilletia controversa* Kühn, is a destructive disease of winter wheat in Ontario. To identify sources of resistance, 285 selected cultivars and germplasm lines obtained from 12 public and private winter wheat breeding programs in North America were evaluated in *T. controversa* inoculated greenhouse trials

and in hill plot field experiments in four environments from 2002-2005. Dwarf bunt developed on susceptible genotypes in all tests. The mean disease incidence in greenhouse trials was 6.9%, ranging from 0-63.4% and in field experiments was 3.9% and 3.4%, ranging from 0-73.2% and 0-45.0%, for 2002-03 and 2004-05, respectively. Twenty-one genotypes, including cultivars Blizzard, Carlisle, and Tarso, were free from infection in all tests and were considered resistance to *T. controversa*. These 21 genotypes have not been previously reported with dwarf bunt resistance and could be used in genetic studies, breeding programs, and possibly as cultivars for production.

P1-47. Towards a Canadian Invasive Plant Framework. C. Lindgren. *Invasive Alien Species Section, Canadian Food Inspection Agency, 59 Camelot Drive, Ottawa, ON K1A 0Y9, Canada.*
An invasive plant is a harmful organism whose introduction or spread threatens the environment, the economy, or society including human health. The number of new plant incursions and their impacts have increased annually accelerating in the last 30 years due to exponential increases in air travel, the increased speeds at which commodities and people traverse the globe, more numerous ports of entry, expanded exports and imports into new international markets, increased interest in the use of exotic plants in gardening and water gardening, and increased access to foreign ecosystems. It is estimated that invasive plants cost the Canadian economy millions of dollars annually. There is a need for a Canadian Invasive Plant Framework that enhances collaboration among governments, economic sectors, stakeholders, and the international community. The Canadian Food Inspection Agency (CFIA) will provide leadership and coordination throughout the overall development of the framework, partnering with other federal departments, provinces and territories, academia, industry and members of the Canadian public concerned with invasive plants. A Canadian Invasive Plant Framework will be consistent with the Invasive Alien Species Strategy for Canada, focussing on prevention, early detection, rapid response and management of invasive plants.

P1-48. The influence of *Ophiostoma novo-ulmi Mitovirus 3a* (*OMV3a*) on respiration and growth of *Sclerotinia homoeocarpa*, the causal agent of dollar spot of turf. A. Orshinsky and G.J. Boland. *Department of Environmental Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*
Sclerotinia homoeocarpa (Bennett) causes dollar spot disease of turf grass. Hypovirulent isolates of *S. homoeocarpa* contain the mitochondrial virus *Ophiostoma novo-ulmi Mitovirus 3a* (*OMV3a*). *OMV3a* has also been detected in asymptomatic isolates with growth rates and virulence comparable to virus-free isolates. In this study, the respiration and growth of hypovirulent, asymptomatic, and virulent isolates of *S. homoeocarpa* were characterized using antimycin a (AA) as a complex III inhibitor and salicylhydroxamic acid (SHAM) as an alternative oxidase (AOX) inhibitor. The respiration of virulent and asymptomatic isolates was significantly reduced by AA but was not affected by SHAM. The respiration of a hypovirulent isolate was not reduced by AA or SHAM. AA reduced the growth of all isolates tested. SHAM also reduced the growth of all isolates; however, the reduction was only significant for asymptomatic and hypovirulent isolates. The effect of SHAM on the growth of all isolates reflects low-level constitutive transcription of *AOX*, which was confirmed by comparing relative transcription of *AOX* by various isolates. Transcription of *AOX* by hypovirulent isolates was higher than that of virulent and asymptomatic isolates. Alternative respiration is believed to be an inefficient means for energy production since it does not directly contribute to the mitochondrial proton gradient. These results confirm that *OMV3a*-associated hypovirulence of *S. homoeocarpa* involves impaired mitochondrial function, resulting in the initiation of the alternative oxidase pathway. The use of the inefficient alternative pathway may be responsible for the reduced growth and virulence of hypovirulent isolates. Additionally, the alternative oxidase pathway appears to be employed by asymptomatic isolates, but to a lesser degree than hypovirulent isolates.

P1-49. White mold control in dry beans: Evaluation of fungicides. J. Lajeunesse and D. Pageau. *Research Farm, Agriculture and Agri-Food Canada, 1468 Saint-Cyrille Street, Normandin, QC G8M 4K3, Canada.*
In Northern Quebec, dry bean (*Phaseolus vulgaris* L.) is an uncommon crop. Dry bean is very susceptible to white mold (*Sclerotinia sclerotiorum* (Lib.) de Bary) and yield losses due to this disease could be severe. In 2005 and 2006, a trial was conducted at the Research Farm of Agriculture and Agri-Food Canada in Normandin to evaluate fungicide application to control *S. sclerotiorum* in narrow-row bean fields. Four fungicide treatments (control, iprodione, vinclozolin and boscalid) and three cultivars (AC Redbond, CDC Pintium and Cirrus) were evaluated. Fungicides were applied at the beginning of the flowering stage and a second application was done 10 days later. Disease index (DI) was assessed for each plot using a scale of 0 to 5 where 0 is no infection and 5 is 100% of the plants infected. In 2005, fungicide application had no effect on DI and grain yields. CDC Pintium had the lowest DI and the highest grain yields compared to AC Redbond and Cirrus. In 2006, fungicide application reduced significantly DI and increased grain yields by 14% compared to control plots. Grain yields were significantly higher (3876 kg ha^{-1}) when boscalid was applied compared to iprodione (3584 kg ha^{-1}) and vinclozolin (3609 kg ha^{-1}). In 2006, AC Redbond produced more grains and was less affected by white mold (DI = 1.7; 3913 kg ha^{-1}) than Cirrus (DI = 2.4; 3449 kg ha^{-1}) and CDC Pintium (DI = 3.6; 3363

kg ha^{-1}). It seems that, under high disease pressure, some cultivars are less susceptible than others to white mold and fungicide applications reduced significantly the disease incidence.

P1-50. Analysis of genes differentially expressed during interaction of potato with the late blight pathogen *Phytophthora infestans*. M.A. Henriquez and F. Daayf. *Department of Plant Science, 222 Agriculture Building, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.* Manitoba is the second largest potato producer in Canada after Prince Edward Island. Potato crop faces many disease problems including the most famous and devastating one, late blight, caused by the oomycete pathogen *Phytophthora infestans* (Mont) de Bary. More than 150 years have elapsed since this disease caused the Irish potato famine, but strategies for managing it often remain unsustainable and costly. With the advent of molecular biology, genetic engineering and now genomics-based approaches, it is possible to initiate studies which can address important questions regarding very complex host-pathogen interactions. Our team has shown that the most aggressive strains of *P. infestans* suppress potato defense mechanisms, through transcriptional inhibition of phenylpropanoid (PAL) and isoprenoid (HMGR) pathways. Therefore, it becomes important to understand the molecular mechanisms governing the suppression of potato defenses by the pathogen. The objective of the current study was to develop a new molecular approach to identify differentially expressed genes of *P. infestans* implicated in the suppression of potato defense genes. Gene expression profiling was accomplished using the IDASH (Integral Differential Amplification of Subtractive Hybridization). IDASH was used with different strains of *P. infestans*, inoculated to both susceptible and tolerant potato cultivars. Using this approach, it was possible to select individual fragments with specific expression patterns at different times after inoculation, which showed relation with *P. infestans* cDNAs potentially involved in suppression and potato cDNAs potentially suppressed.

P1-51. Mycelium growth and pathogenicity of clones of *Sclerotinia sclerotiorum* recovered from canola, borage and purple bugloss. A.S. Shakir, G. Séguin-Swartz, and H. Nair. *Agriculture and Agri-Food Canada, Saskatoon Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; and (H.N.) Bioriginal Food and Science Corp., 102 Melville Street, Saskatoon, SK S7J 0R1, Canada.* The mycelial growth and pathogenicity of clones of *Sclerotinia sclerotiorum* recovered from borage (*Borago officinalis*, clone HN-Bo-03) and purple bugloss (*Echium plantagineum*, clone HN-Ep-05) were compared to that of clone 321, a predominant clone in canola (*Brassica napus*) fields in western Canada. Mycelial growth was measured at 24, 36, 48, 72, 96 and 120 hours post-inoculation on potato dextrose agar (PDA), glucose agar (GA) and on PDA and GA amended with bromophenol blue (BB, 10 ppm). Mycelial growth of the three clones was similar on PDA with or without BB, while the growth of HN-Ep-05 was faster than that of the other clones on GA with or without BB. A preliminary pathogenicity test was conducted in the greenhouse on plants of *B. napus* lines characterized as either susceptible or moderately resistant to clone 321. Plant stems were inoculated with infected plugs of GA with or without BB (10 ppm). Clone HN-Bo-03 was the most aggressive clone, killing all plants of the susceptible line 11 days after inoculation (dpi) and 66% of the plants of the moderately resistant line at 21 dpi. In comparison, at 21 dpi, clone 321 had killed 80% of the plants of the susceptible line and 15% of the plants of the moderately resistant line. Clone HN-Ep-05 was less aggressive on both lines than clone 321.

P2. Plant development and improvement

P2-1. Screening potato genotypes for antioxidant capacity and total phenolics. Q. Chen, J. Su, S. Nandy, and G. Kereliuk. *Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB T1J 4B1, Canada.* Potato is an important vegetable and a good source of antioxidants. Enhancing antioxidant capacity in potato is a good strategy for increasing the consumption of antioxidants to protect human health. In present study, 22 cultivated potatoes with various color and 15 wild *Solanum* species were studied for total phenolic, chlorogenic acid concentration and antioxidant activity using spectrophotometric analysis. The antioxidant activity varied from 240 to 754 ug Trolox / g FW for white to yellow flesh cultivars and 481 to 1591 ug Trolox / g FW for red to purple flesh cultivars. In wild potato species, the antioxidant activity ranged from 343 to 4917 ug Trolox / g FW. The antioxidant activity in Mexican wild species was about 7 times higher than that of white to yellow flesh cultivars. Both total phenolic and chlorogenic acid concentration in wild species were almost 3 times higher than those of cultivated potatoes. Correlation coefficients among the three traits in 37 genotypes were all higher than 0.95. The high correlation coefficient between antioxidant activity and total phenolics indicated that total phenolics were very important for antioxidant capacity in potato and can be used as indirect indicator for potato antioxidant capacity. It's feasible to improve antioxidant activity of cultivated potato by using wild *Solanum* species, especially Mexican wild species as gene pools through genetic breeding approach.

P2-2. Inheritance of resistance gene to Colorado potato beetle in wild potato plant *Solanum pinnatisectum*: A new insight for potato growers. Q. Chen, S. Nandy, D. Beasley, and M.S. Goettel. *Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB T1J 4B1, Canada.*

The wild Mexican potato species, *Solanum pinnatisectum* is an important gene donor for resistance to Colorado potato beetle (CPB) and late blight disease. This work contributes to the genetic and mechanistic basis of *S. pinnatisectum* mediated resistance to CPB in an interspecific hybrid and provides a foundation for future studies to develop CPB resistant potatoes. Diploid progenies segregating for resistance genes to CPB were developed by crossing *S. pinnatisectum* with *S. cardiophyllum*. A resistant hybrid line from this cross was selected and backcrossed as a female to *S. cardiophyllum* in order to generate a backcross family. About 345 lines from this backcross population were selected to analyse the genetic architecture of the CPB resistance gene. The Chi square test result showed a significant 1:3 (Resistance: Susceptible) and 1:2:1 ratio in this backcrossing population, indicating the presence of resistant and susceptible genes in heterozygous condition within the parents. This finding further indicates that resistance in *S. pinnatisectum* to CPB may be controlled by two independently segregating genes having two respective loci, acting in a complementary epistatic manner. The availability of CPB resistance genes, along with late blight resistance genes in *S. pinnatisectum* may enable breeders and geneticists to develop resistant cultivars through the gene pyramiding method.

P2-3. Neural networks to predict cuticle cracking in greenhouse peppers and tomatoes. B.D. Hill, D.L. Ehret, D.A. Raworth, and B. Estergaad. *Lethbridge Research Centre, Agriculture and Agri-Food Canada, P.O. Box 3000, Lethbridge, AB T1J 4B1, Canada; (D.L.E. & D.A.R.) Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1000, Agassiz, BC V0M 1A0, Canada; and (B.E.) Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, Highway 97, Summerland, BC V0H 1Z0, Canada.*

Cuticle cracking is a severe problem affecting the quality of greenhouse-grown hydroponic peppers (*Capsicum annuum* L.) and tomatoes (*Lycopersicon esculentum* Mill.). It is influenced by cultural practices and environment but is not well understood. We monitored pepper and tomato fruit in seven commercial greenhouses in BC from May to September, 2000. Neural network (NN) modelling was used to predict cracking 1 and 4 weeks in advance of the actual fruit harvest. Data records consisted of up to 29 inputs (different biological and environmental variables) paired with the known output (average cracking of 50 fruit using a 0-5 scale) on a case-by-case basis. The best week-1 and week-4 models for pepper consisted of 9 inputs with R^2 of 0.71 and 0.70, respectively. Day and night temperature/humidity, day-time CO_2, radiation and growing media were important inputs. The best week-1 and week-4 models for tomato also used 9 inputs with R^2 of 0.70 and 0.64, respectively. Week of the year, day and night temperature/humidity, number of leaves, and yield were important. NN can predict cuticle cracking in greenhouse peppers and tomatoes up to 4 weeks before harvest.

P2-4. Comparison of media used for evaluating *Rhizobium leguminosarum* for phosphate solubilizing ability. J. Xie, D.J. Knight, M. Leggett, and S. Vick. *Philom Bios, 3935 Thatcher Avenue, Saskatoon, SK S7R 1A3, Canada; and (D.J.K.) Department of Soil Science, University of Saskatchewan, Saskatoon, SK S7N 5A2, Canada.*

Rhizobium leguminosarum are well known for their ability to fix nitrogen. In addition, their capacity to solubilize phosphate has been receiving more attention in recent years. In this study, thirty *R. leguminosarum* isolates were evaluated in broth and solid formulations of three different media, Yeast Mannitol Extract (YEM), Botanical Research Institute Phosphate Nutrient medium (MNBRI) and Pikovskaya medium (PVK), containing dicalcium phosphate ($CaHPO_4$) as the sole phosphate source. Controls were media without *R. leguminosarum* isolates. The *R. leguminosarum* isolates were selected on the basis of their different plasmid profiles, indicative of genetically distinct isolates. All 30 isolates increased the P concentration to varying degrees in broth media but solubilization varied from one medium to another. Furthermore, the ability of the isolates to solubilize P on the solid media was not comparable to the performance of the isolates grown in broth. The component and formulation of medium strongly influenced the amount of $CaHPO_4$ solubility by *R. leguminosarum* isolates, therefore predictors of efficacy obtained through laboratory evaluations will need to be tested and confirmed in greenhouse or field study.

P2-5. Role of the *Arabidopsis thaliana RHD3* gene in root hair tip-growth. D.M. Cooper, A.E. Sutherland, and M.E. Galway. *Department of Biology, St. Francis Xavier University, P.O. Box 5000, Antigonish, NS B2G 2W5, Canada.*

The *ROOT HAIR DEFECTIVE3* (*RHD3*) gene of *Arabidopsis thaliana* encodes a putative GTP-binding protein required for protein transport between endoplasmic reticulum (ER) and Golgi bodies, and for maintaining ER structure. Multiple defects have been reported in plants homozygous for recessive mutations in this gene (*rhd3* and *fra4* mutants). Defects include bundling of the ER and associated actin microfilaments, slow growth, reduced cell elongation, and the presence of thin, cellulose-deficient cell walls in plant stems. The unusual wavy shape of tip-growing root hairs in these mutants has been attributed to differential expansion (bulging) of root hair tips resulting from the misdirected delivery of secretory vesicles, which is known to be an actin-mediated process. We used *rhd3* mutant lines expressing green fluorescent proteins to visualize either the actin microfilaments, endoplasmic reticulum, or lytic vacuoles, confirming that actin microfilaments as well as ER were bundled in the

mutant hairs. Altered vacuole dynamics in mutant hairs may also be linked to actin bundling. Double staining of cellulose and fucosylated xyloglucans in the cell walls of mutant hairs revealed a heterogeneous, patchy distribution of these cell wall components, which is consistent with the previously described defect in secretory vesicle delivery. However, growing mutant seedlings slowly at 5°C produced straighter root hairs with less patchy staining of the cell wall components. It remains to be determined if this phenotypic change is accompanied by changes in the subcellular organization of actin or associated organelles.

P2-6. Potential of fenugreek (*Trigonella foenum-graecum*) as a forage for dairy cattle. J.E. Montgomery, J.R. King, and L. Doepel. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.*

Fenugreek (*Trigonella foenum-graecum* L.) is an annual legume, traditionally used as a spice or dye. Forage-type fenugreek varieties have recently been developed. Benefits of fenugreek for forage include high protein levels throughout the growing season, indeterminate growth, and nitrogen fixation. Two genotypes of fenugreek, 'Quatro' (seed type) and 'F70' (forage-type), were grown at the University of Alberta (Edmonton) in 2006. Bi-weekly harvests were taken to evaluate differences in biomass accumulation, canopy development and leaf to stem ratio. While 'F70' demonstrated higher emergence, and greater initial growth in terms of plant height, biomass, and leaf area, end of season measurements were equivalent across variety. An *in vivo* pilot study using dairy cows showed the dry matter digestibility of 'Quatro' was similar to that of alfalfa, while 'F70' was less digestible. In 2007, the rate of ruminal digestion of fenugreek and alfalfa haylage as well as effects on rumen fermentation, feed intake, and milk production will be determined in lactating dairy cows. Three fenugreek varieties, 'Quatro', 'F70', and 'Canagreen', will be grown in test plots to compare growth characteristics, as in 2006. If fenugreek is found to be equal or superior to alfalfa as forage, producers will have another forage legume that they can feed to dairy cows and use in their crop rotation.

P2-7. Agriculture and Agri-Food Canada and the University of Manitoba's wheat breeding collaboration: The first 3 years. A.P. Kirk, S.L. Fox, and M.H. Entz. *Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada; and (M.H.E.) Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*

Canada exports about $14 M of organically produced wheat each year, representing 1/5 of Canada's total organic food exports. Organic agricultural systems differ from conventional systems in terms of soil fertility, soil microflora distribution and weed management. Organic agriculture may benefit from wheat cultivars specifically tailored to this environment, as wheat cultivars are currently selected under conventional management. In 2004 a collaboration was initiated between Agriculture and Agri-Food Canada and the University of Manitoba to breed wheat targeted for organic production. Organically managed fields at the U of M Glenlea long-term rotation and Carman farm are used to grow Canadian Western Red Spring germplasm from the Cereal Research Centre bread wheat breeding program, in which typical wheat breeding selection activities are performed. F2's were initially planted in 2004, and in 2006 F2 to F5 generations were evaluated. An overview of the organic wheat breeding program is presented, including plant characteristics that are selected for in this environment. While conventional breeding goals are retained, some plant characteristics the breeding program is focusing on differ.

