

8th Canadian Pulse Research Workshop - Calgary, AB
Executive Royal Inn Nov 3-5, 2010

Tuesday, November 2, 2010

Location: Executive Royal Inn Lobby
 6:30-8:30 PM Registration Desk Open and Poster Setup (in Sapphire Room)

Wednesday, November 3, 2010

Location: Emerald Ballroom
 7:30 - 8:15 AM Registration and Breakfast

SESSION 1: Pulse Agronomy, Diseases and Insects **BASF sponsored GOLD session**

Chair: Mark Oostlander/ Sheri Strydhorst

Location: Emerald Ballroom

8:15 AM	WELCOME		Sheri Strydhorst, Chair - 8th CPRW Organizing Committee
8:30 AM	Keynote Speaker Sabine Banniza	Oral-1	Limiting legions of leguminous lesions - pulse pathology research in the Canadian Prairies.
9:15 AM	Chris Gillard	Oral-2	New IPM strategies to control dry bean anthracnose.
9:35 AM	Michael Harding	Oral-3	Oxidized forms of silver as a novel disease management tool for pulse crops.
9:55 AM	Ambuj Jha	Oral-4	Utilization of improved ascochyta blight resistance from wild pea germplasm.
10:15 AM	BREAK		Location: Sapphire Room
10:35 AM	Jianfeng Liu*	Oral-5	Genetic diversity of pea downy mildew, <i>Peronospora viciae</i> f.sp. <i>pisi</i> in Alberta, Canada.
10:55 AM	Robyne Bowness*	Oral-6	Baseline sensitivity of <i>Mycosphaerella pinodes</i> to pyraclostobin fungicide.
11:15 AM	Jennifer Menat*	Oral-7	Lentil anthracnose: Investigating the mating system of <i>Colletotrichum truncatum</i> (Schwein).
11:35 AM	Bruce Gossen	Oral-8	Sensitivity of <i>Ascochyta rabiei</i> to strobilurins and other foliar fungicides in western Canada
11:55 AM	Panel Discussion with Speakers		
12:15 PM	LUNCH		Location: Emerald Ballroom

SESSION 2: Pulses and Environment **Syngenta sponsored GOLD session**

Chair: Denis Tremorin

Location: Emerald Ballroom

1:15 PM	Keynote Speaker Brian McConkey	Oral-9	Soil organic carbon as a measure of sustainable crop production.
2:00 PM	Frank Larney	Oral-10	Wide-row vs. narrow-row production of dry beans in the Vauxhall irrigated rotation study.
2:20 PM	Yantai Gan	Oral-11	Carbon footprints and annual pulses on the Canadian prairie.
2:40 PM	Tony Yang*	Oral-12	Pyrosequencing analysis of chickpea rhizospheric bacterial diversity as influenced by fungicide application.
3:00 PM	BREAK		Location: Sapphire Room
3:20 PM	Rosalind Bueckert	Oral-13	Nitrogen fixation and supply in faba.
3:40 PM	Hossein Zakeri*	Oral-14	Lentil production under varied N regimes and no-till duration in Saskatchewan.
4:00 PM	Dawn Laslop*	Oral-15	Economic costs and benefits of BMP adoption on commercial cropping operations in Alberta.
4:20 PM	Panel Discussion with Speakers		

Poster Display and Interactive Poster Session **Posters 1 through 27**

Chair: Jane King

Location: Sapphire Room
 4:30 - 7:30 PM Cash bar and finger foods
 4:45 - 6:00 PM Poster Display and Interactive Poster Sessions

Evening Dinner on own

Thursday, November 4, 2010**Location: Emerald Ballroom**

7:30 - 8:15 AM Registration and Breakfast

SESSION 3A: Novel Uses of Pulse Crops**Chair: Blair Roth****Location: Emerald Ballroom**

8:00 AM	Keynote Speaker Joyce Boye	Oral-16	Innovative approaches to enhance the use of pulse crops in food, health and industrial applications.
8:45 AM	Yulia Borsuk*	Oral-17	Incorporation of pulse flours (green lentils, navy beans, yellow peas, and pinto beans) of different particle size into pita bread.
9:05 AM	Zhen Ma*	Oral-18	Microstructure, stability and rheological properties of salad dressing-type emulsions supplemented with pulse flours.
9:25 AM	Laura Sawyer	Oral-19	Innovative coatings: Evaluation of pea starch and pea starch/fibre/flour blends in batter, pre-dust and glaze coatings.
9:45 AM	Mary-Lou Swift	Oral-20	Feeding value of peas for swine and poultry - results of feed evaluation/NIRS project.
10:05 AM	Panel Discussion with Speakers		
10:25 AM	Break		Location: Sapphire Room

SESSION 3B: Plant Breeding Initiatives**Chair: Blair Roth****Location: Emerald Ballroom**

10:45 AM	Tamira Delgerjav*	Oral-21	Genotype by environment analysis of the performance of two low phytate pea lines.
11:05 AM	Sarita Khanal*	Oral-22	Quantitative trait loci analysis of folate content in common beans (<i>Phaseolus vulgaris</i> L.).
11:25 AM	Bert Vandenberg	Oral-23	Genetic improvement of lentil in Canada - the next 10 years.
11:45 AM	Bert Vandenberg		CPRW Business Meeting
12:15 PM	LUNCH		
			Location: Emerald Ballroom

SESSION 4: Pulse Nutrition and Health**Novozymes sponsored GOLD session****Chair: Mark Olson****Location: Emerald Ballroom**

1:15 PM	Keynote Speaker Maurice Bennink	Oral-24	Health benefits associated with consumption of dry beans and other pulses.
2:00 PM	Gord Zello	Oral-25	Consumption of a pulse-based diet reduces cardiovascular disease risk factors in older adults.
2:20 PM	Alena Jin*	Oral-26	Identification, quantification and localization of proanthocyanidins in pea seed coats.
2:40 PM	Chris Smith*	Oral-27	Isolated yellow pea protein, but not fibre, suppresses short-term energy intake and postprandial glycemia in young healthy males.
3:00 PM	Break		
			Location: Sapphire Room
3:20 PM	Alfonso Clemente	Oral-28	Exploiting natural variation in legume Bowman-Birk inhibitors to dissect their potential role in human health-promoting programmes.
3:40 PM	Bohdan L. Luhovyy	Oral-29	The effect of pulses on satiation, glycemia and food intake.
4:00 PM	Dil Thavarjah	Oral-30	North Dakota State University pulse quality program - a potential whole food solution to the global human malnutrition.
4:20 PM	Panel Discussion with Speakers		

Poster Display and Interactive Poster Session**Posters 28 through 59****Chair: Sue Arntfield****Location: Sapphire Room**

4:45 - 5:45 PM Poster Display and Interactive Poster Sessions

4:30 - 9:00 PM Cash bar

Banquet, Awards & Entertainment**Saskatchewan Pulse Growers sponsored PLATINUM session****Chair: Kofi Agblor****Location: Emerald Ballroom**