P2-8. Ultrastructural features of the floral nectary in ornamental purple loosestrife (*Lythrum virgatum* x *L. alatum* cv. 'Morden Gleam'). W.D. Caswell and A.R. Davis. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*

Nectar produced by the floral nectary of many species serves as a food reward for pollinators. Ultrastructural studies of floral nectary tissue in the Myrtales are few. Accordingly, to broaden our knowledge within this order of members whose nectar regularly attracts floral visitors, this study represents the first investigation of the fine structure of floral nectaries of the Lythraceae. Three stages of floral development in ornamental purple loosestrife (*Lythrum virgatum* x *L. alatum* cv. 'Morden Gleam') were examined: large, pre-secretory buds; nectar-secreting flowers on the first day of anthesis; and post-secretory flowers (third day of anthesis). The floral nectary lies in a trough formed between the gynoecium base and the calyx tube. Nectar is secreted to outside through modified stomata which are typically solitary and evenly spaced. The floral nectary possesses epidermal cells subtended by several layers of nectariferous parenchyma cells, which surround intercellular spaces. In pre-secretory buds, the parenchyma cells contain many large amyloplasts per cell; each plastid contains several starch grains. Some starch has broken down by the time of anthesis, apparently supplying a portion of nectar carbohydrate. Plasmalemmasomes are observed in nectaries of pre-secretory buds, whereas vacuoles, mitochondria, and endoplasmic reticulum persist throughout. The vacuome of nectariferous cells comprises many small vacuoles in pre-secretory flowers, whereas a large central vacuole occurs post-secretion. A stereological study of various cellular features has been initiated, to quantify ultrastructural changes within nectary tissue throughout floral development.

P2-9. Role of jasmonic acid in leaf senescence in western redcedar (*Thuja plicata*). T. Chan, J. Mehroke, and S. Singh. *Department of Botany, Bioscience Building, University of British Columbia, Vancouver, BC V6T 1Z4, Canada.*

Evergreen trees do not follow the pattern of seasonal senescence observed in deciduous trees in temperate climates. Leaves of these trees, such as western redcedar (*Thuja plicata*), stay green throughout the year. Mineral nutrients (especially nitrogen) deficiency, severe and prolonged water stress and pathogen attack are known to induce senescence in western redcedar leaves. However, the involvement of intrinsic factors such as plant hormones in leaf senescence of western redcedar is not known. The objectives of this investigation were: (i) to study the role of plant hormones in leaf senescence in western redcedar and (ii) to compare seasonal changes in photosynthesis and transpiration rates and protein profiles of western redcedar and red oak (*Quercus rubra*). One-year-old seedlings and excised leaves of western redcedar were treated with plant hormones and growth regulators (100 uM), jasmonic acid, abscisic acid, ethephon and benzylamino purine in both light and darkness. Jasmonic acid was the most effective hormone in the induction of leaf senescence in western redcedar. Jasmonic acid also reduced the levels of rubisco and ATP synthase proteins in excised leaves. Western redcedar leaves, relative to red oak leaves, showed much higher photosynthesis and transpiration rates, and rubisco and ATP synthase levels during September to November. These findings will be discussed in relation to physiological sustainability.

P2-10. Pea (*Pisum sativum* L.) fruit development: Seeds involved in regulation of pericarp gibberellin biosynthesis. C. Nadeau, D.M. Reinecke, and J.A. Ozga. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.*
Gibberellins (GAs) are involved in the regulation of many processes in growth and development of plants. Biologically active GA_1 levels are controlled through the regulation of metabolic and catabolic enzymes in a tissue- and temporal-specific manner including regulation of GA 3β-hydroxylase, the enzyme that converts GA_{20} to bioactive GA_1. To test the importance of GA 3β-hydroxylase (*GA3ox*) gene in pea fruit development, pea plants have been transformed to over-express *PsGA3ox1*. The presence of transgenic *PsGA3ox1* was confirmed by PCR, quantitative RT-PCR, and kanamycin segregation. In the process of characterizing GA transgenic lines we have observed a subset of lines that set seed poorly. Interestingly, even though the seed set poorly the pods did not senesce as is typical of wild-type unfertilized ovaries. When a seed(s) did set, the pod was even longer than would be expected for that number of developing seed. We examined the expression pattern of a poorly setting *GA3ox* seed line using growth measurements and quantitative RT-PCR. Early fruit growth is promoted by active GA_1 produced by GA 3β-hydroxylase (*PsGA3ox1*). Basal expression of *PsGA3ox1* in the transgenic line appears to be sufficient to allow minimal pericarp growth in the absence of seeds. However, normal developmental trends in pericarp *PsGA3ox1* expression depend on the presence of at least one seed. This is evidence to support the hypothesis that seeds are a major factor in inducing expression of GA biosynthesis genes necessary for normal pericarp development. Supported by grants from AARI to JAO and DMR, NSERC to JAO.

P2-11. Developmental morphology of the flower of *Anthurium jenmanii* (Araceae). D. Barabé and C. Lacroix. *Institut de recherche en biologie végétale, Jardin botanique de Montréal, 4101 Sherbrooke Est, Montréal, QC H1X 2B2, Canada; and (C.L.) University of Prince Edward Island, 550 University Avenue, Charlottetown, PE C1A 4P3, Canada.*
The early stages of development of the inflorescence of *Anthurium jenmanii* were examined using scanning electron microscopy. The inflorescence of *A. jenmanii* consists of more than one hundred flowers arranged in recognizable spirals. Each flower has four broad tepals enclosing four stamens that are not visible before anthesis. The gynoecium is formed by two carpels. The ovary is bilocular and contains two ovules. The short style bears a two-lobed stigma. The floral primordia are first initiated on the lower portion of the inflorescence. They increases in size and appear as transversely extended bulges. Early during their development, they assume their typical diamond shape. The two lateral tepals are the first organs to be initiated followed shortly thereafter by the two median tepals. After their initiation, each stamen appears to be associated with a tepal of the same radius; the two lateral stamens are initiated first, directly opposite to the lateral tepals. The two-lobed stigma is clearly visible during the early stages of development of the gynoecium. The mode of floral development observed in *Anthurium* is similar to that reported for *Gymnostachys*. In both genera, the first pair of tepals and stamens to develop are those perpendicular to the axis of the inflorescence. The similarity in mode of development may be linked to structural constraints or phylogenetic relationships.

P2-12. Identification of cytoprotective phytochemicals from western Canadian plants, foods and herbal medicines. D.J.F. Konkin, E. Bol, R. Hughes, and J.E. Page. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; and (E.B., R.H. & J.E.P.) National Research Council of Canada, Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada.*
Phase 2 proteins are a diverse set of enzymes and antioxidant proteins that neutralize electrophiles and reactive oxygen species (ROS) and thereby prevent cellular damage caused by harmful endogenous and exogenous substances. Increasing levels of phase 2 proteins is an attractive means to prevent diseases associated with oxidative and electrophile-mediated stress, including cancer, cardiovascular disease, and neurodegenerative diseases. The production of phase 2 proteins can be increased by consumption of foods rich in

phase 2 protein inducing phytochemicals. In order to identify novel phase 2 protein inducing phytochemicals from plants, 164 methanolic extracts were prepared and screened for activity of the phase 2 protein quinone reductase (QR) in murine Hepa1c1c7 cells. Approximately 10% of extracts tested increased the activity of QR greater than two-fold. *Ligusticum porteri* J.M. Coult. & Rose (Umbelliferae), a plant used in Native American traditional medicine, displayed high activity and has been selected for further study. Bioassay-guided fractionation and a novel mass spectrometry, thiol reactivity based approach will be used to identify active components of a *L. porteri* root extract. Identification of novel inducers from *L. porteri* and other plants is important in order to make use of the health benefits associated with phase 2 protein induction.

P2-13. Identification and characterization of *cis*-acting elements in *CHS7* and *CHS8* gene promoters in soybean seeds. J. Yi and S. Dhaubhadel. *Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, 1391 Sandford Street, London, ON N5V 4T3, Canada.*

Our previous transcriptome analysis during embryo development in soybean has revealed an important role for *CHS7* and *CHS8* genes in the synthesis of isoflavonoids. Towards understanding the molecular details of how these two genes may control isoflavonoid synthesis, we cloned and sequenced two fragments; 1617 bp upstream of *CHS7* and 1556 bp upstream of *CHS8* by Genome Walking procedure. A total of 71 potential transcription factor binding sites (TFBSs) within *CHS7* promoter region and 73 potential TFBSs within *CHS8* promoter region were predicted and annotated by both TSSP and GENOMATIX software. A combination of *in vitro* footprinting and Electrophoretic Mobility Shift Assay was employed to confirm this prediction. Totally, 26 footprints were obtained in *CHS*8 promoter region with nuclear proteins isolated from soybean embryo. A functional genomic approach has been employed to clone and characterize nine candidate Transcription Factors (TFs) from microarray analysis and DFCI Soybean Gene Index (http://compbio.dfci.harvard.edu/tgi/cgi-bin/tgi/gimain.pl?gudb=soybean) followed by heterologous expression in bacteria. Efforts are underway to demonstrate the functional interaction of candidate transcription factors with the *cis*-acting regions of *CHS7* and *CHS8* promoters.

P2-14. Toc complex assembly in chloroplasts of *Arabidopsis thaliana*. L.G.L. Richardson and M.D. Smith. *University of Waterloo, 200 University Ave. W., Waterloo, ON N2L 3G1, Canada; and (M.D.S.) Wilfrid Laurier University, 75 University Ave. W., Waterloo, ON N2L 3C5, Canada.*

Chloroplast biogenesis is essential for plant development, and relies on successful import of thousands of nuclear-encoded proteins. Receptors of the Toc complex responsible for preprotein recognition at the outer chloroplast membrane include the Toc159 and Toc34 families of homologous GTPases. A current model of chloroplast protein targeting implicates Toc159 family members (designated atToc159/132/120 in *Arabidopsis*) as the primary preprotein receptors. In this model, different Toc159 homologues show specificity for different preproteins, and target them to the chloroplast via a GTP-dependent interaction with specific members of the Toc34 family (atToc33/34). The Toc159 homologues have a distinct tripartite structure consisting of conserved membrane-anchor (M-) and GTP-binding (G-) domains, and a non-conserved acidic (A-) domain. Mutant forms of atToc132 and atToc159 in which the A-domains were exchanged, and atToc132 and atToc159 A-domain deletions will be targeted to chloroplasts isolated from two *Arabidopsis* mutants, an atToc33 knockout (*ppi1*) and an atToc34 knockout (*ppi3*), using *in vitro* targeting assays. This study will investigate a potential role for the A-domain in the targeting of Toc159 receptors to Toc complexes, and possible roles for Toc34 family members in Toc complex assembly. Elucidating how Toc complexes are assembled may provide insight into how these translocons mediate import of different groups of preproteins necessary for organelle differentiation and functioning.

P2-15. Transgenic pea plants expressing cell wall invertase have altered carbohydrate status during seed growth and development. P.K. Bhowmik, D.M. Reinecke, and J.A. Ozga. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.*

Invertases are a class of enzymes that hydrolyze sucrose to glucose and fructose. Invertases are considered to be a control element in the changing carbohydrate status of sink tissues. Genetic manipulation of the expression of invertases could be an important molecular breeding strategy for the manipulation of the quantity and type of carbohydrate in the seeds. Our lab has produced transgenic pea (*Pisum sativum* L.) plants that express cell-wall-bound invertase (CWI) under the control of a seed-coat-specific promoter. In this study, several independent transgenic plant lines and wild-type plants were characterized for cell-wall invertase gene expression, enzyme activity, and product levels. Significant increases in hexoses (glucose and fructose) were detected in developing transgenic seeds whereas sucrose was decreased. Both transcript and enzyme activity of cell-wall invertase increased in developing transgenic seeds correlating well with hexose content. The results suggest that the expression of the cell-wall invertase gene involved in sucrose breakdown and hexose accumulation serves as a novel strategy to change the hexose/sucrose ratio in pea. More recently, null control lines that segregated for the loss of the transgene were similarly analyzed, and they show similar trends (although lesser in magnitude) to those observed with the wild-type plant. We are currently analyzing two other

independent CWI transgenic lines to extend the observed data. Modulation of the hexose/sucrose ratio after initiation of the starch accumulation phase could lead to production of different types of starch, variation in starch granule size, and the ratio of starch to protein in the mature seed.

P2-16. RNA binding characteristics of *Arabidopsis thaliana* ribosomal protein S15a. H. Wakely and P.C. Bonham-Smith. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*

Arabidopsis thaliana ribosomal protein (r-protein) S15a (RPS15a), is a putative 18S ribosomal RNA (rRNA) primary binding protein and may play a role in the assembly of the small (40S) ribosomal subunit. RPS15a is encoded by a multi-gene family that is composed of six members: *RPS15aA, RPS15aB, RPS15aC, RPS15aD, RPS15aE* and *RPS15aF*. RPS8, the prokaryotic orthologue of RPS15a, has been mapped to 16S rRNA and also binds to its polycistronic mRNA thereby preventing translation. The binding of RPS15aD, RPS15aE, and RPS15aF to 18S rRNA and to their respective transcripts will be investigated. Recombinant His-tagged RPS15a recombinant proteins were expressed in *E. coli* Tuner (DE3) cells and purified using a Nickel affinity column. Electromobility shift assays (EMSAs) will be carried out with the recombinant r-proteins and the 18S rRNA molecule, fragments of the 18S rRNA molecule, and the individual RPS15a mRNA transcripts. Additionally, to investigate specific RPS15a RNA binding domains, site directed mutagenesis will be performed on the RPS15a isoforms and further EMSAs will determine differences in binding affinities to RNA.

P2-17. Diversity of seed starch and amylose concentration in chickpea mini-core collection. A. Sinha, A. Frimpong, B. Tar'an, B.D. Gossen, and R.N. Chibbar. *Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; (A.F. & R.N.C.) Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; and (B.T.) Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*

As a pulse crop, chickpea (*Cicer arientinum* L.) ranks third globally after beans and peas. It is an important crop in Canadian prairies. In addition to proteins, chickpea seed is also a rich source of carbohydrates. On dry weight basis, almost half of the chickpea seed is made up of water-insoluble starch granules. Two glucan polymers, amylopectin (highly branched) and amylose (rarely branched), constitute the starch granule in the ratio of three- and one-quarter, respectively. Starches rich in amylose are termed resistant starch as these resist digestion in the small intestine but are broken down by bacteria in the large intestine. Therefore, foods rich in resistant starch have low glycemic index (GI) and may be useful in management of type II diabetes. In addition, resistant starch fermentation in colon promotes the growth of bifido bacteria, which may play a role in colon cancer prevention. Chickpea in general has higher amylose than other pulse and cereal grains, but there is an interest to further enhance amylose concentration in chickpea for niche markets. A chickpea mini-core collection of 211 accessions, which represents 1% of the global chickpea gene-pool, was procured from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India, and characterized for its starch quantity and amylopectin-to-amylose ratio. A high performance size-exclusion chromatography technology, previously optimized in our group, was used to determine the ratio. In the mini-core collection, no significant differences were found between desi- and kabuli-type chickpeas for the quantity and amylose concentration of seed starch. However, the total starch concentration varied from 40 to 60%, while the amylose fraction of the seed starch ranged between one-fourth and one-third of the total seed starch. Selected chickpea lines with high, medium and low starch and amylose concentrations have been selected for further analyses.

P2-18. Functional analysis of CIL1 from *Brassica carinata*. S. Gibson and J.L. Taylor. *Department of Biology, University of Saskatchewan, W.P. Thompson Building, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; and (J.L.T.) National Research Council, Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada.*

A cDNA sequence representing a *Brassica carinata* L. (Ethiopian mustard) gene was isolated from a library constructed with mRNA from copper chloride treated leaves. This cDNA sequence was designated *CIL1* (*COPPER CHLORIDE INDUCED* in *LEAVES*). A BLAST search revealed that *CIL1* has similarities to an auxin-induced gene, *AIR12* from *Arabidopsis thaliana* L., suggesting a role in development. Antisense *CIL1* plants had reductions in the phytohormones indole-3-acetic acid, zeatin riboside, and abscisic acid. Bioinformatic analyses suggest that CIL1 is glycosylphosphatidylinositol (GPI) anchored to the plasma membrane and is very similar to AIR12 from *Arabidopsis thaliana*. Preliminary complementation analysis in yeast suggests that CIL1 may be involved with cell wall structure. Antisense *CIL1* leaves also have reduced H_2O_2 production, while roots have reduced superoxide production. CIL1 may be involved with an auxin-signaling pathway, transmitting a free radical signal across the cell wall. Further examination of CIL1 will involve determination of the cellular localization of CIL1, investigation of protein-protein interactions, examination of *CIL1* overexpression plants, and complementation analysis of *AIR12 A. thaliana* T-DNA insertion lines.

P2-19. Nuclear and chloroplast genomic data reveals asymmetrical hybridization in poplars. M. Hamzeh, C. Sawchyn, P. Périnet, and S. Dayanandan. *Biology Department, Concordia University, 7141 Sherbrooke St. West, Montreal, QC H4B 1R6, Canada; and (P.P.) Direction de la recherche forestière, Ministère des Ressources naturelles et de la Faune, 2700, rue Einstein, Sainte-Foy, QC G1P 3W8, Canada.*

The genus *Populus*, commonly known as poplars is one of the most widely used groups of forest trees with high economic, ecological and evolutionary importance. Poplars are well known for their natural and artificial hybrids with superior qualities that are being exploited in breeding programs and plantation forestry. We investigated the direction of natural hybridization between two sympatric *Populus* species in northeastern North America (*Populus deltoides* and *P. balsamifera*) using species-specific single nucleotide polymorphism (SNP) markers in both nuclear and chloroplast genomes. All putative natural hybrid individuals examined had nuclear alleles corresponding to both parental species, while the chloroplast genotypes showed similarity to *P. deltoides*, indicating a unidirectional hybridization with *P. deltoides* as the maternal and *P. balsamifera* as the paternal donor species. The observed asymmetrical hybridization could be attributable to cytonuclear interactions.

P2-20. Isolation of a cDNA encoding a plastidial *sn*-glycerol-3-phosphate acyltransferase from the cold tolerant plant, *Erysimum asperum*. X. Chen, M. Truksa, J. Zhang, C. Snyder, S. Shah, and R.J. Weselake. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; and (J.Z. & S.S.) Plant Biotechnology Laboratory, Alberta Research Council, Vegreville, AB T9C 1T4, Canada.*

Sn-glycerol-3-phosphate acyltransferase (GPAT; EC 2.3.1.15) catalyzes the transfer of an acyl chain from acyl-CoA to the *sn*-1 position of *sn*-glycerol-3-phosphate, the first step in de novo glycerolipid assembly. Plastidial GPAT from cold tolerant plants may be selective for unsaturated substrates so as to increase the degree of unsaturation in the plastid membrane lipid, which in turn would greatly enhance the membrane fluidity and cold tolerance of plants. In the present study, we isolated a cDNA from the wild cold tolerant plant, *Erysimum asperum*, which shows a very high sequence similarity to the published plant plastidial GPAT genes**.** Overexpression of the *E. asperum* GPAT-like cDNA in a GPAT-defective yeast strain confirmed that the gene product has GPAT activity. Future studies will be aimed at examining the acyl-CoA selectivity properties of *E. asperum* GPAT and comparing the acyl-CoA selectivity with other plant plastidial GPATs. If this enzyme is highly selective for incorporating unsaturated fatty acid moieties into the glycerolipids of plastids, it might contribute to the cold tolerance of *E. asperum*.

P2-21. Structure-function relationships in an enzyme involved in acetylene fatty acid formation in plants. S.J. Gagne, P.S. Covello, G.R. Gray, and D.W. Reed. *Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada; and (G.R.G.) Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*

Canonical FAD2-type fatty acid desaturases introduce *cis* double bonds between C12 - C13 in oleic acid-containing substrates. Acetylenases are a subset of FAD2 enzymes which also act at the delta-12 position, but introduce a triple bond in linoleate. In an effort to understand the structure-function relationships among FAD2-like enzymes, fifty FAD2 and acetylenase amino acid sequences were compared. Eleven amino acid residues were identified as being conserved within each separate family but different between the enzyme classes. Specific amino acid residues were then altered by site-directed mutagenesis and the effect on function was determined. Specifically, mutants of the acetylenase CREP1 from *Crepis alpina* (Asteraceae) have been constructed and expressed in *Saccharomyces cerevisiae* and fatty acid content analyzed by gas chromatography. The relevance of the results in understanding the structure-function relationships in FAD2-like enzymes will be discussed.

P2-22. Hydroponic culture induces apoplastic bypasses in *Arabidopsis* roots. K.W. Bender and E. Cholewa. *Department of Biology, Nipissing University, 100 College Drive, North Bay, ON P1B 8L7, Canada.*

Solutes entering roots follow two parallel conduits: the apoplastic and symplastic pathways. The movement of solutes along the radial apoplastic pathway is blocked by Casparian bands (CBs) in the endodermis in mature parts of the root; however, permeability of the entire root system has not been tested. This study demonstrates that no direct apoplastic pathway to the xylem exists in roots by exposing root systems to an apoplastic tracer. We treated roots of *short-root* (*shr*) and *scarecrow* (*scr*) mutants of *Arabidopsis thaliana* (L.) Heynh. with PTS (3-hydroxy-5,8,10-pyrene trisulfonate). This led to the accumulation of the tracer in the leaves of *shr* which lack CBs but not in *scr* whose single cortical layer has CBs. Apoplastic pathways that bypass the CB barrier have been reported to occur at sites of lateral root emergence. The *alf1-1* mutant of *Arabidopsis* exhibits hyperproliferation of lateral roots but did not accumulate PTS in leaves. Therefore, previously reported apoplastic bypasses may be due to injuries from root manipulation during experiments. We compared the accumulation of PTS in leaves of soil- and hydroponic-grown wild-type *Arabidopsis*. PTS accumulated in leaves of hydroponic-grown but not in soil-grown plants. This indicates that hydroponic culture induces root injury creating apoplastic bypasses which do not exist in healthy, undisturbed roots.

P2-23. Developing biotechnological tools to select beans with enhanced folic acid levels. Y.-S. Shim, F. Garabagi, and K.P. Pauls. *Department of Plant Agriculture, Crop Science, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Dry beans (*Phaseolus vulgaris*) have given Canadian farmers the highest rate of return per hectare of all of the field crops for the past few years. Beans are an excellent source of dietary folic acid (Vitamin B), which acts as a cofactor in one-carbon transfer reactions to synthesize components of DNA, RNA, and proteins but levels of this compound can vary more than 3 fold among varieties. Folate deficiency is one of the world's most common human nutrition problems. Folate plays an important role in preventing neural tube disorders in newborns as well as helping to prevent heart disease and cancer. Fragments of six genes of the central folic acid synthesis pathway in *Phaseolus* were cloned and sequenced. The sequences were compared to known sequences from other plant species to confirm their identity. The activities of the folic acid synthesis genes in developing seeds of 10 bean varieties will be measured by RT- PCR and the folate levels in their dry seeds will be assayed by HPLC. This data will be used to identify correlations between gene expression and folate content in bean seeds. This information may allow the development of new tools for the selection of high folate beans.

P2-24. Measuring microbial phosphate solubilization using *in vivo* and *in vitro* methods. S.J. Steckler and M.E. Leggett. *Philom Bios, 3935 Thatcher Avenue, Saskatoon, SK S7R 1A3, Canada.*

Phosphate solubilization by bacteria and fungi has gained interest around the world as a means to improve fertility in soils with poor phosphate availability. Numerous bacterial and fungal isolates have been identified as phosphate-solubilizing microorganisms (PSMs). However, much of this research involves *in vitro* testing on solid and liquid media, and does not examine phosphate solubilization in association with soil or plant roots. Development of an *in vivo* assay to measure the phosphate solubilizing ability of microorganisms in the presence of plant roots and in a soil environment will improve the screening methods for selecting PSMs, and improve understanding of how growth conditions affect the ability of an inoculant organism to solubilize phosphorus. The scope of the project includes using *in situ* methods such as water displacement, anion exchange membranes, and micro-suction cups, to measure changes in soil solution phosphate concentrations. Results from the *in vivo* assays will be compared to the traditional *in vitro* tests to determine their appropriateness as screening tools for potential PSMs.

P2-25. Investigation of isoprenoid biosynthesis in *Artemisia annua* L. utilizing trichome-specific EST's. D.R. Polichuk, K.T. Teoh, D.W. Reed, and P.S. Covello. *Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada.*

Artemisia annua L. (Asteraceae) is a chinese herb that possesses a myriad of terpenoid compounds which are biosynthesized and stored in the 10-cell biseriate glandular trichomes present on the aerial tissues of the plant. Of particular importance is the sesquiterpene lactone artemisinin, which is currently used to produce frontline anti-malarial drugs and also shows great promise in cancer therapy. Abundant monoterpenes in the essential oil include artemisia ketone, camphor and pinocarvone. Investigations into the biosynthesis of artemisinin and monoterpenes have been conducted through the analysis of Expressed Sequence Tags (EST's) from isolated glandular trichomes. Progress in the evaluation of genes involved in terpenoid biosynthesis as well as preliminary work in the cell-specific localization of the artemisinin pathway will be presented.

P2-26. Physiological characteristics of recent Canada Western Red Spring wheat cultivars: Non-grain spike remobilization of dry matter and nitrogen. H. Wang, T.N. McCaig, R.M. DePauw, and J.M. Clarke. *Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1030, Swift Current, SK S9H 3X2, Canada.*

The registration of Canada Western Red Spring (CWRS) wheat cultivars requires a stringent quality standard including high protein concentration and certain kernel visual distinguishability including kernel size, shape and color. The harsh environment on the Canadian prairies including short growing-season, limited rainfall and high temperatures also limit alternatives for yield improvement, such as reducing height and prolonging maturity. Therefore, it is extremely difficult to achieve genetic gains in grain yield for CWRS wheat. A large spike has been recognized as an important characteristic of high-yielding wheat ideotypes. Spike size is also associated with the capacity of the grain to assimilate nitrogen from vegetative tissues. Previous studied showed that some newer high-yield CWRS cultivars had larger spikes than older cultivars. These new cultivars also had lower N concentration in glume and rachis at maturity indicating more N remobilization to the grain from non-grain spike parts. The objective of this study was to investigate genotypic difference in spike dry matter and nitrogen remobilization during grain filling. Results showed that mean non-grain spike dry matter and N remobilizations of six cultivars over three years were 3% of spike grain yield and 12% of spike grain N, respectively. There was no genotypic difference in spike dry matter remobilization, but newer cultivars had significantly higher non-grain spike N remobilization than older cultivars.

P2-27. ***NOT PRESENT***

P2-28. ***NOT PRESENT***

P2-29. ***NOT PRESENT***

P2-30. ***NOT PRESENT***

P2-31. Genetic variation in *Eruca vesicaria* (L.) Cav. S.I. Warwick, R.K. Gugel, C. Gómez-Campo, and T. James. *Agriculture and Agri-Food Canada, Eastern Cereal and Oilseed Research Centre, K.W. Neatby Bldg., Central Experimental Farm, Ottawa, ON K1A 0C6, Canada; (R.K.G.) Agriculture and Agri-Food Canada, Saskatoon Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; and (C.G.-C.) Departamento de Biología Vegetal, Universidad Politécnica de Madrid, 28040-Madrid, Spain.*
Eruca vesicaria subsp. *sativa* (syn. *E. sativa*) is a cruciferous vegetable and oilseed crop that is high in erucic acid. It occurs throughout the Mediterranean region and western Asia, and has been naturalized elsewhere as a crop/weed escape. It is closely related to subsp. *vesicaria* (Spain) and subsp. *pinnatifida* (northwestern Africa). This study evaluated patterns and levels of diversity in the three subspecies based on 234 amplified fragment length polymorphisms (AFLP), and evaluated agronomic and seed quality data in field trials at Saskatoon, Saskatchewan (western Canada). AFLP data revealed three main clusters: 'Sativa' (33 accessions of subsp. *sativa*), 'Vesicaria' (nine accessions of subsp. *vesicaria*) and 'Pinnatifida' (one accession of subsp. *pinnatifida* and three Moroccan accessions of subsp. *sativa*). The Sativa cluster separated into Mediterranean and Asian groups, likely reflecting differences in origin (wild vs. cultivated) or primary usage (vegetable vs. seed oil). The origin of an introduced Mexican population was confirmed as subsp. *sativa*. The highest levels of diversity were found in the Sativa cluster (88% AFLP polymorphisms) and the least in the Vesicaria (56%) and Pinnatifida (39%) clusters. Extensive variation was observed among 159 subsp. *sativa* accessions evaluated in the field trials, and overall findings indicated a favourable agronomic potential for western Canada.

P2-32. Improved somatic embryogenesis yield and biolistic transformation efficiency in *Triticum aestivum* (Superb). M.S. Greer, F. Eudes, and I. Kovalchuk. *University of Lethbridge, Department of Biology, 4401 University Drive, Lethbridge, AB T1K 3M4, Canada; and (F.E.) Lethbridge Research Station, Agriculture and Agri-Food Canada, Department of Cereal Biotechnologies, 5403 1st Ave. S., Lethbridge, AB T1J 4B1, Canada.*
The capability to introduce novel genes into new systems has been shown to be a very powerful tool in humanitarian, scientific and commercial fields. Transformation of crops is still not a routine process and any improvement would of great asset. Our work shows that modification of the media composition leads to 2-2.5-fold increase in the number of somatic embryos regenerated from dissected wheat scutella. We also show that exposure to certain salts are capable of improving the transformation efficiency obtained from microparticle bombardment of wheat tissue. Currently we are analyzed the efficiency of multiple transgene insertions in wheat. In our approach we used the delivery of 3 independent plasmids carrying various transgenes. Preliminary data suggest the increase in the frequency of delivery of these transgenes into wheat tissue. The influence of these salts seems, however, to be cultivar-specific.

P2-33. Integration of SSR and SNP markers using an interspecific cross *C. arietinum x C. reticulatum* for mapping of ascochyta blight resistance. G.K. Kishore, L. Buchwaldt, B. Mooney, H.M. Booker, B. Tar'an, and A. Sharpe. *Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; and (B.T.) Crop Development Centre, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.*
A narrow diversity in cultivated chickpea (*Cicer arietinum* L.) has motivated development of molecular markers based on single nucleotide polymorphism (SNP) for mapping of the genome and for use in marker-assisted selection in breeding programs. A population of 94 recombinant inbred lines (RILs) of an interspecific cross, *C. arietinum* line ILC 72 x *C. reticulatum* line Cr 5-10, was selected to maximize the likelihood of SNP discovery. In order to anchor the new SNP markers to previously published markers the same population was screened with 85 simple sequence repeat (SSR) markers using a Megabace 1000 capillary electrophoresis platform. Line ILC 72 is highly resistant to *Ascochyta rabiei* (Pass.) Lab., which a serious foliar pathogen of chickpea world wide. Phenotyping of the RILs for ascochyta reaction was conducted by inoculation with isolate 3279a in a detached leaf assay. Analysis for the presence of quantitative trait loci (QTL) conferring resistance to ascochyta blight will be reported as well as the SSR linkage map showing integration of the first SNP markers.

P2-34. ***NOT PRESENT***

P2-35. Storage and shelf life assessment of late harvest sweet cherries. F. Kappel and P. Toivonen. *Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, Summerland, BC V0H 1Z0, Canada.*
Changes in the market have increased the importance of sweet cherry (*Prunus avium* L.) storage and shelf life. Cherries are now shipped great distances either by air or sea freight. This research was undertaken to study the response of a number of new late-ripening-cherries to modified atmosphere packaging (MAP) and extended shelf life (SL) tests in 2006. The cultivars 'Lapins', 'Sweetheart', 'Staccato', 'Sovereign', and 'Sentennial' were treated with gibberellic acid (GA) or left untreated, stored for 4 weeks at 1°C in MAP bags (PD 941 polyolefin) then removed from the bags and stored for 5 days at 10°C. At harvest, after storage in MAP, and after

SL tests, fruit quality measurements were taken along with assessments for defects. There were significant interactions between cultivar and GA application for all three defects (pitting, pebbling and stem browning) regardless at which time the ratings were done (at harvest, after MAP storage, or after MAP storage plus 5 day SL test). GA increased the pitting of 'Lapins', 'Sweetheart', and 'Staccato' after the SL test and reduced it for 'Sentennial' and 'Sovereign'. Pebbling was increased significantly by GA on 'Lapins' and reduced on 'Staccato' and 'Sovereign'. There was no difference for 'Sweetheart' and 'Sentennial' after the SL test. After the SL test 'Lapins' had more stem browning when GA was applied whereas all other cultivars had lower stem browning ratings after GA applications.

P2-36. Nectary development, anatomy, and ultrastructure in *Lilium philadelphicum* L. J. Stolar and A.R. Davis. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*

Lilium philadelphicum L. (Saskatchewan's floral emblem) is distributed throughout North America, where it grows in both disturbed and undisturbed habitats. Despite a substantial population decrease on the prairies over the past two centuries, provincial legislation has assisted in its recovery, to the extent that it is currently classified as 'common' in Saskatchewan. Studies in the eastern U.S.A. have shown that flowers of *L. philadelphicum* are visited by insects, especially butterflies and bees, which are attracted by an abundance of floral nectar and pollen. *Lilium* nectar typically contains sucrose, glucose and predominantly fructose. However, studies of nectar composition and nectary structure are unknown for this species in Saskatchewan. We are currently investigating the development, anatomy, and ultrastructure of the floral nectaries of *L. philadelphicum*, which are located at the base of each of the three sepals. Flower buds as well as open flowers, all of increasing age prior to and following anthesis, were examined to study developmental changes in the nectaries. The nectariferous tissue was fixed in 3% glutaraldehyde, post-fixed in 1% osmium tetroxide and dehydrated in ethanol before embedding in epon-araldite resin for ultra-thin sectioning and examination by transmission electron microscopy. Results of transmission electron microscopy are presently being studied. Further studies will involve determining the volumes and solute concentrations of the nectar itself.

P2-37. Transcript and hormone profiling of transgenic *Brassica napus* plants with increased seed oil content. N. Sharma, M. Anderson, A. Kumar, Y. Zhang, D.C. Taylor, S.R. Abrams, and P.R. Fobert. *Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada.*

Seed oil accumulates primarily as triacylglycerol (TAG). While the biochemical pathway for TAG biosynthesis is largely characterized, its regulation remains unclear. Previous research identified two genes, mitochondrial pyruvate dehydrogenase complex kinase (mtPDCK), and microsomal diacylglycerol acyltransferase (DGAT), controlling rate-limiting steps in the pathway. Overexpression of *DGAT* or silencing of *mtPDCK* result in substantial increases in oil content and seed size. To understand the regulation of these key steps in seed oil synthesis, we have initiated transcriptome and metabolome analysis of transgenic canola prototypes. Transcriptome analysis in seeds at the onset of oil accumulation using cDNA microarrays identified a number of genes differentially expressed between the wild type and the transgenic lines, suggesting that altered expression of *DGAT* or *mtPDCK* result in substantial transcriptional changes. A small fraction of genes appeared to be differentially expressed among individual lines, suggesting possible feedback or feed-forward effects associated with altered levels of DGAT or mtPDCK. Metabolome analysis focused on oil content and composition of mature seed and major classes of plant hormones during seed oil deposition. Oil content was elevated by 3-4% with no change in composition of the TAGs, and seed weights increased by 20-29%. Levels of auxins and cytokinins varied between transgenic lines and the wild type while ABA remained unchanged.

P2-38. Regulation of camphor synthesis in lavender. A. Boeckelmann and S.S. Mahmoud. *Centre for Natural Product Research, University of British Columbia Okanagan, 3333 University Way, Kelowna, BC V1V 1V7, Canada.*

Lavender essential oil is valued for its application in cosmetics, perfumery and alternative medicine; however, the lavender oil business is challenged by the divergence between lavender species that produce high oil quantities and those that produce oil of high quality. We analysed the essential oil of several lavender species (*Lavandula* spp.) from three different locations in the Okanagan (British Columbia). Our data confirm previous observations that oil quality and scent are defined by the monoterpenes camphor, limonene and linalool: while high quality oils contain high amounts of limonene and linalool, oil quality deteriorates with increasing camphor levels. Studies in sage (*Salvia officinalis*) suggest that camphor synthesis is regulated through the transcription of camphor specific monoterpene synthases. In addition, high inter- and intra-species homology among monoterpene synthases suggests analogous camphor synthetic pathways in sage and lavender. To gain a better understanding of camphor synthesis and regulation, we will isolate camphor synthases through a homology screen of lavender mRNA and define the site of camphor synthase transcription. Tissue specific transcription will be quantified and compared to absolute amounts of camphor produced, which will indicate whether monoterpene metabolism is regulated transcriptionally or via other downstream mechanisms. Attained results will guide future attempts to

improve lavender essential oils through genetic engineering or revised cultivation practices.