6:30pm Indian Banquet Buffet and Awards Presentation

8:00pm Entertainment - Comedian, Jebb Fink

9:00 PM Cash bar closes

Friday, November 5, 2010

Location: Emerald Ballroom

7:30 - 8:15 AM Registration and Breakfast

SESSION 5: Plant Breeding Initiatives

Alberta Pulse Growers sponsored GOLD session

Chair: Parthiba Balasubramanian

Location: Emerald Ballroom

8:00 AM	Keynote Speaker Hans-Jörg Jacobsen	Oral-31	Present status and prospects of transgenic grain legumes.
8:45 AM	Kirstin Bett	Oral-32	Leveraging legume genomic resources for lentil genetic improvement.
9:05 AM	Andrew Sharpe	Oral-33	454 Transcript profiling for SNP discovery in pulse crops.
9:25 AM	Greg Perry	Oral-34	Sequence comparison of the major resistance QTLs for common bacterial blight in OAC-Rex and HR67.
9:45 AM	Chun (Marcus) Shi	Oral-35	Association mapping of common bacterial blight resistance QTL in Ontario bean breeding populations.
10:05 AM	BREAK		Location: Sapphire Room
10:25 AM	Deng-Jin Bing	Oral-36	Investigation of relationships of yield, seed size, seed protein and starch content and development of varieties with improved protein content of field pea (<i>Pisum sativum</i> L).
10:45 AM	Bunyamin Taran	Oral-37	Interaction of herbicide applications with reaction to ascochyta blight and phenology of several chickpea varieties.
11:05 AM	Anuradha Yadav	Oral-38	In vitro micropropagation in chickpea (<i>Cicer arietinum</i> L.) - a recalcitrant crop.
11:25 AM	Aziz Rehman	Oral-39	Improving chickpea productivity under drought using physiological and molecular approaches.
11:45 AM	Panel Discussion with Speakers		
12:05 PM	Invite to the 9CPRW (2012)		
			Chris Gillard
12:10 PM	CLOSING REMARKS		
			Sheri Strydhorst, Chair - 8th CPRW Organizing Committee

Lunch on own

Wednesday, November 3 - Poster Display and Interactive Poster Session

Chair: Jane King
Location: Sapphire Room
Time: 4:45 - 6:00 PM

Presentation Number	Title	Presenter	Presentation Type
Poster-1	Management of fusarium root rot of field peas with new disease control strategies.	Debra McLaren	Interactive
Poster-2	Esterase activity produced by conidia of <i>Peronospora viciae</i> f. sp. <i>pisi</i> .	Jerry Feng	Interactive
Poster-3	Characterization of mycosphaerella blight resistance, lodging resistance, and selenium concentration in a pea recombinant inbred line population.	Yong Liu*	Student Interactive
Poster-4	Developing a breeding strategy for Stemphylium blight resistance in lentil.	Rajib Podder*	Student Interactive
Poster-5	Anthracoze resistance breeding in lentil.	Leila Zadeh*	Student Interactive
Poster-6	SNP based genotyping of <i>Ascochyta lentis</i> resistance genes in lentil.	Ehsan Sari*	Student Interactive
Poster-7	Anthracoze resistance in lentil - genetic inheritance and molecular markers under development.	Rubeena Shaikh	Interactive
Poster-8	Innovations in pulse crop research and field techniques.	Brent Barlow	Interactive
Poster-9	Searching for a herbicide to control Group 2 (ALS) resistant cleavers (<i>Galium aparine</i>) in pulse crops.	Ken Sapsford	Interactive
Poster-10	Post-emergence rotary hoeing for weed control in pulse crops.	Eric Johnson	Interactive
Poster-11	Field pea effects on subsequent crops and economics of various crop combinations in southeast Peace area of Alberta.	Kabal Gill	Interactive
Poster-12	An overview of PURENet field studies at Scott, SK.	M. Sather	Interactive
Poster-13	Nitrogen cycling in pulse vs. non-pulse rotations: gross mineralization and nitrification.	L.P. Comeau	Interactive
Poster-14	Does the frequency of pea in long-term rotations impact nitrogen fixation?	J.D. Knight	Interactive
Poster-15	Soybean production potential in southern Alberta.	Manjula Bandara	Interactive
Poster-16	Partial field resistance and partial physiological resistance to white mould in dry bean.	Parthiba Balasubramanian	Poster
Poster-17	Inheritance of CBB resistance in a resistant-intercross population of common bean.	Ali Navabi	Poster
Poster-18	Image analysis for accurate quantification of common bacterial blight severity in common bean.	Weilong Xie	Poster
Poster-19	Sensitivity of <i>Ascochyta pinodes</i> populations to prothioconazole.	Goswami	Poster
Poster-20	Effect of downy mildew growth on yield of field pea.	Kan-Fa Chang	Poster - not published in CJPS
Poster-21	Effect of seeding depth, seeding date and seed treatment on downy mildew of field pea.	Kan-Fa Chang	Poster
Poster-22	Assessing the potential for clubroot spore contamination of field pea seed.	Ron Howard	Poster
Poster-23	Field pea response to phosphorous fertilizer in Southeast Peace area of Alberta.	Kabal Gill	Poster
Poster-24	Quantification of glomalin-related soil protein using the Bradford and ELISA methods.	M. Sather	Poster
Poster-25	Carbon fate in pulse vs. non-pulse rotations: A ¹³ C greenhouse study.	L.P. Comeau	Poster
Poster-26	Temporal dynamics of nitrogen rhizodeposition of pea.	M. Arcand	Poster
Poster-27	Yellow pea, lentil, navy bean and pinto bean addition to wheat flour cookies and their effect on physical and nutritional properties	Susan Artfield	Poster