P2-39. Mycovitality, a new concept of plant biotechnology. V. Vujanovic. *Agri-Food Innovation Fund Chair in Agric Microbiology and BioProducts, and Department of Applied Microbiology and Food Science, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.*

This study emphasizes on the new concept of "mycovitalism": the relationship between endophytic fungi and seeds, maintaining their vitality and leading to germination. An innovative fungal bioassay to address the question of orchid seed viability is described in which viability is evaluated using co-culture with compatible *Fusarium* strain. In viable seeds, this leads to seed coloration and germination. This *Fusarium* phylogenetical status was defined based on sequences of the EF-1 alpha gene. The culture-independent PCR-DGGE fingerprinting method was optimized to select promising strains for orchid seed viability testing in orchid production using biotechnology. The *Orchidaceae* were selected as a model system for future studies on plants with minute seeds.

P2-40. Bio-prospecting new accessions of *Lonicera caerulea* (Blue honeysuckle) from boreal ecosystems in Saskatchewan. J. Treloar and R. Bors. *Fruit Breeding Program, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*

Blue honeysuckle, *Lonicera caerulea*, is an emerging fruit crop on the Canadian prairies. Accessions of Blue honeysuckle, with potential to introduce important genetic material into the Fruit Breeding Program at the University of Saskatchewan, can be found in boreal ecosystems of Saskatchewan. Successful plant improvement expeditions to boreal areas of Saskatchewan in spring and summer of 2006 have produced new genetic material to be used to improve existing lines of Blue honeysuckle. The Fraser Herbarium in the College of Agriculture and Bioresources housed a collection of *Lonicera villosa* (caerulea) samples collected in northern boreal ecosystems of Saskatchewan. Commonly the plant was located in marshy areas, black spruce peat lands, treed fens, or adjacent to creekbeds, rivers and lakes, supporting available literature describing Canadian *Lonicera caerulea* habitat (Lahring and Heinjo, 2003). Plants co-existing with *Lonicera caerulea* included Labrador-tea *Ledum groenlanicum*, Sphagnum moss *Sphagnum fuscum*, and Small Cranberry *Oxycoccus microcarpus* Turcz. Successful plant collecting missions to six locations in Saskatchewan were completed in May-August 2006. Information collected at each site included coordinates, elevation, date, and plant development stage. Early to mid May was found to be the optimum collection time. *Lonicera caerulea* is one of the first species in the ecosystem to break dormancy; early leaf growth stands out amongst adjacent, dormant plants. One hundred and twenty eight accessions from six sites were collected and propagated. In March 2007, the Fruit Breeding Program successfully crossed Saskatchewan accessions with existing germplasm from Japan, Russia, and the Kuril Islands.

P2-41. Effects of grafting techniques on plant growth and fruit yield of greenhouse tomatoes. X. Hao, Q. Wang, S. Khosla, and S. Borhan. *Greenhouse and Processing Crops Research Centre, Agriculture and Agri-Food Canada, 2585 County Road 20, Harrow, ON N0R 1G0, Canada; and (S.K.) Ontario Ministry of Agriculture, Food and Rural Affairs, 2585 County Road 20, Harrow, ON N0R 1G0, Canada.*

Grafted transplants are being adopted in Canada to increase plant vigour and fruit yield in greenhouse tomato (*Lycopersicon esculentum* Mill.) production. However, there has been little research on methods for preparing grafted transplants and their effects on crop performance. This study evaluated the crop performance of the transplants prepared with different post-grafting methods. Two trials were carried out from Jan. to Sept. 2006. The post-grafting treatments included R (regular, non-grafted), G-TS (grafted single-head), G-TT (grafted seedlings were topped at 2 true leaf stage to generate the twin heads) and G-CT (grafted seedlings were topped at cotyledon stage to generate twin heads). Two beefsteak cultivars, 'Macarena' and 'Big-Dina', and one cluster cultivar, 'Clarance', were grafted on root stock 'Maxifort'. Topping of the grafted seedlings to generate two heads delayed the growth of the transplants and the first fruit harvest by 6 days. As a result of this delay, the early fruit yield with the twin-heads (G-CT and G-TT) was lower than that with the single head (R and G-TS). The total marketable yield of grafted plants was similar (for 'Macarena' and 'Clarance') or higher (for 'Big-Dina') than non-grafted plants even if the fruit harvesting period was shorter. Proper scheduling for raising grafted transplants is essential for achieving full benefits of grafting.

P2-42. Antioxidant activities of newly developed Day-neutral and June-bearing strawberry lines. S. Khanizadeh, S. Tao, S. Zhang, R. Tsao, D. Rekika, R. Yang, and M.T. Charles. *(S.K. & S.T.) Horticultural Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Blvd., St-Jean-sur-Richelieu, QC J3B 3E6, Canada; (S.T. & S.Z.) Nanjing Agricultural University, 1 Weigang, Nanjing, Jiangsu Province 210095, P.R. China; and (R.T. & R.Y.) Food Research Program, Agriculture and Agri-Food Canada, 93 Stone Road West, Guelph, ON N1G 5C9, Canada.*

This study was carried out to evaluate the total antioxidant capacity, total phenolic content and composition of known and new advanced selections among June-bearing and Day-neutral genotypes using ferric reducing/antioxidant power (FRAP), Folin-Ciocalteu (FC) and high performance liquid chromatography (HPLC) assay. The parameters varied between different genotypes. Mean of

total phenolic content and total antioxidant capacity in Day-neutral strawberries were estimated to be 1341 µg/g and 2062 mg/g, respectively, which were higher than those in June bearing genotypes (1119 µg/g and 1917 mg/g), there was a positive correlation between total phenolic content and total antioxidant capacity. Conversely, June-bearing strawberries had higher mean of each group of phenolics than those in Day-neutral genotypes, no correlation between individual compound and total antioxidant activity (FRAP) was obtained. These results revealed the importance of genetic background for the content of total phenolics, showed the potential value of certain new cultivars and advanced lines as parents in a breeding program to produce new strawberry cultivars with higher levels of antioxidant capacity.

P2-43. Phytochemical distribution of selected apple lines and cultivars for fresh market and processing. S. Khanizadeh, L. Ding, R. Tsao, D. Rekika, R. Yang, M.T. Charles, and H.P.V. Rupasinghe. *Horticultural Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Blvd., St-Jean-sur-Richelieu, QC J3B 3E6, Canada; (R.T. & R.Y.) Food Research Program, Agriculture and Agri-Food Canada, 93 Stone Road West, Guelph, ON N1G 5C9, Canada; and (H.P.V.R.) Tree Fruit Bio-product Research Program, Nova Scotia Agricultural College, P.O. Box 550, Truro, NS B2N 5E3, Canada.*

The phenolic composition in the flesh and peel of nineteen advanced apples breeding lines and cultivars to be released for fresh market and processing was determined by high performance liquid chromatography (HPLC). Total phenolic content (TPC) by the Folin-Ciocalteu (FC) method and total antioxidant capacity using ferric reducing/antioxidant power (FRAP) were also determined. HPLC analysis revealed the presence of several sub-classes of phenolics: proanthocyanidins, hydroxycinnamate acids, flavan-3-ols, flavonols, and dihydrochalcones. The profile of phenolic compounds varied among the nineteen tested genotypes and the peel showed higher concentrations than the flesh. Proanthocyanidins were the most predominant sub-class in both flesh and peel and contributed 49.7% and 48.7% of the total phenolic index (TPI), respectively. Flavonols were not found in the flesh, except for quercetin 3-rhamnoside, which was detected in almost all tested genotypes. In contrast to all other genotypes, flavan-3-ols were not detectable in the flesh of 'Eden'. Cyanidin glycosides were exclusively found in the peel, except for 'Floribunda Rosea' which contains in both peel and flesh. 'Floribunda Rosea' was found to possess the highest concentrations of polyphenols and TAC, whereas 'Eden' had the lowest. The significant variation in total antioxidant capacity (TAC), TPI and TPC indicates the potential use of some new cultivars and advanced lines as parents in breeding programs targeted toward developing superior apple genotypes with higher levels of antioxidants.

P2-44. Browning potential of new apple varieties. J. DeEll, P. Toivonen, S. Khanizadeh, and C. Hampson. *Ontario Ministry of Agriculture, Food and Rural Affairs, Simcoe, ON, Canada; (P.T. & C.H.) Agriculture and Agri-Food Canada, Summerland, BC, Canada; and (S.K.) Agriculture and Agri-Food Canada, St-Jean-sur-Richelieu, QC, Canada.*

One of the largest costs in producing fresh-cut apple slices is the anti-browning solution. Therefore, the elimination or any reduction in the amount of solution required would be very beneficial to the producer. Some apple varieties brown more quickly and severely than others upon cutting, depending on the inherent amount of responsible enzymes and antioxidant levels. The objective of this work has been to evaluate the browning potential of several new apple varieties, including 'Ambrosia', Aurora Golden Gala™, 'Galarina', 'GoldRush', 'Honeycrisp', and a recent release (SJCA38R6A74 = Eden™) and a selection (SJCA16R5A15) from Quebec. Fruit from each variety were harvested either in Ontario and/or British Columbia during commercial harvest and stored at 0-1°C for 1-3 months. Several fruit were then removed periodically throughout the storage duration and sliced within 1 hour. After cutting, the slices were rinsed in running tap water, allowed to drip dry, and placed into zip-lock bags. Slices in bags were held at 4.5-5°C for 1-3 weeks and then assessed for browning. Overall, Eden™ and the other Quebec selection showed the least amount of browning, with slight to none. The other varieties all exhibited some degree of moderate to severe browning at one or both locations (Ontario and BC). When post-cutting treatments were evaluated for ON and BC-grown 'Ambrosia', results on quality retention were similar for both growing areas.

P2-45. 'Hanhong' pear. M. Zhang, L. Ding, Q. Wang, M. Feng, G. Xing, and S. Khanizadeh. *Pomology Institute Academy of Agriculture Science of Jilin Province, Gongzhuling 136100, P.R. China; and (S.K.) Agriculture and Agri-Food Canada, Horticultural Research and Development Centre, 430 Gouin Blvd., St-Jean-sur-Richelieu, QC J3B 3E6, Canada.*

'Hanhong' (*Pyrus ussuriensis* Maxim × *P. bretschneideri* Rehd.) is a new high quality asian pear with excellent firmness, crispness and long shelf life. Fruit of 'Hanhong' are very attractive and the tree is very winter hardy. The fruit and leaves are resistant to pear scab (*Venturia pirina* Aderh) and black spot (*Alternaria kikuchiana* Tannka) disease. 'Hanhong', tested as 86-1-32, is a progeny resulting from a cross between 'Nanguoli' (*Pyrus ussuriensis* Maxim.) × 'Jinsu' (*Pyrus bretschneideri* Rehd.) made in 1986 at the Pomology Institute Academy of Agriculture Science of Jilin Province and was released in 2003 by the author (MZ). 'Hanhong' tested in Jilin province with minimum winter temperatures between -30°C to -35°C which sometimes drop to as low as -45°C in extreme years with little snow cover. Limited quantities of non-indexed budwood are available for research

purposes from the author (MZ) after signing a non-propagation agreement. Nurseries can obtain a multiplication license from Meiosis Inc. (Bradbourne House, Stable Block, East Malling, Kent, UK ME19 6DZ).

P2-46. 'SJCA38R6A74' (Eden™). S. Khanizadeh, Y. Groleau, A. Levasseur, M.T. Charles, R. Tsao, R. Yang, J. DeEll, C.R. Hampson, and P. Toivonen. *Agriculture and Agri-Food Canada, Horticultural Research and Development Centre, 430 Gouin Blvd., St-Jean-sur-Richelieu, QC J3B 3E6, Canada; (R.T. & R.Y.) Agriculture and Agri-Food Canada, Food Research Program, 93 Stone Road West, Guelph, ON N1G 5C9, Canada; (J.D.E.) Ontario Ministry of Agriculture, Food and Rural Affairs, 4890 Victoria Ave. N., P.O. Box 8000, Vineland Station, ON L0R 2E0, Canada; and (C.R.H. & P.T.) Agriculture and Agri-Food Canada, 4200 Highway 97, Summerland, BC V0H 1Z0, Canada.*
'SJCA38R6A74' is a new high quality cultivar with improved firmness, crispness and much longer shelf life than 'McIntosh' and 'Cortland'. The fruit has superior flavor and does not abscise at maturity. The flesh is juicy, firm, crisp and resistant to bruising. Flesh resists browning, making it an excellent candidate for fresh fruit slices, fruit salad, dried apple chips and processing (juice, cider and ice-cider). The Trade Mark 'Eden' is used for sale, distribution and marketing. 'SJCA38R6A74' originated from a cross made in 1971 between 'Linda' and 'Jonamac' at the Agriculture and Agri-Food Canada (AAFC), Quebec. 'Eden' is aromatic, sweet, juicy, firm and crisp, resistance to browning, most likely due to low levels of phenolic compounds such as chlorogenic acid and epicatechin, the key substrates for enzymatic browning in apples. Mature fruit of 'SJCA38R6A74' does not fall off from the tree and even hangs on during the winter. In laboratory tests the new apple remained crisp with no signs of browning after 2-3 days at room temperature make it ideal for fresh eating in salads, packaged as dried apple chips or processed for juice or apple cider. Nonexclusive licenses can be obtained from AAFC or from Meiosis (Bradbourne House, Stable Block, East Malling, Kent, UK ME19 6DZ).

P2-47. 'St-Jean d'Orléans' strawberry. S. Khanizadeh, M. Deschênes, A. Levasseur, O. Carisse, M.T. Charles, D. Rekika, L. Gauthier, A. Gosselin, R. Tsao, R. Yang, J. DeEll, and J.A. Sullivan. *Agriculture and Agri-Food Canada, Horticultural Research and Development Centre, 430 Gouin Blvd., St-Jean-sur-Richelieu, QC J3B 3E6, Canada; (L.G. & A.G.) Les Fraises de l'Île d'Orléans Inc., St-Laurent, Île d'Orléans, QC, Canada; (R.T. & R.Y.) Agriculture and Agri-Food Canada, Food Research Program, 93 Stone Road West, Guelph, ON N1G 5C9, Canada; (J.D.E.) Ontario Ministry of Agriculture and Food, P.O. Box 587, 1283 Blueline Road & Highway 3, Simcoe, ON, Canada; and (J.A.S.) Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada.*
'St-Jean d'Orléans' is a new June bearing strawberry cultivar (*Fragaria* x *ananassa* Duch.) released by Agriculture and Agri-Food Canada, Horticultural Research and Development Center, Quebec. 'St-Jean d'Orléans' was introduced because it has large, very firm, light red shiny fruit, with excellent shelf life and resistance to leaf diseases. 'St-Jean d'Orléans' is a selection resulting from a cross between 'L'Acadie' and 'Joliette'. 'St-Jean d'Orléans' is recommended for Eastern Central Canada, especially in areas where the climate is similar to that of Quebec (winter temperatures down to –30°C and warm and humid summers with unpredictable mixture of sun and rain). Nonexclusive multiplication licenses can be obtained from Agriculture and Agri-Food Canada, or from Meiosis Ltd. (Bradbourne House, Stable Block, East Malling, Kent, UK ME19 6DZ).

P2-48. Evaluation of *in vitro* regeneration of *Arabidopsis thaliana* using shoot apical meristem gene markers. C.R. Bird, M.S. Kahlon, and E.C. Yeung. *University of Calgary, #301 Biological Sciences, 507 Campus Drive NW, Calgary, AB T2N 1N4, Canada.*
Plants are able to be propagated by *in vitro* regeneration of somatic tissue. While useful for propagation of valuable plants, regeneration often occurs at very low rates or results in developmental abnormalities. A critical step in successful regeneration is the formation and maintenance of a *de novo* shoot apical meristem (SAM). If a functioning SAM is established and maintained, it will give rise to a functional shoot. Genes involved in the initiation and maintenance of a functioning *Arabidopsis thaliana* SAM are known, and include the homeodomain transcription factors wuschel (wus) and shoot meristemless (stm). In this study, we use β-glucoronidase fused downstream of wus and stm *A. thaliana* promoters to visualize the origin and maintenance of the regenerated SAM. This technique gives us criteria to evaluate regeneration systems beyond simply waiting to see the final product, as we are able to demonstrate a genetic commitment to SAM formation in somatic tissue earlier than evidence of SAM morphology, as well as see a continued genetic commitment within the potential SAM. We are then able to systematically tailor our tissue culture environment to specifically optimize the initiation and maintenance of SAM genes.

P2-49. High throughput screening of plant mutants for identifying the numbers of T-DNA insertion loci and copies using quantitative PCR technology. S. Wei, K. Narayanan, B.Y. Yu, and A. Hannoufa. *Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*
Agrobacterium mediated T-DNA activation tagging and knockout technologies are widely used for plant mutagenesis. Identification of T-DNA insertion locus and copy numbers in the mutated plants is crucial for further molecular characterization of the mutants. However, the conventional T-DNA insertion identification methods such

as Southern bolt are laborious and time consuming. In this study, quantitative PCR technology was employed for high throughput screening of plant mutants. About 60 Arabidopsis mutants (Columbia) with T-DNA activation tagging fragment from the binary vector pSKI015 (Weige et al., Plant Physiol. 2000, 122, pp. 1003–1013) and differing seed colours from wild type's were used for qPCR screening. Arabidopsis single-copy genes encoding high-mobility-group protein (Y10836) and glyceraldehyde-3-phosphate dehydrogenase (AT2G24270) were employed as internal reference genes. qPCR analyses were performed using Invitrogen SYBR® Green qPCR SuperMix-UDG Kit according to manufacturer's protocol. Mutant T-DNA insertion copy numbers were identified by comparing the fluorescent intensities of inserted *Bar* gene and internal reference gene. Mutants with multiple T-DNA insertion copies would be subject to a further qPCR analysis using the primers which cover all the combinations of T-DNA co-integration in one locus for the purpose to identify the insertion locus number. The two-step analyses can be combined together and completed in one or two qPCR reactions.

P2-50. Enhancing carotenoid content of *Brassica napus* seeds by downregulation of lycopene epsilon cyclase. B. Yu, D.J. Lydiate, U.A. Schäfer, and A. Hannoufa. *(B.Y.) Department of Applied Microbiology and Food Science, Agriculture Building, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; and (B.Y., D.J.L., U.A.S. & A.H.) Agriculture and Agri-Food Canada, Saskatoon Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

The accumulation of carotenoids in higher plants is regulated by the environment, tissue type and developmental stage. In *Brassica napus* leaves, β-carotene and lutein were the main carotenoids present while petals primarily accumulated lutein and violaxanthin. Carotenoid accumulation in seeds was developmentally regulated with the highest levels detected at 35-40 days post anthesis. The carotenoid biosynthesis pathway branches after the formation of lycopene. One branch forms carotenoids with two β- rings such as β-carotene, zeaxanthin, antheraxanthin and violaxanthin, while the other introduces both β- and ε-rings in lycopene to form α-carotene and lutein. We used two RNAi constructs of lycopene ε-cyclase (ε-*CYC*) to alter carotenoid accumulation in seeds of *B. napus*. Transgenic seeds expressing this construct had increased levels of β-carotene, zeaxanthin, violaxanthin and, unexpectedly, lutein. The higher total carotenoid content in ε-CYC silenced seeds suggests that this enzyme is the rate-limiting step in the carotenoid biosynthesis pathway.