Thursday, November 4 - Poster Display and Interactive Poster Session

Chair: Sue Arntfield
Location: Sapphire Room
Time: 4:45-5:45 PM

Presentation Number	Title	Presenter	Presentation Type
Poster-28	The capacity of symbiotic N fixation of pulse crops grown on the Canadian prairie.	Xiaoyu Wang	Interactive
Poster-29	Barley crop response to preceding cool season pulses in Alberta.	Christina Williams*	Student Interactive
Poster-30	Effects of plant growth regulators on crop maturity, seed yield and seed quality of the Kabuli chickpea cultivar CDC Frontier in southern Alberta.	Prabhath Lokuruge*	Student Interactive
Poster-31	Exploiting response to photoperiod to improve adaptation and yield of chickpea in the Canadian Prairies.	Ketema Daba*	Student Interactive
Poster-32	Quality assessment of pulse crops grown in North Dakota.	Kevin McPhee	Interactive
Poster-33	Anti-inflammatory activity of flavonoids isolated from the seed coat of coloured beans (<i>Phaseolus vulgaris</i> L.) on murine macrophages.	Karen Pitura*	Student Interactive
Poster-34	Biochemical and molecular characterization of two low phytate pea lines.	Arun Shunmugam*	Student Interactive
Poster-35	Understanding the genetic basis for carotenoid pigments in lentils.	Zesong Ye*	Student Interactive
Poster-36	Lactic acid assisted wet fractionation improved the purity and physicochemical properties of field pea (<i>Pisum sativum</i> L.) starches.	Sabaratnam Naguleswaran*	Student Interactive
Poster-37	Development of an oilseed pea.	Ehsan Khodapanahi*	Student Interactive
Poster-38	Linkage between genotype and phenotype in wild lentil.	M. Fedoruk*	Student Interactive
Poster-39	KnowPulse: A breeder-focused web portal that integrates genetics and genomics of pulse crops with model genomes.	L. Sanderson	Interactive
Poster-40	Characterization of <i>Phaseolus acutifolius</i> as a source for developing genetic variability in dry bean breeding.	Perumal Vijayan	Interactive
Poster-41	Wilderness adventures: Using wild germplasm to sustain genetic improvement of cultivated lentil.	Abebe Tullu	Interactive
Poster-42	Techniques for quantifying nitrogen fixation of pulse crops on the Canadian prairie.	Xiaoyu Wang	Poster
Poster-43	Ureide concentrations in faba genotypes.	Rosalind Bueckert	Poster
Poster-44	The feasibility of winter pulses grown in Alberta agro-ecological environments.	Mark Olson	Poster
Poster-45	Acidification, microbial growth, physical and rheological properties of yogurt supplemented with lentil flour.	Joyce Boye	Poster
Poster-46	Angiotensin I-converting enzyme in vitro inhibitory activity of nine <i>Phaseolus vulgaris</i> legume tryptic hydrolysates.	Joyce Boye	Poster
Poster-47	The feed value of field pea and five other annual crops harvested prior to seed fill.	Shirley Ross	Poster
Poster-48	Physicochemical and functional properties of fiber fractions from pulses.	Ning Wang	Poster
Poster-49	Comparison of protein films mechanical properties made from common dry bean (<i>Phaseolus vulgaris</i>) varieties and storage protein deficient lines.	Loo-Sar Chia	Poster
Poster-50	Low phytic acid lentil: an answer for micronutrient malnutrition?	Vincent See	Poster
Poster-51	Cooking and canning quality of selected dry bean genotypes grown in Manitoba.	Gina Boux	Poster

Poster-52	Lentils (<i>Lens culinaris</i> L.) as an ingredient in emulsified ovo-vegetarian sausages: nutritional, sensory and physicochemical property evaluation.	Dil Thavarajah	Poster
Poster-53	Capturing market opportunities for Canadian pulses: Pulse flour milling and utilization project description.	Heather Maskus	Poster
Poster-54	Worldwide dry bean germplasm collections useful for cultivar development for production in Canada.	Anfu Hou	Poster
Poster-55	Double, double, toil and trouble - new technologies for lentil.	Hai Yuan	Poster
Poster-56	Genetic diversity of selected chickpea elite lines and their progenitors based on microsatellite markers.	Marwan	Poster
Poster-57	Development of temperature-switch PCR (TS-PCR) markers for SNP genotyping in common bean.	Kangfu Yu	Poster
Poster-58	Development of SNP markers for lentil breeding.	Kirstin Bett	Poster
Poster-59	Genetic control of post-harvest darkening in pinto bean.	Kirstin Bett	Poster



**EIGHTH
CANADIAN
PULSE RESEARCH
WORKSHOP**

**November 3 - 5, 2010
Calgary, AB**

It is our pleasure to invite you to the 8th Canadian Pulse Research Workshop in Calgary, Alberta on November 3 - 5, 2010. Building on the success of previous bi-annual workshops, pulse crop researchers will present their latest results within the areas of: Nutrition and Health; Plant Breeding Initiatives; Novel Uses of Pulse Crops; Pulse Agronomy, Diseases and Insects; Pulses and the Environment.

Schedule of Events

November 3, morning: Pulse Agronomy, Diseases and Insects

Keynote speaker: Sabine Banniza, Associate Professor (Plant Pathology)
Crop Development Centre, University of Saskatchewan

November 3, afternoon: Pulses and the Environment

Keynote speaker: Brian McConkey, Research Scientist
Agriculture and Agri-Food Canada, Swift Current, SK
Soil organic carbon as a measure of sustainable crop production

November 4, morning: Novel Uses of Pulse Crops

Keynote speaker: Joyce Boye, Scientist
Agriculture and Agri-Food Canada, St-Hyacinthe, QC

November 4, afternoon: Pulse Nutrition and Health

Keynote speaker: Maurice Bennink, Professor
Michigan State University

November 4, evening: Indian Banquet Buffet

Entertainment: Jebb Fink, Comedian, www.callbackent.com/Jebb-Fink.html

November 5, morning: Plant Breeding Initiatives

Keynote speaker: Hans-Jörg Jacobsen, Head Plant Biotechnology
Leibniz University, Hannover, Germany

Key Deadlines

- August 3rd, 2010 • Student travel award application due
- October 1st, 2010 • Title and short abstract due
- October 1st, 2010 • Hotel registration deadline for guaranteed room and rate
- October 1st, 2010 • Regular registration deadline
- December 3rd, 2010 • Two page summary of poster or oral presentation

ORAL - 1

Limiting legions of leguminous lesions - pulse pathology research in the Canadian prairies.

S. Banniza, B. Vandenberg, B. Tar'an, T. Warkentin and K. Bett. Crop Development Centre, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8.

Since the first pulse crops were growing in the Canadian prairies substantial progress has been made in managing the diseases that sooner or later have infested those crops. Some significant improvements have been made in resistance breeding, most notably against ascochyta blight and anthracnose in lentil. More challenging in this regard have been ascochyta blight and mycosphaerella blight of chickpea and pea, for which good resistance has remained elusive. Wild germplasm has become a valuable source of new resistance, and is being used experimentally in all pulse breeding programs at the Crop Development Centre. Good resistance remains the most efficient and economical tool in disease management and efforts continue to improve resistance to the primary as well as some secondary diseases that can cause major damage. Regular disease and fungal population surveys are essential for the identification of resistance break-down and shifts in the disease spectrum, not only for effective resistance breeding programs, but also for disease management. Agronomic research in terms of crop rotation and crop management over the years has highlighted some basic approaches to breaking disease cycles, but the use of fungicides, whether as seed treatments against seed and root rotting pathogens, or as foliar applications, continues to be an important tool. The decision to apply a fungicide has always been challenging for producers, requiring thorough field scouting and early recognition of disease symptoms, as well as a good knowledge of disease progression and impact, in terms of biology and economy. Most recently, producers have been confronted with the emergence of fungicide insensitivity primarily in the population of *Ascochyta rabiei* to strobilurins. A considerable amount of research has been conducted on determining thresholds for intervention as well as best application practices, in particular in chickpea. For the past 10 years, attempts have been made to introduce decision support and disease forecasting systems for pulse crop diseases as an aid to producers. Implementation and uptake of these systems have been met with mixed results for various reasons. As farms become larger and economic margins on farms become narrower, it will be important to develop effective technology transfer strategies so that pulse production indeed benefits from all the research conducted on disease management.

ORAL – 2

New IPM strategies to control dry bean anthracnose. C.L. Gillard¹, R.L. Conner², P. Balasubramanian³ and G. Boland⁴. ¹University of Guelph Ridgetown Campus, Ridgetown, Ontario, ²Agriculture and Agri-food Canada, Morden, Manitoba, ³Agriculture and Agri-food Canada, Lethbridge, Alberta, ⁴University of Guelph, Guelph, Ontario.

In Canada, anthracnose (*Colletotrichum lindemuthianum*) infection frequently results in yield and seed quality losses in dry bean. In 2005, a national anthracnose project was initiated. Studies were conducted in Manitoba and Ontario, the leading dry bean producing provinces. One of the project objectives was to update the Integrated Pest Management (IPM) strategy for anthracnose. Surveys of commercial fields determined that race 73 was the predominate race, accounting for 96.2% of the isolates submitted between 2005 and 2007. Several studies were conducted to determine the movement and survival of anthracnose. In an overwintering study (still ongoing), anthracnose survived on stem and pod tissue for at least 16 months, and seed tissue for at least 6 months. Survival was greater for residue placed on the soil surface, versus residue buried 15 cm in the soil. Similar findings were found in a simple rotational experiment conducted in 2006-08. A disease transmission study was conducted using common agricultural materials (leather, rubber, painted metal and denim) that were soaked in a concentrated anthracnose spore solution (1×10^7), and then passed through wet and dry bean canopies. Infection occurred at the Manitoba site in 2007, the Ontario site in 2008, and both sites in 2009. When infection occurred, it occurred in all

treatments in both the wet and dry crop canopies, except the control treatment. The degree of disease transmission was influenced by the humidity in the crop canopy at a site, and differences in the humidity between sites. To disinfect these materials, a 10% bleach solution (0.525% sodium hypochlorite) was found to be the most effective, followed by chlorine dioxide (Aquacare) and chloroxyleneol (Dettol). As well, several studies were conducted to determine the efficacy and timing of chemical controls. The seed treatment DCT (diazinon/captan/thiophanate-methyl) was superior to Apron Maxx (fludioxonil/metalaxyl-M). The addition of azoxystrobin to Apron Maxx provided results similar to DCT. The best seed treatments suppressed disease symptoms for approximately 45 days after planting. Foliar fungicides are effective in providing in-crop disease suppression. Pyraclostrobin was found to be superior to azoxystrobin, increasing economic returns by \$69-163 ha⁻¹. A late vegetative (V6) application timing of either fungicide gave the best disease control at low disease levels, while an early to mid-flower application timing (R1-R2) gave the best disease control under moderate to high disease scenarios. A late timing at 10 days after full flower (R4) consistently provided the poorest results. A sequential fungicide application at early (R1) and full flower (R2) consistently provided better results, compared to any single application timing. In studies combining seed treatments with foliar fungicides, it was found that the addition of DCT seed treatment generally allowed for a delay in the first application of either foliar fungicide, while the addition of Apron Maxx did not. Combining azoxystrobin with Apron Maxx provided similar results to DCT. In this study, a sequential fungicide application was still superior to a single fungicide application, particularly under high disease pressure.

ORAL – 3

Oxidized forms of silver as a novel disease management tool for pulse crops. M.W. Harding¹, D.A. Sowa¹, R.J. Howard², and M.E. Olson¹. ¹Innovotech Inc., 101, 2011-94 St., Edmonton, Alberta, Canada T6N 1H1, ²Crop Diversification Centre South, Alberta Agriculture and Rural Development, 301 Horticultural Station Rd. E., Brooks, Alberta, Canada T1R 1E6.

Oxidized forms of silver are highly effective antimicrobial compounds. For example, oxysilver nitrate is bactericidal and fungicidal, and demonstrated to eradicate a number of plant pathogenic microorganisms from seed surfaces. Oxysilver nitrate is effective against biofilms of dry bean bacterial blight pathogens at concentrations 10 to 100 times lower than current seed treatment standards such as streptomycin sulphate and cupric hydroxide. Furthermore, oxysilver nitrate is a multi-site fungicide with a reduced risk of resistance development in target organisms. In a number of instances, small-plot replicated field studies in Alberta have confirmed that oxysilver nitrate is an effective seed treatment for control of seed-borne bacteria and fungi on pulse crops. More recently, oxysilver nitrate has been tested as a foliar-applied treatment for control of bacterial blights and ascochyta blights on pulses. The research described indicates that oxysilver nitrate has significant potential as a broad spectrum disease management tool for pulse producers in Canada.

ORAL – 4

Utilization of improved ascochyta blight resistance from wild pea germplasm. A.B. Jha, V. Gurusamy, B. Tar'an, S. Banniza, and T. Warkentin, Crop Development Centre, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8.

Ascochyta blight caused by *Mycosphaerella pinodes* is the most important pea disease in the world. It reduces yield, seed quality and limits the areas in which field pea can effectively be grown. Several studies have indicated a high level of resistance to ascochyta blight disease in some accessions of *Pisum fulvum*, a wild relative of field pea. The objective of this study is to identify ascochyta blight resistant wild pea accessions for use in introgression program into Canadian pea germplasm. For this study, 53 wild pea (*P. fulvum*) accessions, and several wild

sub-species accessions (subsp. *elatius*, *transcaucasicum*, *asiaticum*, *arvense* and *abyssinicum*) obtained from USDA, Pullman, WA and IFAPA, Spain were used. Wild accessions along with checks, CDC Striker (fair resistance) and Alfetta (poor resistance), were artificially inoculated with *M. pinodes* isolate MP25 (Crop Development Centre, University of Saskatchewan pulse pathology group collection) and scored for ascochyta blight disease severity under greenhouse and field conditions. Thirteen accessions had lower disease score than CDC Striker (1.9) and had less area under the disease progress curve (AUDPC) than CDC Striker (26), while Alfetta had a 3.3 disease score and an AUDPC value of 53. On the basis of these results, 4 wild accessions namely, PI 344538 (*P. sativum*, ssp. *elatius*), PI 560061 (*P. fulvum*), W6 15017 (*P. fulvum*) and P 651 (*P. fulvum*) were selected and used in crossing with the susceptible check cultivar Alfetta (*P. sativum*) for further genetic studies. Four successful interspecific crosses have been confirmed by hybridity analyses, and these populations are currently in the F₂ generation. Recombinant inbred lines (RILs) will be generated from these crosses then used for QTL analysis to identify SNP markers for ascochyta blight resistance.

ORAL – 5

Genetic diversity of pea downy mildew, *Peronospora viciae* f.sp. *pisi* in Alberta, Canada. J.F. Liu¹, K.F. Chang², S.F. Hwang³, and S.E. Strelkov¹. ¹Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, Alberta T6G 2P5, Canada; ²Field Crop Development Centre, Alberta Agriculture and Rural Development, Lacombe, Alberta T4L 1W8, Canada; ³Crop Diversification Centre North, Alberta Agriculture and Rural Development, Edmonton, Alberta T6G 2P5, Canada.