P2-51. ***NOT PRESENT***

P2-52. Plant micropropagation in wild sage (*Salvia multicaulis*). H.R. Ghasempour, D. Kahrizi, and S. Borzoo. *Biology Department, Razi University, Kermanshah 67149, Iran; and (D.K.) Plant Breeding and Biotechnology Department, Faculty of Agriculture, Razi University, Kermanshah, Iran.*

Salvia multicaulis is an important medical plant of west – Iran. Root and aerial parts of this plant is containing variety of essential oil. An efficient plant regeneration protocol of the wild sage (*Salvia multicaulis*) from cotyledon was developed. Excised cotyledon explants from *in vitro* seedling after 6 days of germination were cultured on MS medium containing 30 gr/l sucrose, 0.6% agar and 0, 2, 5, 10 mg/l BAP for production of leaf. For proliferation, explants cultured on MS mediums containing different concentrations (0, 10, 20 and 30 gr/l) of sucrose. Proliferated microshoots were rooted on MS medium with 0, 1, 3 mg/l IBA. Results indicated that leaf number was highest for each explants cultured on a MS medium containing 2 and 5 mg/l BAP. There was not significant difference on the leaf number and length of plantlet with changing of sucrose concentration. Microshoots cultured on MS medium without a growth regulator exhibited the highest rooting.

P2-53. ***WITHDRAWN***

P2-54. ***NOT PRESENT***

P2-55. ***NOT PRESENT***

P2-56. ***NOT PRESENT***

P2-57. ***NOT PRESENT***

P2-58. ***NOT PRESENT***

P2-59. ***NOT PRESENT***

P3. Plant responses to the environment

P3-1. Seed yield, quality and sulphur uptake of different *Brassica* oilseed crops in response to sulphur fertilization. S.S. Malhi, Y. Gan, and J.P. Raney. *Agriculture and Agri-Food Canada (AAFC), P.O. Box 1240, Melfort, SK S0E 1A0, Canada; (Y.G.) AAFC, Swift Current, SK S9H 3X2, Canada; and (J.P.R.) AAFC, Saskatoon Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Field experiments were conducted in 2003, 2004 and 2005 to determine seed yield, quality and sulphur (S) uptake response of different *Brassica* oilseed species/cultivars to S fertilization on a S-deficient Gray Luvisol (Boralf) soil near Star City, Saskatchewan. *Brassica juncea* canola 'Arid', *B. juncea* canola 'Amulet', *B. juncea* mustard 'Cutlass' and *B. napus* 'InVigor-2663' were tested with five rates of S fertilizer (0, 10, 20, 30 and 40 kg S ha^{-1}). All *B.* species/cultivars gave a positive response for most

parameters to S fertilizer in all 3 years, but the magnitude of response varied with species/cultivar and year. Seed yield was highest for *juncea* mustard in a dry year (2003), but was highest for Invigor-2663 hybrid canola in years with above-average precipitation (2004 and 2005). Seed yield was maximized at 30 kg S ha^{-1} rate for all species/cultivars. Oil concentration in seed increased with S fertilization for all species/cultivars. There was also significant (but small) increase in protein concentration of seed due to S fertilization. Regardless of S application, *juncea* mustard, as expected, had considerably higher concentrations of glucosinolates in seed than the other *B.* species/cultivars, and S uptake in seed was highest for this species in all years. Our findings suggest similar S fertilizer requirements for optimum seed yield for all *B.* species/cultivars on S-deficient soils.

P3-2. Essential oils as sprout inhibitors and their effects on potato seed tuber performance. X. Song, C. Neeser, M. Bandara, and K.K. Tanino. *Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; and (C.N. & M.B.) Crop Diversification Centre South, Alberta Agriculture and Food, 301 Horticultural Station Road East, Brooks, AB T1R 1E6, Canada.*

Increasing concerns regarding the safety and environmental impact of traditional sprout inhibitors (chloropropham) has increased interest in alternate sprout inhibitors including essential oils. This study examined the impact of concentration and application duration of dill, spearmint and clove oils on potato sprout growth and the yield potential of seed tubers treated with essential oils. Dill and spearmint oils were applied as vapors to 'Russet Burbank' tubers in one-liter containers at 0, 0.5, 5, 15, 50 and 200 mg/L airspace. Increasing concentrations of both essential oils had significant linear and quadratic effects on sprout growth. A dose of 26.8 mg/L airspace would produce a 50% reduction in sprout growth at 30 days after dormancy break. Spearmint oil applied at 30 mg/L airspace or higher had a greater sprout suppressing effect on 'Piccolo' tubers than dill or clove oil. This could be due to the higher content of carvone in spearmint oil (82.3%) than in dill oil (30.5%). When 'Piccolo' seed tubers were treated with the three essential oils at 0, 15, 30, 60, 120 and 240 mg/L airspace for 7 days prior to planting, neither the source of essential oil nor the concentration had any significant effect on tuber yield/plant.

P3-3. Interactive effect of nitrogen and sulphur fertilizer on canola in S-deficient soils. S.S. Malhi. *Agriculture and Agri-Food Canada, Research Farm, Highway 6 South, P.O. Box 1240, Melfort, SK S0E 1A0, Canada.*

Knowledge on the interactive effect of nitrogen (N) and sulphur (S) is essential for maximizing crop productivity. This study determined the interactive effects of N (0, 50, 100 and 150 kg N ha^{-1}) and S (0, 10, 20 and 30 kg S ha^{-1}) fertilizer rates on seed yield, quality, and S and N uptake of canola on Gray Luvisol (Boralfs) soils deficient in available N and S in north-eastern Saskatchewan. In the absence of S application, increasing N rates increased S deficiency symptoms and reduced seed yield and quality. When S was applied, yield, S concentration, and S and N uptake in seed increased with increasing N rates. Irrespective of S rate, fertilizer N had no consistent effect on S concentration, but reduced oil concentration and increased protein concentration. With S fertilization, seed yield, S and N uptake, as well as S and oil concentrations were substantially increased, whereas there was no consistent effect on protein concentration. Response of these parameters to S application was generally greater at higher N rates. In conclusion, at high N rates an increased amount of S is needed on S-deficient soils in the Parkland region to adequately meet S requirements for optimum seed yield and quality of canola.

P3-4. Productivity and water-use efficiency in *Populus trichocarpa* and *P. balsamifera.* V.M. Pointeau and R.D. Guy. *Department of Forest Sciences, Faculty of Forestry, University of British Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4, Canada.*

Increasing net carbon sequestration through the establishment of hybrid poplar plantations could play a substantial role in Canada's continued efforts to reduce greenhouse gases. In order to take full advantage of lands currently available for such projects, however, hybrids must be developed that combine cold hardiness with both high productivity and high drought tolerance, thus demanding a better understanding of links between water-use efficiency (WUE), photosynthesis, endogenouse gibberellin (GA) levels, nitrogen-use efficiency (NUE), and other physiological traits linked to growth and productivity. Poplars for use in carbon sequestration programs would ideally combine high WUE with high productivity, thus implying high photosynthetic capacity. This project will determine the basis for variations in WUE within selected populations of *Populus trichocarpa* and *Populus balsamifera*, along with correlations between WUE, NUE, C isotope content ($\delta^{13}C$), photosynthetic capacity, stomatal conductance, endogenous GA concentrations, and overall productivity. It is expected that genotypes displaying positive correlations between $\delta^{13}C$ values (proxy for long-term WUE) and productivity will also display a high photosynthetic capacity; that genotypes displaying high WUE together with high net photosynthesis will also contain relatively high levels of inherent GAs; and that genotypes displaying relatively high WUE as a result of high sink-driven photosynthetic capacity will show a lower or absent trade-off between NUE and WUE.

P3-5. Responses of five canola and mustard species to varying environments and nitrogen fertilization in

Saskatchewan. Y. Gan, S.S. Malhi, S. Brandt, and F. Katepa-Mupondwa. *Agriculture and Agri-Food Canada, Research Centre, P.O. Box 1030, Swift Current, SK S9H 3X2, Canada; (S.S.M.) Research Farm, P.O. Box 1240, Melfort, SK S0E 1A0, Canada; (S.B.) Research Farm, P.O. Box 10, Scott, SK S0K 4A0, Canada; and (F.K.-M.) Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Brassica juncea canola provides producers in western Canada with an alternate oilseed crop. This study compared fertility responses of *juncea* canola to *napus* and *rapa* canola, *juncea* mustard, and *Sinapis alba* mustard across various environments. The five oilseed species were grown under seven N fertilizer rates at 11 site-years in Saskatchewan. Flowering began 40 days after seeding (DAS) for *alba* mustard and *rapa* canola, 46 DAS for *juncea* canola, and 49 DAS for *napus* canola. *Juncea* canola had longest flowering duration and *napus* canola the shortest. The *napus* canola and *juncea* mustard produced the highest (2045 kg ha^{-1}) seed yields across environments. The N fertilizer required for maximum seed yield in low-yielding environments was 160 kg N ha^{-1} for the mustard species, and 121 kg N ha^{-1} for the canola species. *Juncea* canola had similar responses to N fertilizer as the other oilseeds in low-yielding environments but expressed low N use efficiency at high-yielding environments. We conclude that *juncea* canola is a suitable alternative oilseed in low-yielding environments, and that new cultivars with improved N use efficiency are required to make *juncea* canola a viable alternative in more favorable environments.

P3-6. ***WITHDRAWN***

P3-7. Nitrogen use efficiency and N uptake in five canola/mustard species across the varying environments of Saskatchewan. Y. Gan, S.S. Malhi, S. Brandt, and F. Katepa-Mupondwa. *Agriculture and Agri-Food Canada, Research Centre, P.O. Box 1030, Swift Current, SK S9H 3X2, Canada; (S.S.M.) Research Farm, P.O. Box 1240, Melfort, SK S0E 1A0, Canada; (S.B.) Research Farm, P.O. Box 10, Scott, SK S0K 4A0, Canada; and (F.K.-M.) Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Brassica juncea canola is well adapted to the semiarid regions of western Canada. This study was conducted at 11 site-years in Saskatchewan to determine N-related responses of *juncea* canola, *napus* and *rapa* canola, *juncea* mustard, and *Sinapis alba* mustard. As N fertilizer rates increased from 0 to 250 kg N ha^{-1}, N use efficiency (NUE) (defined as seed yield / amount of N uptake in zero-N control plus amount of applied N) and N fertilizer use efficiency (NFUE) (defined as seed yield in N fertilizer treatment minus seed yield in zero-N control / amount of applied N) decreased for all five species. Minimum NUE and NFUE were achieved with N fertilizer rates >100 kg N ha^{-1}. Nitrogen uptake was the most important covariable explaining trial site variability for NUE. With N fertilizer rates <100 kg N ha^{-1}, NUE differences among sites became more prominent, with low total N uptake resulting in the greatest NUE. The highest-yielding oilseeds (InVigor2663 and Cutlass) had the greatest NFUE when N fertilizer rates were below 100 kg N ha^{-1}. Nitrogen losses due to export of N from harvested seed was greatest for mustard crops, particularly when total N uptake was greater than normal.

P3-8. Microbial communities in the turfgrass phyllosphere. D. Benedetto and T. Hsiang. *Department of Environmental Biology, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Non-plant-pathogenic microorganisms on leaf surfaces have diverse interactions with pathogenic organisms. However, relatively little is known about these apparently innocuous foliar inhabitants. In this study, fungal and bacterial populations on turfgrass leaves were assessed. Healthy leaves of *Agrostis stolonifera* (L.) and *Poa pratensis* (L.) were collected monthly over 10 months. Five to 10 leaves per sample were washed with 1 ml of 0.85% NaCl solution, and 50 µl of this leaf washing plated on potato dextrose agar. After 1 week at 10°C, the number of colony-forming units was counted. Some pure cultures obtained, and the internal transcribed spacer regions of ribosomal DNA (ITS) of fungal isolates and the ribosomal 16S gene for bacterial isolates were amplified for sequencing or digested with restriction enzymes to obtain ribotypes. All *A. stolonifera* microbial groups increased in spring reaching a maximum number in summer. Throughout the summer, filamentous fungi remained near peak numbers, while yeast and bacterial populations declined. In fall, bacteria and yeasts increased in number, while filamentous fungal populations decreased dramatically. Microbial populations from *P. pratensis* slightly decreased from spring to summer. Yeast morphotypes showed the same patterns as the total yeast population, except for *Rhodotorula graminis* (pink morphotype), which increased in summer. In both grasses, *Epicoccum nigrum* (red morphotype) did not change in number, while the black morphotype composed of several species, abruptly decreased from summer to fall.

P3-9. Characteristics of seed shattering and yield losses in five oilseed crops. Y. Gan, S.S. Malhi, S. Brandt, and F. Katepa-Mupondwa. *Agriculture and Agri-Food Canada, Research Centre, P.O. Box 1030, Swift Current, SK S9H 3X2, Canada; (S.S.M.) Research Farm, P.O. Box 1240, Melfort, SK S0E 1A0, Canada; (S.B.) Research Farm, P.O. Box 10, Scott, SK S0K 4A0, Canada; and (F.K.-M.) Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Use of appropriate harvest management can minimize the yield loss caused by seed and pod shattering in crucifer crops. This study determined the difference among five canola/mustard species/cultivars in the degree of resistance to seed shattering and yield losses. *Sinapis alba* mustard

'AC Base', *Brassica juncea* canola 'Amulet', *Brassica juncea* mustard 'Cutlass', *Brassica rapa* canola 'Hysyn', and *Brassica napus* canola 'Invigor2663' were grown at seven site-years in Saskatchewan. Seed yield was highest for *napus* canola (2146 kg ha^{-1}), followed by *juncea* mustard (1971 kg ha^{-1}), and lastly by *juncea and rapa* canola. Straight combining resulted in 13% greater seed yield than swathing for *juncea* canola and *juncea* mustard, and 7% greater for *rapa* canola, while *napus* canola did not show any yield difference between the two harvest regimes (*alba* mustard was not swathed). Under high pod shattering conditions, *juncea* mustard shed about 400 pods m^{-2}, significantly greater than the four other species, and *rapa* canola had the lowest number of shed pods. Largest yield loss during straight combining occurred with *juncea* mustard and *napus* canola (7% of the total seed yield), followed by *alba* mustard (5.2%), and lastly by *rapa* and *juncea* canola (<4%). Selection of species and cultivars coupled with the adoption of straight combining will minimize harvest yield loss in the production of crucifer species.

P3-10. Litter accumulation in Manitoba pastures. S.J. Neufeld and M.H. Entz. *Department of Plant Science, University of Manitoba, 222 Agriculture Building, 66 Dafoe Road, Winnipeg, MB R3T 2N2, Canada.*

Plant litter, which is made up of all dead plant material either standing or lying on the soil surface, is important for soil moisture conservation. Therefore, the management of litter accumulation in pastures has the potential to increase available moisture through the growing season, and to reduce temperature stress during hot months. Grazing intensity affects litter accumulation through the removal of plant biomass and the enhancement of litter decomposition rates; optimal grazing practices can increase forage production through the promotion of the litter layer. The objective of the current study is to identify rates of litter accumulation on Manitoba pastures. Paired litter samples were collected in June 2006 from inside and outside permanent grazing exclosures erected in 2004. The 12 sampling sites were located in four regions across Manitoba: North West (near Dauphin), South West (near Brandon), Central (MacGregor), and South East (Sprague, East Braintree, and Lac du Bonnet), mostly on crown-owned land. The average level of litter was found to be 1200 kg/ha. Rates of accumulated litter outside the exclosures ranged from 76 kg/ha to over 4000 kg/ha, while rates inside the exclosures ranged from 250 kg/ha to 4000 kg/ha. Species composition, regional variation, and soil quality may contribute to the amount of accumulated litter at each site.

P3-11. Shade avoidance and the regulation of cell wall extensibility in *Stellaria longipes.* R. Sasidharan, L.A.C.J. Voesenek, R. Pierik, and C.C. Chinnappa. *Department of Biological Sciences, University of Calgary, Calgary, AB T2N 1N4, Canada; and (L.A.C.J.V. & R.P.) Plant Ecophysiology, Institute of Enivronmental Biology, Utrecht University, Sorbonnelaan 16, 3584 CA, Utrecht, The Netherlands.*

Plants avoid canopy shade in dense vegetations primarily via enhanced shoot elongation and leaf hyponasty. This is the 'shade avoidance syndrome', initiated by changed light quality in a canopy shade (primarily a lowered R/FR ratio and low blue light). Enhanced shoot elongation requires cellular expansion, brought about by a combination of increased turgor and cell wall extensibility. Cell wall extensibility involves a modification of the molecular network of the cell wall leading to 'wall loosening' via the action of wall loosening proteins such as expansins and xyloglucan endotransglucosylase/hydrolases (XTHs). Two ecotypes of *S. longipes*, the alpine and the prairie, that show contrasting shade avoidance traits, were used to investigate the light regulation of cell wall extensibility. It is observed that there is a genotypic variation in phytochrome mediated shade avoidance responses. These responses correlate well with expansin activity, with the XTHs probably playing a secondary role and a possible regulation via blue light receptors only.

P3-12. Genome segregation and genetic drift in arbuscular mycorrhizal fungi. E. Zimmerman, M. Hijri, and M. St-Arnaud. *Institut de Recherche en Biologie Végétale, 4101 rue Sherbrooke Est, Montréal, QC H1X 2B2, Canada.*

The arbuscular mycorrhizal fungi (AMF) are a group of asexual, root-inhabiting, symbiotic fungi which have recently been found to be multigenomic. Spores are multinucleate at maturity and it is thought that many or all of these nuclei migrate directly into the spore from the subtending hypha. It is not known, however, how different genomes segregate into sister spores during sporulation, or whether differential segregation leads to genetic drift over multiple generations in a given environment. The objective of this study is to quantify the amount of genetic variation due to segregation and drift using markers corresponding to different alleles of the two-copy gene PLS (*POL1*-like sequence), found in the AMF species *Glomus etunicatum* Becker & Gerdemann. PLS alleles have been cloned, separated using single-strand conformational polymorphism (SSCP) and sequenced. At present, nine different alleles have been sequenced from forty clones. These markers will be compared using denaturing gradient gel electrophoresis (DGGE) to the PLS allele content of groups of sister spores of *G. etunicatum* grown over several generations on different hosts. Groups of sister spores produced on two different plant hosts by the same mycelium will also be analyzed to determine the effect of microenvironment on the segregation of nuclei. This research will be an important step towards understanding the behaviour of populations of nuclei in multigenomic organisms.

P3-13. Assessment of heavy metals in our food and feed crops in the Canadian Prairie agro-ecosystems. E. Poscher, M.P. Schellenberg, J.M. Clarke, M.R. Fernandez, and T.N. McCaig. *Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, 1 Airport Road, P.O. Box 1030, Swift Current, SK S9H 3X2, Canada.*

Worldwide pollution is at an all-time high. Among the most serious pollutants are heavy metals, such as Cd, Cr, Pb, Hg, and Ni. Once mobilized, these and other heavy metals accumulate in the atmosphere, in waters, soils, sediments, plants, fauna, and humans. Medical and biochemical studies have shown that some chronic diseases are metal-related (i.e., Alzheimer's, MS, autism, cancers, *inter alia*). In 2006, the WHO finally issued a statement saying that "the contamination of food by chemical hazards is a worldwide public health concern and is a leading cause of trade problems internationally". Due to the high pollution levels, it should not be surprising that agricultural crops have been found contaminated with heavy metals and metalloids, such as the cases of Cd in durum wheat, flax, and sunflower, and, in 2006, selenium in yellow peas. Sources of crop contamination have remained unknown, however. The objectives of this research are to survey the major food and feed crops including corresponding soil samples for possible heavy metal and metalloid accumulation in the major agro-ecosystems of Saskatchewan, and to identify potential heavy metal sources in agricultural production systems with the perspective of enhancing food quality and safety of our food system. With this research, we envision developing a risk-management plan with research tools and cost-effective monitoring activities to reduce, possibly eliminate, future incidents of crop contamination and providing site-specific crop cultivar recommendations adjusted to the prevalent combination of soil characteristics and heavy metal levels in the Canadian Prairies.

P3-14. Effect of elaiosome removal in relation to increasing water potential on germination of leafy spurge (*Euphorbia esula* L.) seeds. P.D. Lerner and A.R. Davis. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; and (P.D.L.) Universidad Nacional de La Pampa, Av. Uruguay 151, 6300, Santa Rosa, La Pampa, Argentina.*

Leafy spurge is a perennial invasive species of wide distribution in North America. Its seeds possess a lipid-rich fleshy appendage called an elaiosome that can be removed by ants during seed dispersion stages, otherwise leaving the seeds intact. Elaiosome removal can be a treatment that breaks seed dormancy and enhances germination. On the other hand, hygroscopic properties of the elaiosomes could be involved in facilitating water imbibition to the embryo, potentially a crucial step for rapid seed germination when water availability is limited. We studied the effect of elaiosome removal and incubation water potential on seed germination. Seed was collected from Douglas Provincial Park, south-central Saskatchewan. Elaiosomes were removed by hand, mimicking ant treatment. A water potential gradient was created by polyethylene glycol solutions of 0, -0.25, -0.50, -0.75, -1.0, -1.5 MPa. We used a completely randomized design with four replications, there being 50 seeds per experimental unit. The units were incubated in a growth chamber at 20°C for 16 h and 30°C for 8 h, in darkness, for 28 days. Germination decreased with increasing water stress ($P < 0.001$), but germination was higher with elaiosome removal at 0 ($P < 0.05$), -0.25 ($P < 0.001$) and -0.50 MPa ($P < 0.05$). Unlike reports in other species, presence of the elaiosome in seeds of leafy spurge may not be an advantage for germination in conditions of water shortage. On the contrary, removal of the elaiosome improved germination under different water availability conditions.

P3-15. Effect of soil type and host tree species on epiphytic lichen in sub-boreal British Columbia. J. Campbell and A.L. Fredeen. *Natural Resources and Environmental Studies Institute, University of Northern British Columbia, 3333 University Way, Prince George, BC V2N 4Z9, Canada.*

Differences in epiphytic lichen diversity and abundance, and lichen nitrogen and carbon stocks were examined across old growth sub-boreal spruce and fir forests in central British Columbia. Abundance and diversity of epiphytic lichens was contrasted between the two dominant host tree species: Interior hybrid spruce (*Picea engelmannii* Parry x *glauca* (Moench) Voss) and Subalpine fir (*Abies lasiocarpa* (Hook.) Nutt.), as well as between the two primary soil texture types: fine (clay-rich) and coarse (sand-rich) soils. Trees were accessed using single-rope climbing techniques. Lichen abundance was assessed using visual estimates on all branches and epiphyte diversity was recorded on a selection of branches from different canopy heights. Forty-four epiphytic macrolichen species were identified across the study area. Hair lichen species, particularly non-sorediate *Bryoria* species, were more abundant in spruce on coarse-textured soils, while cyanolichens were more abundant on subalpine fir on fine-textured soils. However, overall macrolichen biomass and carbon pools were greatest in subalpine fir trees on coarse-textured soils. The tripartite species *Lobaria pulmonaria* was the dominant macrolichen, particularly over fine-textured soils, where its stand level biomass was greater than all other species combined. The nitrogen pools of *L. pulmonaria* in combination with the less abundant, nitrogen-rich bipartite cyanolichens (e.g. *Nephroma helveticum*) amounted to 7.5±1.9 kg N ha^{-1} on fine-textured soils. These results indicate that epiphytic cyanolichens may make substantial contributions to ecosystem nitrogen despite their relatively small contributions to overall forest biomass and carbon stocks. Future experiments aim to quantify epiphyte contributions to forest nitrogen.

P3-16. Seed ecology of two tropical dry ever-green forest lianas in India. D.R. Chillakuru, J.P. Christopher, and K.B. Prakash. *Department of Botany, Plant Ecology Laboratory, Madras Christian College, Chennai 600 059, India; and (K.B.P.) Seed Science and Technology, Indian Institute of Horticultural Research, Hessarghatta, Bangalore-560 089, India.*

Seed germination ecology provides information on the timing of germination and explains how it is controlled in nature. *Combretum albidum* Linn and *Ventilago maderaspata* Gaertn are tropical dry, ever-green forest lianas and of ethno-botanical importance. The leaves of *C. albidum* are used as fodder and consumed by locals and the root of *V. maderaspatana* is highly medicinal and is also a source of red dye 'ventilagin', for coloring cotton and tassar silk. The objective of this study was to investigate the seasonality of reproductive events and the mode of dispersal in relation to climate, as well as dormancy and mechanism of germination in both species. The study indicated that the two species are strongly seasonal in their phenological characteristics and their fruiting coincides with the dry season. Both species are dispersed by wind. The two species showed contrasting germination mechanism that was epigeal and hypogeal for *C. albidum* and *V. maderaspatana*, respectively. The results shed light on the natural regeneration of these two species.

P3-17. Modulation of RNA processing by abscisic acid. F.A. Razem, S. Kumar, and R.D. Hill. *Department of Plant Science, Agriculture Building, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*

The phytohormone abscisic acid (ABA) regulates various developmental and stress-induced processes in plants. Several ABA response genes encode for RNA-binding or RNA-processing proteins and recent studies on Arabidopsis ABA-sensitivity mutants have shown ABA involvement in post-transcriptional mRNA processing. Arabidopsis genome encodes more than 200 putative RNA-binding proteins; half of which are plant-specific. RNA-binding proteins mediate mRNA synthesis, splicing, transport, translation and degradation and by influencing transcript abundance, RNA-binding proteins provide a major regulatory role in fine-tuning cellular protein expression. The objective of our research is to investigate possible involvement of ABA in regulating RNA processing, determining of RNA binding specificity, and in the interactions of the RNA-binding proteins. Here we present the first direct link between ABA and post-transcriptional mRNA processing, particularly in mRNA splicing of the ABA receptors FCA and ABAP1.

P3-18. Expression profiling and gene silencing reveal that monolignol biosynthesis plays a critical role in epidermal defense in wheat in response to powdery mildew attack. N.H. Bhuiyan, Y. Wei, and J. King. *Department of Biology, University of Saskatchewan, Saskatoon, SK S7N 5E2, Canada.*

Lignin is a complex polymer of hydroxylated and methoxylated phenylpropane units, linked via oxidative coupling. For a long time, it has been believed that lignin accumulation is directly involved in cell wall apposition (CWA) formation during cereal defense responses to powdery mildew invasion. However, no genetic evidence for this has been shown so far. We isolated a complete set of genes (*TmPAL*, *TmC3H*, *TmCOMT*, *TmF5H*, *Tm4CL*, *TmCCoAOMT*, *TmCCR* and *TmCAD* encoding phenylalanine ammonia lyase, *p*-coumarate 3-hydroxylase, caffeic acid *O*-methyltransferase, ferulate 5-hydroxylase, 4-hydroxycinnamoyl-CoA ligase, caffeoyl-CoA *O*-methyltransferase, cinnamoyl-CoA reductase and cinnamoyl-alcohol dehydrogenase, respectively) involved in monolignol biosynthesis from a cDNA library derived from the epidermis of diploid wheat infected with *Blumeria graminis* f. sp. *tritici* (*Bgt*) to investigate the regulation of monolignol biosynthesis during powdery mildew infection. We found differential expression patterns for these genes in susceptible and resistant plants after *Bgt* infection. Transcripts of *TmPAL*, *TmCOMT*, *TmF5H*, *TmCCoAOMT* and *TmCAD* were highly induced, in epidermis. Interestingly, RNA interference mediated independent transient gene silencing of *TmPAL*, *TmCOMT*, *TmCCoAOMT* and *TmCAD* in epidermis led to higher penetration efficiencies of *Bgt* than in controls but to varying degrees. Co-silencing of *TmPAL* and *TmCAD* led to greater penetration of *Bgt* than when either was silenced, separately. These results suggest that monolignol biosynthesis during the formation of CWAs in wheat is critically important for host defense in the response to powdery mildew invasion.

P3-19. Nitric oxide scavenging is an essential function of plant haemoglobin. K.H. Hebelstrup and E.Ø. Jensen. *Department of Molecular Biology, University of Aarhus, Gustav Wieds Vej 10C, 8000 Aarhus C, Denmark; and (K.H.H.) Present address: University of Manitoba, Department of Plant Science, 222 Agriculture Building, Winnipeg, MB R3T 2N2, Canada.*

It is well known that haemoglobin plays an important role in the transport of oxygen from lungs or gills to muscles, brain and other oxygen-consuming organs. But some haemoglobins are also found at low concentrations in cells where oxygen transport seems unlikely. It has long been known that some plant species can form symbiotic root nodules with nitrogen-fixing bacteria and that these nodules contain leghaemoglobin, which bind and facilitate diffusion of oxygen. However, haemoglobin has been identified in other plant organs and in families of plant which are incapable of forming symbiotic nodules. Here we present data suggesting that plant haemoglobins play an essential role in all plants, a role different from oxygen transport. Plant haemoglobin rather works as a part of an enzyme system which scavenges nitric oxide (NO). By a

series of experiments with haemoglobin gene promoter reporter, silencing- and over-expression lines of *Arabidopsis thaliana*, we have been able to show that the interaction of plant haemoglobin with NO in Arabidopsis is controlling important processes such as growth, organ development, bolting and adaptation to hypoxia. This suggests that oxygen transport in plant nodules by leghaemoglobin has evolved from a NO scavenging mechanism as has been proposed for animal haemoglobin. However, in plants, this NO scavenging mechanism seems to be essential because haemoglobin-silencing produces severe phenotypes.

P3-20. Alternative respiratory pathway: A way to reduce imbalance between source and sink activity. A. Gandin, P. Dizengremel, and L. Lapointe. *Département de biologie, Université Laval, QC G1K 7P4, Canada; and (P.D.) UMR 1137, Nancy Université-INRA Écologie et Écophysiologie Forestières, BP239, Vandoeuvre, France.*
Several functions have been attributed to the alternative respiratory pathway (AP). AP is believed to be involved in burning excess C not used by metabolism, growth or storage. We tested this hypothesis using *Erythronium americanum*, a common understory plant in North-American hardwood forests. We have already shown that the plant becomes rapidly sink limited during the growing season and that respiration increases under high CO_2. We exposed plants to CO_2 concentrations of 400 and 1000 ppm and to ozone concentrations of 0 and 80 ppb to modulate the source activity in order to test the impact of these treatments, which affect sink/source relationships, on bulb growth and respiratory activity. While photosynthetic rates increased with increasing CO_2, it decreased in presence of O_3. However, bulb growth and biomass were fairly similar under all conditions. The extra C fixed under high CO_2 appears to be respired mainly in the bulbs and the AP activity was stimulated. In presence of ozone, leaves respired more to sustain repairs, while bulbs respired less in accordance with the fact that they received less C from the leaves. Respiration in *E. americanum* probably regulates sugar accumulation in the bulb; otherwise this accumulation could down regulate the photosynthetic activity and induce early leaf senescence.

P3-21. Assessment of inoculation, nitrogen fertilizer and application timing on soybean yield and seed quality in Manitoba. P.J. Gervais, J.C. Froese, R. Karamanos, and B. Brolley. *Department of Plant Science, Agriculture Building, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; (R.K.) Western Co-operative Fertilizers Ltd., Calgary, AB T2C 4M5, Canada; and (B.B.) Manitoba Agriculture, Food and Rural Initiatives, Carman, MB R0G 0J0, Canada.*
Little research has been conducted under Manitoba conditions to determine the effect of nitrogen fertilization on soybeans (*Glycine max* L. Merr.). The objective of this research was to determine the effect of inoculation, nitrogen fertilizer rate and timing on soybean yield and seed quality. Three years of trials were conducted in southern Manitoba. Nitrogen fertilizer (urea) was applied at six rates (0, 25, 50, 75, 100, 125 kg N ha^{-1}) using three methods: at seeding without inoculant, at seeding with inoculant, or as a split-application (25 kg ha^{-1} applied at seeding and the balance applied at the R3.5 stage) with inoculant. Data was collected on emergence, nodulation, biomass, yield, seed size, as well as seed protein and oil content. In 2006, the split-application method resulted in significantly higher emergence populations and seed protein content at all locations. The split-application method also resulted in a significant yield increase at one location. Results for the effects of rate were mixed, but suggested that higher rates reduced emergence, increased seed protein and decreased seed oil content. Yield was increased significantly due to rate at only one location. These results indicate that inoculation may not be necessary in soils with established populations of soybean-specific rhizobia and that increases in seed protein content can be obtained with nitrogen fertilizer using a split-application method.

P3-22. Inorganic carbon acquisition in the chrysophyte algae. S. Bhatti and B. Colman. *York University, Department of Biology, Toronto, ON M3J 1P3, Canada.*
Algae exist in an aquatic environment where they experience restraints in photosynthetic carbon assimilation because the diffusion of CO_2 is slow and in alkaline waters they are CO_2-limited. Consequently many microalgae have evolved the capacity to take up CO_2 and HCO_3^- by active transport and accumulate inorganic carbon (Ci) intracellularly, a process called a 'CO_2 concentrating mechanism' (CCM) by which CO_2 is concentrated at the primary carboxylase, Rubisco. Chrysophytes occur in neutral to acid lake and circumstantial evidence indicates that they depend entirely on the diffusive uptake of CO_2. Photosynthetic characteristics of several chrysophytes, *Mallomonas papillosa*, *Synura uvella*, and *Synura petersenii* were investigated to determine whether they have a CCM. All species lack external CA, have no capacity for active HCO_3^- transport and a low affinity for HCO_3^-. Monitoring of CO_2 and O_2 fluxes in *Mallomonas* by mass spectrometry demonstrated a slow uptake of CO_2 upon illumination suggesting that *Mallomonas* takes up CO_2 by diffusion. The K_m[Ci] Rubisco of *M. papillosa*, *S. petersenii*, and *S. uvella* were found to be 3.44 and 4.2 mM Ci respectively and thus $K_m[CO_2]$ Rubisco were 19.5 and 23.9 μM respectively. These results suggest that these chrysophytes rely on a Rubisco enzyme which has a high affinity for CO_2 to fix the CO_2 taken up by diffusion into the cell. These data indicate that the $K_m[CO_2]$ Rubisco determines the $K_{1/2}[CO_2]$ of the whole cell.

P3-23. ***WITHDRAWN***

P3-24. Photosynthetic properties of *Arabidopsis thaliana* and contrasting ecotypes of *Thellungiella salsuginea* grown under different growth conditions. N. Khanal and G.R. Gray. *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.*

The objective of this study was to characterize the photosynthetic properties of the Yukon and Shandong ecotypes of *Thellungiella* with reference to *Arabidopsis* under growth regimes optimal for these genotypes. Light-response curves were constructed for the parameters of electron transport (ETR), photosystem II excitation pressure (1-qP) and non-photochemical quenching (NPQ). Under the *Arabidopsis* growth regime no difference was observed in ETR between genotypes. Responses of 1-qP and NPQ showed a similar trend with highest values being presented by *Arabidopsis* followed by Yukon and then Shandong. No differential change in ETR or 1-qP was observed between the *Thellungiella* ecotypes under the Shandong growth regime. However, in *Arabidopsis* ETR was lowest and 1-qP was highest. Values of NPQ were highest in Shandong, followed by *Arabidopsis* and then Yukon. Under the Yukon growth regime ETR was highest in Shandong, followed by Yukon and then *Arabidopsis*. Values of 1-qP were highest in *Arabidopsis*, followed by Yukon and then Shandong while NPQ was highest in Shandong, followed by *Arabidopsis* and then Yukon. Though Yukon and Shandong growth regimes seemed to be more conducive for efficient photochemistry than the *Arabidopsis* growth regime for all genotypes, there were differential trends between all the genotypes across growth regimes, suggesting a complex interaction of growth irradiance, photoperiod and temperature are involved in modulating photosynthetic responses.

P3-25. The effect of salt treatment on the growth and morphology of four *Rosa* species. J.P. Young, M. Rutherford, K. Golob, E. Rapaport, and A. Booth. *University of Northern British Columbia, 3333 University Way, Prince George, BC V2N 4Z9, Canada.*

The Sustainable Landscape Initiative project at UNBC involves working with the City of Prince George to establish low maintenance, salt tolerant native plantings. A part of this research was testing the effect of different concentrations of NaCl on the growth and morphology of three native species, *Rosa acicularis* Lindl., *R. woodsii* Lindl., and *R. nutkana* K. Presl, and one known salt tolerant Japanese species, *R. rugosa* Thunb. The solutions (0, 10, 30, 70 or 140 mM NaCl) were added to the soil over a 9 week period in the greenhouse (24°C/18°C day/night; 18-h photoperiod). Plant height and leaf number were determined weekly, and shoot biomass was found at the end of the experiment. Electrical conductivity (EC) and pH of the soils were measured after harvest. Using a two-way ANOVA statistical design, preliminary analysis has found that all *Rosa* species were generally unaffected by salt treatments between 0 and 30 mM NaCl. Height and leaf number were not significantly affected by treatment, but biomass of all species was found to be significantly lower for the two higher salt treatments. Soil EC increased and soil pH decreased with concentration. These data will be provided to the City of Prince George for choosing plantings at sites with relatively high salt accumulation.