Downy mildew, caused by the obligate parasite *Peronospora viciae* f.sp. *pisi*, is a common disease of pea. In 2009, 37 commercial pea fields located in the Mannville, Fort Saskatchewan and Vermillion areas of central Alberta were surveyed for downy mildew, with disease severity found to range from 0% to 26%. As the genetic structure of *P. viciae* populations from Alberta is not known, RAPD markers were used to investigate genetic diversity among 23 isolates of the pathogen collected from 19 infested fields. A total of 47 polymorphic bands were produced using nine arbitrary primers. Based on analysis with the POPGENE program, the 23 isolates were clustered into six groups, which were not associated with pea cultivar or location of origin. Five of the *P. viciae* isolates collected from the most severely infested field clustered in three groups. Studies of the population structure of *P. viciae* in Alberta may be useful in helping to manage downy mildew of field pea, by providing an understanding of the diversity of pathogen populations.

ORAL – 6

Baseline sensitivity of *Mycosphaerella pinodes* to pyraclostobin fungicide. R. Bowness^{1,5}, K.F. Chang¹, B.D. Gossen², R.S. Goswami³, S.F. Hwang⁴, C. Willenborg^{4,5}, and S.E. Strelkov⁵. ¹Alberta Agriculture and Rural Development, Lacombe, Alberta, ²Agriculture and Agri-Food Canada, Saskatoon, Saskatchewan, ³North Dakota State University, Fargo, ND, ⁴Alberta Agriculture and Rural Development, Edmonton, Alberta, ⁵University of Alberta, Edmonton, Alberta.

Mycosphaerella pinodes (Berk. and Blox.) Vestergren (anamorph *Ascochyta pinodes* L.K. Jones) is the dominant pathogen in the Ascochyta blight complex that attacks field pea in Western Canada. Symptoms of the disease include necrotic lesions on the leaves, stems and pods. This leads to foot rot, lodging, and reduced yields. The most effective management strategy is the repeated application of foliar fungicides. Several fungicides are registered for this use, but pyraclostobin, a strobilurin fungicide, is highly effective and frequently used across western Canada. Strobilurins have a site-specific mode of action and so repeated applications may lead to the development of fungicide-insensitivity in pathogen populations. To determine if insensitivity

is developing in a pathogen population, it is useful to know the baseline or initial reaction of the unexposed population. This information simplifies and facilitates implementation of a monitoring program to detect shifts in sensitivity. The pyraclostrobin sensitivity of isolates of *M. pinodes* that were never exposed to this chemistry, originally collected from Saskatchewan, Alberta and North Dakota and kept in long-term storage, were compared with recently (2009 and 2010) collected isolates from the same geographical areas, in order to determine if there had been any change in response as a result of exposure to the fungicide. A baseline sensitivity assessment was made using radial growth and conidial germination assessments on potato dextrose agar amended with concentrations of pyraclostrobin ranging from 0 µg/ml to 10 µg/ml for conidial growth, and 0 µg/ml to 1000 µg/ml for radial growth. The concentration of fungicide that effectively inhibited 50% of germination or growth (EC₅₀) was determined for each isolate in the baseline collection. In the radial growth assessments, the EC₅₀ values ranged from about 0.3 µg/ml to about 0.8 µg/ml. In the assessments using conidial germination, EC₅₀ values were lower, ranging from about 0.1 µg/ml to about 0.5 µg/ml. Determining these values is the first step in developing a vital monitoring system to measure pathogen sensitivity changes to this fungicide.

ORAL – 7

Lentil anthracnose: Investigating the mating system of *Colletotrichum truncatum* (Schwein.). Andrus & W.D. Moore. J. Menat and S. Banniza. University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8.

Lentil anthracnose, caused by the ascomycetous fungus *Colletotrichum truncatum*, is responsible for severe yield losses in Saskatchewan lentil fields. Infection and dispersal is caused by the anamorphic stage, which is the only form to have been described in the field. The teleomorph, (*Glomerella truncata* Armstrong-Cho & Banniza), has been obtained under laboratory conditions only recently, and the mating system of this species remains unstudied. In most heterothallic ascomycetes, the mating system is controlled by a single mating-type gene called MAT, with the two alleles MAT1 and MAT2 determining two mating types (monoallelic bipolar mating system). However, studies performed on several other *Glomerella* species suggest that a different system determines mating compatibility in this genus. This study investigated the mating system of *G. truncata* through classical crossing assays in order to: 1) understand mating compatibility in this species, and 2) verify if different mating types cohabitate in the field at a small scale. The crosses were performed by soaking sterile lentil stems into a mix of spore suspensions of isolate pairs or of a single isolate in the case of selfings, then transferring the stems on agar Petri dishes lined with filter paper. Dishes were incubated for two weeks at 22°C in the dark and subsequently screened for perithecia with a stereomicroscope. To determine mating compatibility in *G. truncata*, 21 field isolates from Saskatchewan and Manitoba were crossed in all possible combinations, including selfings. To determine if different mating types are present in the field, 15 isolates sampled in close proximity were tested against two cross-fertile isolates. The results of this study suggest that *G. truncata* is a heterothallic species with two mating compatibility groups. It also shows that isolates of both groups are present in the field in close proximity, sometimes on the same plant, which makes mating in natural conditions a possible event. Genetic studies are currently undertaken to obtain a better understanding on mating compatibility and the inheritance of mating types from parents to progeny.

ORAL – 8

Sensitivity of *Ascochyta rabiei* to strobilurins and other foliar fungicides in western Canada.

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Foliar fungicides are required each year for management of ascochyta blight, caused by *Ascochyta rabiei* (Pass.) Labr. (teleomorph *Didymella rabiei*) on chickpea (*Cicer arietinum* L.) in western Canada. Extensive and repeated use of strobilurin fungicides starting in 2003 led to widespread insensitivity to strobilurins in *A. rabiei* across the region by 2007. A similar pattern of fungicide usage and loss of sensitivity has been reported from adjacent areas of the USA. To assess the competitive ability of QoI-insensitive isolates, four sensitive and four insensitive isolates were inoculated onto a susceptible chickpea cultivar in a greenhouse trial and the study was conducted three times. There were no differences in ascochyta blight severity, lesion counts, or time to first lesion development and pycnidia initiation between the sensitive and insensitive isolates. This indicates that the gene for insensitivity will likely persist in the population for a long time in the absence of strobilurin fungicide application. A previous study had indicated that sensitivity to the multi-site protectant fungicides chlorothalonil and mancozeb might be declining, but no evidence of insensitivity to either fungicide was identified in 27 isolates of *A. rabiei* collected in Saskatchewan in 2007. To quantify the baseline sensitivity of *A. rabiei* to penthiopyrad (a new succinate dehydrogenase inhibitor (SDHI) fungicide), 50 isolates collected in 2008 and never exposed to this fungicide were assessed. EC₅₀ values for radial growth ranged from 0.002 to 0.30 µg/mL, with a mean of 0.10 µg/mL. To screen a wider population of isolates for sensitivity, isolates from Saskatchewan collected in 2008 and 2009 were assessed on a discriminatory dose of 0.3 µg/mL penthiopyrad; 15% of the isolates (12 of 79) exhibited less than 50% inhibition of radial growth. A discriminatory dose of 0.5 µg/mL penthiopyrad is recommended for future monitoring. However, there was no correlation in response between penthiopyrad and boscalid, a SDHI fungicide that is widely used on chickpea in the region.

ORAL – 9

Soil organic carbon as a measure of sustainable crop production. B.G. McConkey¹, D. Cerkowniak², W. Smith³, and R. Desjardins³. ¹Agriculture and Agri-Food Canada, Swift Current, S9H 3X2; ²Consultant, 2126 McKinnon Ave. Saskatoon, S7J 1N4; ³Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, K1A 0C6.

The question of whether food is produced in a sustainable way is not only important to primary producers but increasingly to consumers and major food processors and retailers. Soil organic carbon (SOC) is a powerful indicator of soil quality because it is important to nutrient cycling, soil biota richness, soil structure and tilth, and water movement and storage. The change in SOC integrates the net difference between soil building and soil degrading processes. Increasing SOC also represents a sink for the greenhouse gas CO₂. Despite its value, SOC is not regularly used as a sustainability indicator for particular foodstuffs. Total SOC by itself is not a reliable indicator of soil quality as many site factors affect this value that are unrelated to sustainability. Total SOC relative to standard management practice has more utility. Although the change in SOC is a more reliable indicator of sustainability, it has challenges to measure and estimate. Pulses can be associated with improving SOC quantity and quality because of their rotational benefits and good fit in cropping systems with reduced summerfallow and reduced tillage. There are both opportunities and challenges to attributing a quantity of SOC change to a tonne of pulses – the measure that is becoming progressively more desired in the marketplace. Generally, SOC change is difficult to document on an individual producer basis but SOC change quantification becomes simpler and more accurate when considering many producers together.

Oral – 10

Wide-row vs. narrow-row production of dry beans in the Vauxhall irrigated rotation study.

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An irrigated rotation study with potatoes (*Solanum tuberosum* L.), sugar beet (*Beta vulgaris* L.), dry beans (*Phaseolus vulgaris* L.) and soft wheat (*Triticum aestivum* L.) was initiated in 2000 to examine the impact of conventional and sustainable rotations on crop yield and quality and soil properties. The sustainable rotations (3 to 6 yr in length) were built around four specific soil management practices: (1) reduced tillage; (2) cover crops; (3) feedlot manure compost application and (4) where beans occurred in the rotation, solid-seeded narrow-row beans vs. conventional wide-row beans. This presentation will focus on dry bean production in wide-row (60 cm) spacing (conventional management) vs. solid-seeded narrow-row (20 cm) beans (sustainable management). Dry bean cultivars (UI-906, 2000-03; AC Redbond, 2004-09) were grown in both wide- and narrow-rows in 3 yr and 4 yr rotations as well as in narrow rows in 5 and 6 yr rotations. The narrow-row beans in the 3 yr rotation were direct seeded with a double disc press drill into fall rye burnoff while those in the 5 yr rotation were direct seeded into shredded wheat stubble. In the early years of the study, weed control in the narrow row beans was more of a challenge due to the inability to inter-row cultivate as with the wide-row beans. Significant rotational effects occurred for average bean yields in the first three years (2000-02), e.g. 4 yr wide-row beans averaged 2339 kg ha⁻¹ which was significantly higher than the 3, 5 and 6 yr narrow-row rotations (1525-1929 kg ha⁻¹). After that (yields averaged over 2000-03, 2000-04 and 2000-05) rotational and row-spacing effects were non-significant as the narrow-row beans 'caught up' with conventional wide-row. By 10 yr of the study (2000-09), average yields on the 3 yr wide-row beans were not significantly different than those on the 3 yr narrow-row (2035 vs. 1918 kg ha⁻¹). However, on the 4 yr rotations, the difference between wide-row and narrow-row was significant (2186 vs. 1976 kg ha⁻¹). The narrow-row beans on the 6 yr rotation (2003 kg ha⁻¹) were not significantly different from the 3 yr wide-row beans (2035 kg ha⁻¹) but were significantly lower than the 4 yr wide row beans (2186 kg ha⁻¹). Of all the rotations, the narrow row beans direct seeded into wheat stubble on the 5 yr rotation were the lowest yielding treatment on average (1811 kg ha⁻¹). Over 10 yr (2000-09), the average yield of the two wide-row rotations (3 and 4 yr) was 2111 kg ha⁻¹ which was 9.5% higher than the average (1927 kg ha⁻¹) of the four narrow row rotations (3, 4, 5 and 6 yr).

ORAL– 11

Carbon footprints and annual pulses on the Canadian prairie. Y. Gan¹, C. Liang², and C.

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Carbon footprint is defined as the amount of greenhouse gas emissions associated with a product or a service, expressed in carbon dioxide equivalence (CO₂e). There is an increased public demand for carbon footprint labeled farm products. This paper compared carbon footprints of pulse crops with oilseeds and cereal crops grown on the Canadian prairie and determined the effect of pulse-based crop sequences on the carbon footprint of a subsequent durum wheat. The values of carbon footprints were estimated based on emissions from the decomposition of crop straw, roots and seeds; the manufacture of N and P fertilizers and their application rates to the production of a specific crop; the production of herbicides and fungicides; and miscellaneous farm field operations including planting, spraying, land preparation, tillage and harvest. Our results showed that the production and application of N fertilizers accounted for about 57 to 65% of the total footprints, those from crop residue decomposition 16 to 30%, and the rest of the

footprints were associated with P fertilizers, pesticides, and field operations. One kg of crop product requires 0.71 kg CO₂e for canola, 0.42~0.63 kg CO₂e for mustard, flaxseed and spring wheat, and 0.17~0.26 kg CO₂e for chickpea, lentil, and dry pea. Durum crop preceded by a pulse crop produced had a carbon footprint of 673 kg CO₂e, 20% lower than when the durum crop was preceded by a cereal crop. Similarly, carbon footprint of durum preceded by an oilseed was 744 kg CO₂e, 11% lower than when was preceded by a cereal. Carbon footprint intensity was 0.25 and 0.28 kg CO₂e per kg of grain of durum grown, respectively, after a pulse and after an oilseed crop, which was significantly lower than 0.37 for the crop grown after a cereal. Crop choices and crop sequences significantly affected carbon footprint of field crops on the Canadian prairie.

ORAL– 12

Pyrosequencing analysis of chickpea rhizospheric bacterial diversity as influenced by fungicide application. C. Yang^{1,2}, C. Hamel², Y.T. Gan², and V. Vujanovic¹. ¹Food and Bioproducts Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, ²Semiarid Prairie Agricultural Research Centre, AAFC, Swift Current, Saskatchewan.

Fungicide application in field crops may have hidden non-target effects on the agro-ecosystem. In this study, amplicon sequencing with 454 GS FLX Titanium technology was applied to unveil the effects of three fungicide application programs commonly used to control *Ascochyta* blight (*Ascochyta rabiei*) on the rhizosphere bacterial communities of two chickpea cultivars. Treatments were replicated four times in complete blocks, in the field, in 2008 and 2009, in Swift Current, Saskatchewan. Results showed that operational taxonomic units (OTUs) of the bacterial communities under different treatments changed significantly ($P < 0.05$), indicating negative effects of fungicide application on soil bacterial variant in the chickpea rhizosphere. Fungicide treatments also had a selective effect on bacterial taxa, as revealed by Ribosomal Database Project (RDP) classification analysis of identified DNA fragments. We conclude that the control of foliar diseases with fungicide applications can modify the composition of the rhizosphere bacterial community, which could further affect their associated functions.