P3-26. The role of reactive oxygen species in the retrograde chloroplast-nucleus signalling pathway. P. Brzezowski, G.R. Gray, and K.E. Wilson. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*

Endosymbiotic processes were the defining events in the evolution of eukaryotic organisms. As current chloroplasts evolved on this course, the development of an efficient communication system between the chloroplast and nucleus was required. Such a signalling system is one of the most crucial factors for any "symbiotic consortium" to function properly. Signalling between the chloroplast and nucleus is especially important during times of environmental challenge. Many environmental stresses can cause oxidative damage. The photosynthetic apparatus of the chloroplast is the main source of reactive oxygen species (ROS) generation in plant cells. A glutathione peroxidase homolog (*Gpxh*) and a glutathione-S-transferase (*GST*) are two chloroplast localized proteins that are encoded by nuclear genes. Both are transcriptionally upregulated during photosynthetic oxidative stress in *Chlamydomonas*, by singlet oxygen ($^1O_2$) and hydrogen peroxide (H_2O_2), respectively. Thus changes in their transcription must be regulated via retrograde signalling pathways from the chloroplast. By fusion of either the *Gpxh* or *GST* promoter with a promoterless arylsulfatase (Ars) reporter gene it is possible to test the levels of induction by ROS by measuring levels of Ars expression. *Chlamydomonas reinhardtii* -$^1O_2$ and -H_2O_2 reporter strains that stably express arylsulfatase gene are being submitted to a secondary mutation screen to identify signalling components involved in the ROS responsive retrograde signal pathway.

P3-27. Proteomic approaches towards a comprehensive understanding of plant biology at molecular level. U.K. Aryal, D.J.H. Olson, and A.R.S. Ross. *National Research Council of Canada, Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada.*

Genomic studies have opened up a new era for plant biologists by initiating, and enabling, a systems biology approach towards understanding plant function at molecular levels. Proteomics involves the identification and expression profiling of proteins, and has increasingly been used for better understanding of the processes involved in plant growth, development and stress responses. However, this approach still presents significant challenges due to complexity of plant proteome, abundance of secondary metabolites, and prevalence of post-transcriptional (splicing) and post-translational

modifications, the latter often playing a critical role in protein function (e.g. phosphorylation). To help address these challenges, we have developed a simple fractionation procedure for obtaining organellar 'sub-proteomes' from plant seed. Pre-fractionation reduces sample complexity and enhances identification of sub-cellular proteins by mass spectrometry (MS). A number of proteins involved in cell signaling were identified in plasma membrane fractions using this approach. As a part of our post-translational proteomics research, we are also developing methods for targeting and identifying phosphorylated proteins. We will report on the use of metal oxide affinity chromatography (MOAC) for purifying intact phosphorylated proteins, and a novel method for enriching phosphorylated peptides prior to MS analysis and identification. This poster reports on our work-in-progress to develop and evaluate different analytical methods for identifying plant proteins of interest to biologists and crop developers.

P3-28. The multi-layered exodermis of *Iris germanica* roots: Its development and permeability to water and NaCl. C.J. Meyer, E. Steudle, and C.A. Peterson. *Department of Biology, University of Waterloo, 200 University Ave., Waterloo, ON N2L 3G1, Canada; and (E.S.) Department of Plant Ecology, University of Bayreuth, D-95440 Bayreuth, Germany.*

Iris germanica roots are intriguing because they can develop a multi-layered exodermis in which the Casparian band (CB) extends through both the tangential and the anticlinal cell walls to become continuous around the root circumference. All exodermal cells also have suberin lamellae (SL). This unusual anatomy allows the permeability of the CB and SL to water and ions to be tested. Roots with a single-layered exodermis were generated by growing plants hydroponically. The multi-layered exodermis was induced in the basal part of a root by lowering the solution level, exposing this region to humid air. (Endodermal development was not affected.) The permeability of whole roots to water, as measured with a root pressure probe, was the same regardless of the presence or absence of the basal multi-layered exodermis ($0.4\text{-}0.6 \times 10^{-8}$ m s^{-1} MPa^{-1}). However, when permeability to NaCl was tested, also using the pressure probe, root segments with a single-layered exodermis were slightly permeable (0.06×10^{-9} m s^{-1}), but those with a multi-layered exodermis were impermeable. It is concluded that the continuous CB can prevent the apoplastic movement of solutes, but not water. The cells of the exodermis remain alive, providing a pathway for the movement of ions through the symplast. This is the first report of the use of a pressure probe to measure the permeability of a multi-layered exodermis.

P3-29. Functional analysis of transcription factors affecting nicotine biosynthesis through virus induced gene silencing (VIGS). A.T. Todd, E. Liu, S.L. Polvi, and J.E. Page. *National Research Council of Canada, Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada.*

Nicotiana species synthesize the pyrrolidine alkaloid nicotine in their roots and transport it to their leaves in response to several stimuli, including wounding and jasmonate signaling. However, the transcriptional regulation of this metabolic pathway remains unclear. We have developed a rapid functional assay to screen for transcription factors involved in regulating nicotine biosynthesis. Clones with sequence homology to known transcription factors were identified from a subtractive cDNA library and VIGS was used to post-transcriptionally silence the corresponding endogenous genes. Leaf nicotine content was analyzed by HPLC before and after methyl-jasmonate treatment of the silenced plants. Altered nicotine levels were seen following the silencing of six putative transcription factors when compared to controls: four exhibited significantly decreased nicotine content while two showed increased nicotine. The sequences of the corresponding endogenous genes have been used to produce stably transformed overexpression and RNAi knockout transgenic lines. Preliminary data suggest that in the absence of methyl-jasmonate induction, RNAi lines exhibit the same effects on nicotine production as seen in the VIGS screen, while overexpression can also significantly alter nicotine accumulation. In addition to being able to generate *Nicotiana* plants with considerably enhanced or reduced alkaloid levels, the identified transcription factors could also be used to metabolically engineer increased production of significant bioactive compounds in other species.

P3-30. Response of three *Echinacea* species to salinity stress. A. Sabra and S. Renault. *Department of Botany, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*

A greenhouse study was designed to investigate the effects of different salt concentrations (0, 50, 75 and 100 mM NaCl) on growth, gas exchange and electrolyte leakage of three *Echinacea* species (*E. pupurea*, *E. pallida* and *E. angustifolia*). Six- month old plants were transferred to nutrient solutions supplemented with NaCl in aerated hydroponic systems for two weeks. Survival of the salinity exposed plants was 98.6% in *E. purpurea* and *E. pallida* compared with 73.6% in *E. angustifolia*. Photosynthetic rate, stomatal conductance and transpiration rate were significantly decreased with increasing salt concentrations in all species. The largest decrease was observed in *E. angustifolia*. Higher salt concentrations (75 and 100 mM NaCl) significantly reduced shoot dry weight and leaf area in *E. pupurea* and *E. pallida*, while the differences were not significant in *E. angustifolia*. Electrolyte leakage increased with increasing salt concentrations in all species with the greatest extent in *E. angustifolia*. Results suggest that *E. angustifolia* is more affected by salinity than *E. purpurea* and *E. pallida*. Further work is being conducted to study the effect of salinity on the active

constituents (phenolic compounds, alkamides and essential oil) of the selected *Echinacea* species.

P3-31. Transcriptome comparison of high and low cadmium accumulating near isogenic lines of durum wheat. N.S. Harris, M.J. Bryman, C.J. Pozniak, and G.J. Taylor. *Department of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9, Canada; and (C.J.P.) Crop Development Centre, Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*

Cadmium (Cd) concentrations in durum wheat (*Triticum turgidum* L. ssp. *durum*) grain grown in prairie soils often exceed proposed international trade standards. Genotypic differences in grain-Cd concentration are poorly related to root or whole-plant Cd accumulation. Rather, differences in root-to-shoot Cd translocation are most closely associated with Cd concentrations in grain. To identify genes that are potentially involved in regulating Cd accumulation in grain, we compared gene expression in roots of pairs of durum wheat near-isogenic lines (NILs), high and low for Cd accumulation in grain, using a 17,000-spot wheat microarray. Less than 40 genes were differentially expressed between the high and low Cd-accumulating NILs. These include genes encoding β-glucosidases, chitinases, germins, fatty acid desaturases, and late embryogenesis abundant proteins. One quarter of the differentially expressed genes showed homology to unannotated genes. The expression of these genes is being confirmed by quantitative RT-PCR. The information gained from these microarray experiments will be used to identify candidate genes specifically involved in low grain-Cd accumulation, and these will be the focus of subsequent genetic mapping and functional analysis.

P3-32. Do escaped transgenes persist in nature? Introgression of a transgene in weedy bird rape (*Brassica rapa* L.). S.I. Warwick, A. Légère, M.-J. Simard, and T. James. *Agriculture and Agri-Food Canada (AAFC), Eastern Cereal and Oilseed Research Centre, Ottawa, ON K1A OC6, Canada; (A.L.) AAFC, Saskatoon Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; and (M.-J.S.) AAFC, Soils and Crops Research and Development Centre, 2560 Hochelaga, QC G1V 2J3, Canada.*

Transgenic bird rape × canola (*Brassica napus* L.) F1 hybrids were detected under field conditions in 2001 in two Québec bird rape populations (St-Henri and Ste-Agathe). This represented the first documented case of transgene movement into a natural weed population from a commercial transgenic crop. We monitored these two populations in 2002, 2003, and 2005 to determine the fate of the HR transgene under normal agro-environmental conditions. Progeny were grown from three putative hybrid/introgressed plants collected in 2005 from the St-Henri population. All plants were scored for the HR trait (HR+/HR-), presence of species-specific AFLP molecular markers from both parental species, pollen viability, and ploidy level. We observed many hybrid types and identified one plant in 2005 that was diploid, contained the transgenic HR trait, scored negative for canola-specific AFLP markers, and whose progeny had bird rape characteristics and segregated 1:1 for the HR transgene. This confirms that a crop HR transgene, after being introduced into a weedy relative by gene flow, can persist over time in the absence of selection pressure (the herbicide), and in spite of the fitness cost associated with hybridization.

P3-33. Mycorrhizal soil infectivity: A new approach for its determination. C. Plenchette, T. Fraser, and C. Hamel. *Institut National de la Recherche Agronomique, 17 rue Sully, 21065 Dijon Cedex, France; and (T.F. & C.H.) Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, 1 Airport Road, P.O. Box 1030, Swift Current, SK S9H 2X3, Canada.*

A more sustainable agriculture should aim at maintaining a high biodiversity in the agro-ecosystems, and better exploit soil-plant-microbe interactions for plant nutrition and protection against pests. Among the soil borne microorganisms, AM fungi that colonize roots of most of crops to form mycorrhizae, have co-evolved with plants since 400 million years and their beneficial effects are well recognized. In order to plan a strategy of maintenance, enhancement, or replacement of indigenous AM fungi, it is necessary to know the level of the population of these fungi in the field, *i.e.* the soil infectivity. Methods used to determine soil infectivity are time consuming as they involve the cultivation of a test plant on soil dilution series. The method most commonly used, the "Most Probable Number" (MPN) method, gives a measure of the number of propagules (spores, vesicles, hyphal pieces) of AM fungi per gram of soil. The fatty acid 16:1ω5 is found in large amounts in AM fungi. We found that the amount of this fatty acid in the neutral fraction of soil lipid extracts is correlated with the number of propagules of AM fungi as determined by the MPN method. A biochemical test is proposed to replace the MPN method by a more rapid measurement of soil infectivity.

P3-34. Sympatry and hybridization of canola and bird rape (*Brassica rapa* L.) in Québec. M.-J. Simard, A. Légère, and S.I. Warwick. *Agriculture and Agri-Food Canada (AAFC), Soils and Crops Research and Development Centre, 2560 Hochelaga, QC G1V 2J3, Canada; (A.L.) AAFC, Saskatoon Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; and (S.I.W.) AAFC, Eastern Cereal and Oilseed Research Centre, Ottawa, ON K1A 0C6, Canada.*

Hybridization between herbicide resistant (HR) transgenic canola (*Brassica napus* L.) and weedy bird rape has been documented in Québec. We evaluated the actual hybridization potential based on range overlap and *in situ* rates. We mapped the distribution of canola fields and bird

rape herbarium specimens in Québec; collated information on the presence of bird rape in certified canola seed production fields; and surveyed for bird rape in, or close to canola field margins. Progeny from these populations was screened for herbicide resistance (HR) and for the presence of the HR transgene. Significant sympatry was observed in several areas and hybridization occurred in all eight populations (1.1-17.5% hybrid seed) located in field margins and in one (1.1%) out of three populations located less than 10 m from a canola field. Hybridization rates decreased exponentially as bird rape density increased, but inter-plant rates (0 to 68%) were highly variable. At present, there are no compelling data suggesting that the presence of an HR transgene in a wild/weedy relative is inherently risky. However, our current knowledge might not fully describe the risks posed by other transgenes, particularly those that convey fitness-enhancing traits.

P3-35. Endomycorrhizal colonization of Bt corn. J.A. Traquair and B.L. Singh. *Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, 1391 Sandford Street, London, ON N5V 4T3, Canada.*
Growing corn cultivars that have been genetically modified to express genes for the toxin produced by the biological control agent, *Bacillus thuringiensis* Al Hakam, is a popular approach to the management of insect pests such as corn borer. A challenge is to minimize risk to the environment by restricting the activity of the biological agent to target species. We examined the non-target effects of Bt genes on the receptivity of corn to arbuscular mycorrhizal colonization in a Bt corn cultivar compared with an isogenic non-Bt line from Syngenta Seeds. Seedlings grown in the greenhouse in clay-loam or Pro-Mix and sand were inoculated with commercial endomycorrhizal inoculum, MYKE Pro-Endo, (Premier Tech, Rivière-du-Loup) containing *Glomus intraradices* Schenck & Smith or with natural, arbuscular mycorrhizal fungi from local clay-loam corn fields. After 8 weeks, aerial parts of plants grown in pots with mycorrhizal or non-mycorrhizal soils (autoclaved inoculum) were weighed. Random samples of roots from these treatments were fixed, stained with Trypan blue in lacto-glycerol, and assessed for endomycorrhizal colonization. There was no significant difference ($P = 0.05$) between the mean growth of mycorrhizal Bt (N29-A2) *versus* mycorrhizal non-Bt (N29-G7) corn.

P3-36. Photosynthesis rate, transpiration rate and protein profiles of *Hydrangea anomala*, *Magnolia grandiflora*, *Mahonia nervosa* and *Polystichum munitum* in response to environmental changes during the year. N. Rafati, R. Pettersson, R. Lau, C. Chanis, A. Wang, J. Mehroke, and S. Singh. *Department of Botany, Bioscience Building, University of British Columbia, Vancouver, BC V6T 1Z4, Canada.*
The objective of this study was to monitor the influence of seasonal changes on photosynthesis rate, transpiration rate, and protein profiles in leaves of four diverse plant species, *Hydrangea anomala*, *Magnolia grandiflora*, *Mahonia nervosa* and *Polystichum munitum*. Leaf photosynthesis and transpiration rates were measured by Li-cor Gas Exchange system, and SDS-PAGE and Western blots were employed to determine protein profiles. *Hydrangea anomala* leaves exhibited the most dramatic changes in photosynthesis rate during the year, with a much higher rate of photosynthesis during May to August before gradually declining to a negligible level in December. In general, the rates of photosynthesis and transpiration in leaves of all species examined started to decrease during the months with lower temperature and light intensity. The level of photosynthetic proteins (e.g. rubisco, ATP Synthase and LHC II) increased between April and August in all species except that of *Mahonia nervosa* which remained relatively constant throughout the year. The significance of the influence of environmental factors such as temperature and light intensity on gas exchange, and protein expression in leaves of these diverse plant species will be discussed.

P3-37. Abscisic acid negatively regulates ethylene-responsive genes in salt-stressed tomato (*Lycopersicon esculentum* Mill) roots. A. Kwok and A.L. Plant. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada.*
Experiments to characterize the role of abscisic acid (ABA) and ethylene (ET) in regulating a salt-responsive α-dioxygenase (*Leα-DOX*) gene uncovered a positive regulatory role for ET in salt-stressed tomato roots. *Leα-DOX1* expression is markedly responsive to the ET precursor 1-aminocyclopropane-1-carboxylic acid (ACC) and we have previously found that ABA antagonizes ACC-responsive expression of *Leα-DOX1*. To further investigate the role of ET and the interaction between ET and ABA in salt-stressed roots, the expression of genes encoding transcription factors (*JAMYC2*, *ERF1*, *ERF3*) or enzymes for the biosynthesis of ET (*ACS3*, *ACO1*) and ABA (*NCED1*) was examined. In addition, we assessed the expression of these genes in roots with altered levels of ABA and/or ET. A positive regulatory role for ET was substantiated by the salt-induced expression of *ACS3*, *ACO1*, *JAMYC2*, *ERF1* and *ERF3* in roots. *NCED1* was positively regulated by ABA and its expression in salt-stressed root required ABA. ABA negatively regulated the expression of *ACO1*, *JAMYC2*, and *ERF1* and, in general, was a "dominant" signal capable of suppressing ET-responsive gene expression.

P3-38. Nitrogen and non-nitrogen benefit of legumes to a subsequent spring barley crop. J. Lafond and D. Pageau. *Research Farm, Agriculture and Agri-Food Canada, 1468 St-Cyrille Street, Normandin, QC G8M 4K3, Canada.*

Annual legume crops, in rotation with cereal, contribute to nitrogen soil supply and can reduce the mineral nitrogen fertilizer demand of the following crop. The objectives of this project were to determine the nitrogen and non-nitrogen benefit of dry pea, soybean and red clover on grain yields of barley seeded the following year and their impacts on the soil nitrate. Plots of barley, dry pea, soybean and red clover were initially seeded. The following year, barley plots were established and fertilized with four rates of mineral nitrogen (0, 40, 80 and 120 kg ha^{-1}). The productivity of barley increased by 13 to 50% following a legume crop compared to barley grown two-years in a row and these increments were attributed to the non-nitrogen benefit of legumes. Nitrogen benefits were estimated at 57 kg N ha^{-1} for pea, 52 kg N ha^{-1} for soybean and 26 kg N ha^{-1} for red clover. However, grain yield increments associated with the nitrogen benefit were less important than yield increments associated with the non-nitrogen benefit. Soil nitrate at harvest was higher under barley, dry pea and red clover compared to soybean. However, previous crops had no significant effect on soil nitrate in the following spring. Under these experimental conditions, nitrogen and non-nitrogen benefit associated with legumes should reduce mineral nitrogen fertilizer demand.