ORAL – 13

Nitrogen fixation and supply in faba. R. Bueckert, J. Pritchard and A. Vandenberg. Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan S7N 5A8.

Pulses can supply most of their N requirements through N₂ fixation, and they also contribute N to the succeeding rotation crop. Our goal was to assess 15 genotypes (cultivars and breeding lines) of faba (*Vicia faba*) in the field at two locations in Saskatchewan in 2009 for their ability to take up and to fix N. The N in the shoot was partitioned into leaf, stem, pod and seed portions. A range of yield, biomass and nitrogen accumulation was seen for Rosthern 2009. Saskatoon 2009 was drier and yields were slightly lower, along with less biomass and slightly less N accumulated. Florent, Taboar, Melodie, FB22_10 and Divine had the highest total plant N accumulation, coming from vegetative parts but especially from reproductive growth. Faba had a ratio of about 2 parts of total N per unit area in the seed compared to 1 part in the stover. Assuming all N from vegetative biomass at maturity became available to succeeding crops, faba genotypes supplied between 10 and 15 g N m⁻², or 100 to 150 kg N ha⁻¹. The yield portion removed an additional 20 to 35 g N m⁻², or 200 to 350 kg N ha⁻¹, due to faba being a high yielding crop with a high seed protein content (about 30%). Faba was efficient at partitioning biomass to yield with harvest indices ranging from 0.34 to 0.45 in a cool, dry year. For Rosthern, cultivars had significantly different yields, ranging from 499 to 617 g m⁻² (4,990 to 6,170 kg ha⁻¹). At Saskatoon, yield differences were less obvious among the 15 faba genotypes, ranging from 447 to 650 g m⁻². Snowbird had the highest yield at both locations. At Rosthern, Snowbird, NPZ5_7680, Divine and Imposa were in the high-yielding group (617-590 g m⁻²). So far, faba's physiological

characteristics show a reasonably efficient crop with lower variability when compared to chickpea and lentil, and high amounts of N accumulated in yield and stover.

ORAL – 14

Lentil production under varied N regimes and no-till duration in Saskatchewan. H. Zakeri¹, R.A. Bueckert¹, G.P. Lafond², J.J. Schoenau³, and A. Vandenberg¹, ¹Department of Plant Sciences, ²Indian Head Research Farm, RR# 1 Gov Road, PO Box 760, Indian Head, Saskatchewan, S0G 2K0, ³Department of Soil Science, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan S7N 5A8, Canada.

Lentil is increasingly grown in the Black soil zone of Saskatchewan, where short seasons together with plentiful soil nitrogen (N) and late season rainfall delay crop maturity and reduce yield. Response of maturity and yield to the source and timing of N and duration of no-tillage was investigated in a series of field and greenhouse studies during 2006-2009. Commercial rhizobia inoculant and N fertilizer treatments did not delay the days to maturity compared to an untreated control. Reduced N availability in the control lowered both yield and harvest index. When N availability to lentil was reduced, post-flowering N accumulation was reduced in vegetative biomass, thereby lowering yield. In the second field experiment, days to maturity were not affected by the duration of no-till practices in the Black soil zone of the province; however, yield was significantly lowered by long-term no-till in one out of three years. Apparently, longer no-till practices reduced the soil temperature and lowered both harvest index and yield. In a greenhouse study, post-flowering N fertilizer application improved the yield and harvest index compared to an inoculated treatment. From these results, we do not recommend applying N fertilizer instead of rhizobia as a tool to hasten maturity in lentil. Further investigations on source-sink associations as well as the effects of no-till on crop residues, soil temperature and lentil yield are needed.

ORAL– 15

Economics of beneficial management practices adoption on commercial cropping operations in Alberta. D.E.T. Laslop, S.R. Jeffrey, and J.R. Unterschultz. Department of Rural Economy, University of Alberta, Edmonton, Alberta, Canada, T6G 2H1.

Crop production “interacts” with the environment in the sense that cropping activities impact on environmental quality. In some cases, the effects are positive while in other cases crop production can have negative effects on the surrounding environment, resulting in external costs to society. Beneficial management practices (BMPs) are production practices that can potentially mitigate the negative impacts. However, currently the economic viability of these BMPs is unknown. This study examines the on-farm costs and benefits of adoption of BMPs, including the addition of pulse and cereal crops in cereal-oilseed rotations and the addition of management practices on representative commercial crop farms in Alberta. Specifically, the adoption of alfalfa hay, field peas, and oats in pre-existing crop rotations will be examined, with the addition of legume green manures as a partial replacement for fallow in applicable regions. Changes in management practices include the adoption of on-farm shelterbelts, buffer strips and crop residue management. Farms are defined to be representative of different regions of Alberta and to have features typical of each region. A total of five farms are considered to represent cropping operations in Alberta: dryland farms in each of the Brown, Dark Brown, Black, and Dark Grey soil zones and one farm under irrigated production located in the Brown soil zone. Representative farms differ by farm size, crops produced, and management decisions. Models are developed to replicate the economic performance of each representative farm using modified net cash flow methods. Monte Carlo simulation is used to account for price and yield risk encountered in cropping operations. Cash flows are calculated over a 40 year planning horizon. These cash flows are used to determine an overall net present value for each farm, under each scenario. Farm performance prior to BMP implementation is evaluated and individual and combined effects post BMP adoption is

estimated. Pre- and post- BMP adoption net present values are compared to determine the feasibility of BMP adoption on commercial crop farms in Alberta. Preliminary findings suggest that some of the previously mentioned BMPs may be costly to producers to implement and producers may need monetary incentives for adoption to occur. However some rotational changes have minimal adoption cost and it is thought that after further analysis, long term benefits may occur. Results from this study are valuable to producers for specific BMP adoption feasibility. Governments may also find value in the results of this study as policy incentives may be necessary to compensate producers for implementing BMPs that are beneficial to society.

ORAL – 16

Innovative approaches to enhance the use of pulse crops in food, health and industrial applications. J.I. Boye. Food Research and Development Centre, Agriculture and Agri-Food Canada, 3600 Casavant Boul West, St Hyacinthe, QC Canada J2S 8E3

The last few decades have seen tremendous progress in the development of novel food products and innovative processing technologies. Global markets indicate that the trend is only likely to grow as food manufacturers seek ways to remain competitive domestically and internationally while meeting the demands of consumers for better tasting, nutritious foods at affordable costs. Pulse crops and their derived ingredients can be positioned to take advantage of these markets due to their great versatility and suitability for use in the feed, food, health food, pharmaceutical and industrial sectors. Thus, knowledge generation on ways to diversify the functionality of whole pulse products and pulse ingredients will be critical to sustaining and supporting their application in sectors of interest. The presentation will review cost effective technologies for the processing of whole pulses, pulse flours and pulse fractions and for mapping their functionality. Recent research on the composition of pulse bioactives and potential health properties and approaches for harnessing these benefits will be discussed. Additionally, novel current and potential applications in allergen-free food development, probiotic beverages, salad dressings, pharmaceutical hydrogels and biofilms will be presented. As innovation and speed-to-market are the lynchpins in spurring uptake in new areas of application, the presentation will also address current challenges as well as opportunities presented by other food and industrial sectors.