P3-39. Phosphorus and potassium fertilization of flax grown under a cool climate. D. Pageau, J. Lajeunesse, and J. Lafond. *Research Farm, Agriculture and Agri-Food Canada, 1468 St-Cyrille Street, Normandin, QC G8M 4K3, Canada.*

Oilseed flax (*Linum usitatissimum* L.) is a new crop in Québec and there is presently no phosphorus (P) and potassium (K) fertilization recommendations. The objective of this study was to determine the effects of P and K fertilization on the productivity of flaxseed in a northern agricultural area of Québec. Five P (0, 20, 40, 60, and 80 kg ha^{-1}) and three K application rates (0, 50, and 100 kg ha^{-1}) were evaluated in two fields in each of two years (2005 and 2006). Fertilizers were broadcast in a single application prior to seeding the cultivar 'AC Bethune'. In 2005 and 2006, the soil of the first field had a P content of 21 and 33 kg ha^{-1} and a K content of 147 and 223 kg ha^{-1}, respectively. The soil of the other field had a P content of 184 and 137 kg ha^{-1} and a K content of 413 and 347 kg ha^{-1} in 2005 and 2006, respectively. In 2005 and 2006, P application had no significant effect on grain yield. Potassium fertilization had no significant effect on grain yield in 2005 but it slightly reduced grain yield in 2006 in the field with the higher soil K content. Phosphorus and K fertilization had no significant effect on seed oil concentration. Our results suggest that that there is no advantage in applying P and K fertilizer on flax grown under cool conditions on soils with more than 27 kg P ha^{-1} and 185 kg K ha^{-1}.

P3-40. Effect of management zone and nitrogen fertilizer rates on potato yield, preliminary results. A.P. Moulin and N. Tremblay. *Agriculture and Agri-Food Canada (AAFC), Brandon, MB, Canada; and (N.T.) AAFC, St. Jean-sur-Richelieu, QC, Canada.*

Potato yield varied due to landform and application of N fertilizer in a study west of Carberry in 2005. Management zones were delineated with image analysis based on color values of cereal stubble in the year prior to potatoes, and assessed with landform analysis of digital elevation data. The analysis showed 3 potential management zones which were correlated with upper, middle and lower slope positions within the field. In general irrigated potato yield decreased from lower to upper slope positions. Nitrate nitrogen, organic carbon and total nitrogen decreased from lower to upper slope positions. Yield response to nitrogen fertilizer applied at 0, 75, 150 and 225 kg ha^{-1}, and split application at 75+75, 75+150 and 75+225 kg ha^{-1} was different in each of the management zones. Yield of potatoes responded to fertilizer in the middle and upper slope positions, though the effect of split application of nitrogen fertilizer was not clear. Data field research during 2006 and 2007 will be analyzed to further assess these trends.

P3-41. Identification of functional allantoinase sequences from soybean. A. Shahid and C.D. Todd. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*

Ureides are nitrogenous compounds formed in the nodules of soybean and other warm season legumes during symbiotic biological nitrogen fixation. They are synthesized in the non-infected cells of the nodule and are involved in the transport of fixed nitrogen out of the nodule to the rest of the plant. In leaves and other sink tissues ureides are broken down through a multi-step pathway, with nitrogen eventually being converted to ammonium for assimilation through the GS-GOGAT cycle. In soybean and other ureide-exporting legumes, regulation of ureide catabolism is still not well understood despite the importance of this pathway to plant growth and development. The first metabolic conversion in the breakdown of ureides in plants is catalyzed by the enzyme allantoinase ([S]-allantoin amidohydrolase, E.C. 3.5.2.5), converting allantoin to allantoate. Allantoinase cDNAs have been identified from *Arabidopsis thaliana* (L.) Heynh. and the tree legume *Robinia pseudoacacia* L. (Black Locust). In order to better understand the regulation of ureide catabolism in ureide exporting legumes, we sought to clone allantoinase from soybean, *Glycine max* (L.) Merr., and confirm its function by heterologous expression of the predicted coding sequence in yeast mutants defective in allantoin catabolism.

P3-42. Arbuscular mycorrhizal fungi from the Athabasca oil sands. X. Bao, J.F. Basinger, and S. Kaminskyj. *Department of Biology, University of*

Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; and (J.F.B.) Department of Geological Sciences, University of Saskatchewan, 114 Science Place, Saskatoon, SK S7N 5E2, Canada.

The arbuscular mycorrhizal (AM) symbiosis is a mutualistic relationship formed between plant roots and AM fungi that has a significant impact on plant health and consequently on ecosystem function. AM supply mineral nutrients to plants and receive carbohydrates produced by photosynthesis through characteristic structures called arbuscules and hyphal coils. We examined AM and other endophytic fungi in dandelion plants (*Taraxacum officinale*) collected from unimpacted, extracted and remediated sites in the Athabasca Tar Sands. Hydrocarbons are extracted from oil-sand recovered from open-cut mines using hot water, lye, and gasoline. The extracted sand is eventually remediated for revegetation, but can also be colonized by weedy species. AM colonization levels were assessed using lactofuchsin-stained lateral roots and epifluorescence microscopy, and a multiple quantitation microintersect method. *Taraxacum* root samples had high AM colonization even in the extracted soil sites, although the extraction process initially seemed likely to have removed all possible soil microbes. In addition, roots hosted abundant fine endophytes and septate endophytes. Corresponding soil samples are being studied to determine AM spore viability and diversity by baiting with plants that are highly receptive to AM colonization. This research will be beneficial for application of AM in bioremediation in the oil sands.

P3-43. Morphology and diversity of arbuscular mycorrhizal fungi colonizing roots of dandelion and chive. Y. Li, J.F. Basinger, and S. Kaminskyj. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; and (J.F.B.) Department of Geological Sciences, University of Saskatchewan, 114 Science Place, Saskatoon, SK S7N 5E2, Canada.*

Arbuscular mycorrhizas (AM) form between AM fungi and the roots of about 90% of plant species. AM help plants to capture phosphorus and micronutrients from the soil. Typically, plant roots colonized by AM have one of two fungal morphologies, called *Paris* (hyphal coils) and *Arum* (highly branched arbuscles) after the plant genera where they were first characterized. Finding both AM morphologies in the same root has seldom been reported. AM colonization was studied in dandelion (*Taraxacum*) and chive (*Allium*) using confocal microscopy, each of which had both AM types, perhaps due to multiple AM fungi or one AM fungus producing both morphologies. An anatomical and ultrastructural study explored possible relationships between AM morphotype and the host root features. The assumption that more air space could facilitate the rapid growth of intercellular hyphae will be discussed. The taxonomy of the AM fungi is unclear, and these species lack sexual stages. Traditional AM identification using morphological data from asexual spores can be combined with molecular DNA methods. DNA extracted from colonized roots was PCR amplified with fungal specific primers, cloned into a TOPO-TA vector and sequenced. Sequence results will be discussed.

P3-44. Root-associated fungi in *Equisetum* species from Western and Arctic Canada are diverse and abundant. F. Shahid, E. Hodson, J.F. Basinger, and S. Kaminskyj. *Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada; and (J.F.B.) Department of Geological Sciences, University of Saskatchewan, 114 Science Place, Saskatoon, SK S7N 5E2, Canada.*

Mycorrhizal fungi are associated with roots of ~95% of land plants, and are important for plant mineral nutrition. Mycorrhizae are seldom reported for *Equisetum*, the only extant genus from the ancient Class Equisetopsida that included *Calamites*. *Equisetum* is relatively rare in developed and agricultural areas, but is abundant on the tundra and is an important understory plant in boreal forests, including disturbed sites. We describe mycorrhizal fungi and root endophytes associated with *Equisetum* collected from Ellesmere Island (82°N), Axel Heiberg Island (80°N), and from sites in Yukon Territory and the Prairie Provinces (67°-51°N). Fungal colonization was assessed using a multiple quantitation method for lactofuchsin-stained roots examined with epifluorescence microscopy. For 85 specimens from 24 sites, total colonization per length of root averaged 30 ± 3%, range 0-97%. Colonization rate by wide aseptate hyphae characteristic of arbuscular mycorrhizae (5 ± 1%) was significantly less than for fine endophytes (20 ± 3%) or septate endophytes (17 ± 2%). Fine endophytes are closely related to arbuscular mycorrhizae and have similar symbiotic relationships. Septate endophytes are from a distinct fungal group that form root symbioses. *Equisetum* fungal endorhizal associates likely have broad ecological relevance.

P3-45. Fossil remains of the walnut family (Juglandaceae) from the Eocene forests of Axel Heiberg Island, Canadian High Arctic. R.F. Wilson, D.R. Greenwood, and J.F. Basinger. *Department of Geological Sciences, University of Saskatchewan, 114 Science Place, Saskatoon, SK S7N 5E2, Canada; and (D.R.G.) Department of Zoology, Brandon University, 270 18th Street, Brandon, MB R7A 6A9, Canada.*

The Eocene fossil forests of Axel Heiberg Island (45 million years old) provide insight into the vegetation and climate of ancient polar environments. Remains of Cupressaceae (dawn redwood, swamp cypress, cedar), Fagaceae (oak), Betulaceae (birch, alder), Pinaceae (pine, spruce, larch, golden larch), Ginkgoaceae (ginkgo), and others are exquisitely preserved and reveal the existence of lush forest ecosystems throughout the far north during a time of warm global climate. Fossil nuts of the

Juglandaceae (walnut family) have been found within these deposits. Comparison with living and fossil Juglandaceae indicates that the remains represent nuts of three new extinct species of two genera, *Juglans* L. (walnut) and *Carya* Nutt. (hickory). Since the Eocene, global climatic cooling, leading ultimately to Pleistocene glaciation, has transformed high latitude vegetation, and has resulted in the American/Eurasian disjunct distribution found in many north-temperate families, of which the Juglandaceae is typical. The Axel Heiberg Island fossil nuts are the earliest records of both *Juglans* and *Carya* in the polar regions and are among the oldest specimens from either genus. As important components of the ancient polar landscape, members of the Juglandaceae have played a significant role in the evolution of temperate forest ecosystems.

P3-46. Functional analysis of the RCD-SRO (RADICAL INDUCED CELL DEATH SIMILAR TO RCD) gene family in salt treated roots. G. Babajani and A.L. Plant. *Department of Biological Sciences, Simon Fraser University, Burnaby, BC, Canada.*

JWL-26 is a novel salt-regulated gene that was isolated from the roots of tomato (*Solanum lycopersicum* L.). BLAST-based homology searches revealed similarity between JWL-26 and several *Arabidopsis* proteins that include RCD1 (Radical-induced Cell Death 1) and the SRO (Similar to RCD-One) family members. These proteins play a role in regulating hormone signalling cascades involved in programmed cell death. Two full length cDNA clones (LeRCD1-likeA and LeRCD1-likeB) with similarity to *RCD1* were obtained from tomato. JWL-26 shares 65% similarity to the SRO5 (At5g62520.1) protein. The 3′UTR of *SRO5* and the gene encoding Δ1-pyrroline-5-carboxylate dehydrogenase (*P5CDH*) overlap in a cis-antisense manner, which results in the cleavage of *P5CDH* mRNA via generation of siRNAs. The loss of P5CDH results in a reduction of proline degradation and enhanced salt tolerance. JWL-26, LeRCD1-likeA and B are being analysed to determine their function in salt-stressed roots. To achieve this transgenic lines have been generated to over-express LeRCD1-likeA and LeRCD1-likeB cDNAs in the *rcd1* mutant to see if they can complement the mutant phenotype. JWL-26 was over-expressed in wild-type Arabidopsis and an *SRO5* knock-out line. Data obtained to date will be presented.

P3-47. Long-term versus short-term zero-till effects on lentil yield and nitrogen uptake. H. Zakeri, R. Bueckert, and G. Lafond. *Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; and (G.L.) Indian Head Experimental Farm, Agriculture and Agri-Food Canada, P.O. Box 760, Indian Head, SK S0G 2K0, Canada.*

Higher amounts of N, C and microbial biomass are associated with zero tillage systems. Higher N supply however, may not be favorable in certain crop systems in cold short season climates. Lower yield may come from delayed seedling and subsequently delayed maturity and may be exacerbated in zero tillage. In this study we compared the yield and N uptake of five cultivars of lentil under long (>20 yr) and short (<10 yr) term zero-till systems in the Black soil at Indian Head, Saskatchewan. Total dry matter, N uptake and plant N concentration were significantly higher in short term zero-till than long term. More nodes and branches were produced by plants under short term than long term as a result of more nitrogen uptake. Yield for short term (264 g/m^2) was almost significantly higher ($p=0.06$) than long term (195 g/m^2) zero tillage. Cultivars of 'CDC Milestone' and 'CDC Robin' produced more yield than 'CDC Redcap' and 'CDC Sedley' with the 'CDC Vantage' being intermediate (range of 172 to 293 g/m^2). However, the Harvest index for tillage systems and cultivars were similar. Application of 60, 45, 15 and 0 kg N ha^{-1} for 'CDC Sedley' in the second experiment also resulted in higher yields in the short-term zero-tillage. But N uptake was not consistent among treatments. In summary, for one site year (2006), lentil yield was more favorable in the short term zero-till. Ongoing research will elucidate the role of nitrogen to crop growth and yield.

P3-48. Inorganic and organic nitrogen forms in forest soils and their contributions to plant nutrition. R.J. Metcalfe. *Centre for Forest Biology, University of Victoria, P.O. Box 3020, Station CSC, Victoria, BC V8W 3N5, Canada.*

Available soil nitrogen (N) is a major factor limiting forest growth. While inorganic N forms (ammonium and nitrate) have been the focus of plant N nutrition studies, a growing body of research shows direct uptake of organic N forms (including amino acids) is common across the plant kingdom. However, there are few quantitative examinations of the contribution amino acid N makes to plant nutrition, especially in temperate forest regions. Two main objectives of this study were to determine relative availabilities of amino acid N to inorganic N in coastal forest soils, and to compare uptake of inorganic versus organic N using two economically important conifers *Picea sitchensis*, and *Pseudotsuga menziesii*, and two of their common competitors *Vaccinium ovalifolium* and *Rubus spectabilis*. Biomass results from plants given inorganic and organic (amino acid) N forms indicated plant growth was significantly greater when ammonium was the dominant N form for all species. Competitor shrub species were more plastic in N form use and grew proportionately more when given nitrate and amino acids than conifers. Mycorrhizal status did not influence biomass accumulation except for *P. menziesii*, where growth was significantly reduced for mycorrhizal tree seedlings when given amino acids as the sole N source. Soil N form availability will also be presented. This information may help explain

species abundance patterns, plant diversity and competitive interactions.

P3-49. Characterization of transgenic *Arabidopsis* lines expressing a choline oxidase gene from *Arthrobacter pascens*. J. Huang, U.A. Schäfer, V.S. Bhinu, K. Rozwadowski, and A. Hannoufa. *Agriculture and Agri-Food Canada, Saskatoon Research Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*
Glycinebetaine (betaine) is ubiquitous and affords protection against stressful environmental conditions. Betaine-accumulating plants occupy very saline or xeric environments. Many oilseed crops such as *B. napus* and *Linum usitatissimum*, however, only accumulate small amounts of betaine, opening the potential for engineering effective betaine synthetic pathway into such crops to improve their stress tolerance. In higher plants, the first step of converting choline to betaine aldehyde is catalyzed by a soluble flavoprotein choline monooxygenase (CMO) in the chloroplasts; the second step of oxidizing the intermediate to final product of betaine is catalyzed by an NAD^+-dependent betaine aldehyde dehydrogease (BADH; EC 1.2.1.8) in all organisms. We have introduced the choline oxidase (*COX*, EC 1.1.3.17) gene from *Arthrobacter pascens* into *Arabidopsis sct* T-DNA insertion mutant lacking sinapoylcholine (sinapine) due to a null sinapoylglucose: choline sinapoyltransferase activity in the seeds. The *Arthrobacter pascens COX* enables one step conversion of choline to betaine aldehyde, and further oxidization of betaine aldehyde to betaine. Several *COX*-positive lines with high *COX* transcript levels in the siliques were more tolerant than WT and the *sct* mutant under osmotic stress when varying levels of choline substrate was supplemented. COX enzyme assay, endogenous choline, and betaine levels and germination and seedling responses to other stress conditions are currently underway.

P3-50. The role of microtubules in low temperature sensing and signalling. K.A. Sproule, P.C. Bonham-Smith, and I.A.P. Parkin. *Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; and (P.C.B.-S.) Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK S7N 5E2, Canada.*
Microtubules are dynamic components of the cytoskeleton that are essential for plant growth and development and also appear to be involved in controlling the plants low temperature response. Cold acclimation is a complex process where plants acquire increased freezing tolerance following exposure to low, non-freezing temperatures, and multiple lines of evidence suggest that the cytoskeleton is involved in this process. Traditional freeze tests, microtubule disrupting chemicals and fluorescent imaging tools were used to help characterize the involvement of microtubule reorganization in cold acclimation in *Arabidopsis thaliana*, and we found that microtubule reorganization has a considerable impact on the cold acclimation process in this plant. Microtubule binding proteins are likely to play a key role in the low temperature response, because they control not only the activity and organization of microtubule arrays, but also induce signalling cascades that cause gene expression changes that could potentially confer cold tolerance. Three candidate genes that had been previously shown to both interact with microtubules and respond to low temperatures were selected for characterization. Fluorescent protein tagging, gene knock-out and gene over-expression studies are being used to determine if and how these genes are involved in the low temperature response in *Arabidopsis*.

P3-51. Managing crop nitrogen for weather in Canada. T.W. Bruulsema. *International Plant Nutrition Institute, 18 Maplewood Drive, Guelph, ON N1G 1L8, Canada.*
The weather controls a great deal of the variation in crop response to nitrogen. The recently-introduced calculator for corn (*Zea mays* L.) nitrogen recommendations in Ontario is based on a stepwise regression model that explained no more than one-third of the observed variability in optimum rates. The application of models integrating soil water flow, soil nitrogen dynamics, and plant uptake can potentially improve prediction of crop nitrogen needs in response to weather conditions. A recent Soil Science Society of America symposium held in November 2006 featured 16 presentations by scientists studying cropping systems across three continents. They described experimental data and experiences of applying models and methods to manage nitrogen application rate, timing and placement in a manner that addresses the variability imposed on the soil-plant system by the dynamics of weather. This study summarizes approaches with relevance to Canadian crops, and outlines the research and extension needs required to develop and apply weather-based nitrogen recommendations for cropping systems in Canada.

P3-52. *WITHDRAWN*


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