ORAL – 17

Incorporation of pulse flours (green lentils, navy beans, yellow peas, and pinto beans) of different particle sizes into pita bread. Y. Borsuk¹, S. Arntfield¹, and O. Lukow². ¹Department of Food Science, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2, ²Agriculture and Agri-Food Canada, Winnipeg, Manitoba, Canada R3T 2M9

As Canadian grown pulse crops have not received adequate attention in terms of pulse based products, incorporation of pulse flours into pita bread was studied. Health and nutritional benefits of pulses and their by-products have been broadly studied and recognized as they are rich in protein, fibre, antioxidants, some minerals and vitamins. In this study, commercial dehulled yellow pea flour (*Pisum sativum* L.) of fine particle size and other pulse flours including dehulled green lentils (*Lens esculenta*), navy beans (*Phaseolus vulgaris*) with the hull, and pinto beans (*P. vulgaris*) with the hull, which were ground into fine and coarse fractions, substituted wheat flour in the pita formula. Flour blends were prepared with various percentages of pulse flours (25, 50, 75, and 100%) and wheat flour, and made into pita bread. A commercial food graded system of hydrocolloids (cellulose gum, guar gum, and xanthan gum) was included in the formula at 0.4% of the flour as a texture improver. The amount of water required for mixing was evaluated based on Farinograph absorption of the flour blends. The blends made from coarse pulse flours demonstrated higher rates of water absorption compared to the blends made from small particles. Pita bread quality was estimated objectively according to its specific loaf volume, texture, crust color, diameter, and a pocket height. Subjective evaluation of pita bread quality for absence of

cracks and quality of separation of the layers was also performed. Specific loaf volume of all pulse-based pitas decreased with increasing level of pulse substitution compared to that of the wheat control. However, specific loaf volumes of pitas containing 25% coarse lentil and 25% coarse navy bean flours were similar to the control. Regarding texture, pitas containing 25% coarse navy bean and 25% coarse pinto bean flours had lower values for the force than those for the control in an extension test, and the remaining pitas had higher values. Pitas containing coarse and fine navy bean flours at all the levels demonstrated the lowest decrease in whiteness index for the top crust compared to that of the wheat control, and pitas containing pea flour had the highest decrease in the whiteness. All the pulse-based pitas had pockets superior to the control in height. Overall, navy and pinto bean flours appear to be more suitable for wheat flour substitution at higher levels in pita bread compared to pea and lentil flours.

ORAL – 18

Microstructure, stability, and rheological properties of salad dressing-type emulsions supplemented with pulse flours. Z. Ma¹, J.I. Boye², B.K. Simpson¹, and S.O. Prasher¹.

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Significant opportunities for developing health promoting foods from pulses exist as consumers look for functional foods with disease prevention effects. Salad dressings are an important type of oil-in-water food emulsions frequently consumed in North America and in many countries around the world. It is therefore a good vehicle to target for the introduction of pulse ingredients for the development of innovative value-added pulse products. The goal of this study was to develop high quality products that will be acceptable to the North American consumer and which could help to increase pulse consumption in the Canadian diet. In this study, physical stability, rheological properties, and microstructure of salad dressing supplemented using pulse flours prepared from Desi chickpea, Kabuli chickpea, red lentil, green lentil, and yellow pea (with and without decortication) were evaluated. In general, salad dressing emulsions supplemented with pulse flours were stable for up to 28 days. An average decrease of 3.62% in back scattering was noticed in the 45-50 mm zone of the storage tube after 28 days, which indicated some coalescence at the top of the tube. Samples supplemented with dehulled Desi chickpea showed significantly higher L^* and b^* values and lower a^* value, indicating a lighter, greener and yellower hue compared to the other samples. Variations in a^* and b^* values during 28 days of storage was slight, and L^* values remained stable for all samples. The effect of storage on the rheological properties of the supplemented salad dressing was studied. A significant decrease in storage (G') and loss (G'') moduli, representing the elastic and viscous components of the sample respectively, was observed for salad dressing samples supplemented with dehulled green lentil, green lentil with hulls, dehulled red lentil, dehulled Desi chickpea, and dehulled yellow pea after 12 days of storage at 4 °C indicative of a decrease of viscoelastic properties during storage. The plateau modulus, G_N^0 , another important viscoelastic parameter, also tended to decrease during storage. This is likely due to the slight increase in particle diameters and the changes occurring as a result of interactions between droplets in the emulsions during the 12 days. The results were supported by microstructure images taken of the fresh and stored samples. Flow curves (shear stress vs. viscosity) of the fresh and stored emulsions were fitted with a power law model. All samples exhibited a pronounced shear thinning behaviour over the shear rate range from 0.02 to 300 s⁻¹. The consistency coefficient (m) in the power law model tended to decrease with increasing days of storage, suggesting that the stored samples were less structured compared to the fresh samples. $Q(t)\%$, a measure used to estimate the elasticity of the materials, was compared for all samples by applying a creep and recovery test. All samples at day 0 showed slightly higher $Q(t)\%$ values compared to samples stored for 12 days, indicating a slight decrease in strain recovery and

decreased elasticity with storage. Overall, our results suggest that pulse flours may have good potential to be used as value-added food ingredients for salad dressing type applications.

ORAL – 19

Innovative coatings: Evaluation of pea starch and pea starch/fibre/flour blends in batter, pre-dust, and glaze coatings. L.L. Sawyer, A.C. Utioh, L.M. Humiski, and J. Meseyton. The Food Development Centre, Portage la Prairie, Manitoba, Canada R1N 3J9.

Canada is the global leader in pea (*Pisum sativum*) production. Peas offer unique nutritional benefits as non-GMO (genetically modified organism), low glycemic index, gluten-free foods that are high in protein and fibre but low in fat. Dry and wet milling and fractionation technologies have been developed and commercialized in Canada and elsewhere for production of pea flour, pea starch, pea protein, and pea fibre. These fractions have excellent functional and nutritional attributes and are well-suited for commercial food ingredients. The objective of this project was to evaluate the feasibility of using yellow pea starch and a combination of pea starch and other fractions (flour and fibre) in batter, pre-dust and glaze dry mixes to replace traditional corn and wheat ingredients. The performance of dry mixes containing dry or wet milled pea fractions was evaluated in 3 meat applications: 1) ready-to-cook tempura battered chicken nuggets, 2) ready-to-cook breaded fish nuggets and 3) fully cooked glazed chicken breasts. In the chicken nugget application it was possible to replace 100% of traditional corn starch and wheat flour in the pre-dust and batter with pea starch and pea flour. Pea fibre was successfully added to the two-step tempura batter coating to meet the Canadian nutritional labelling regulations for a “source of fibre” claim, and with acceptable sensory attributes. In the fish nugget breading system pea starch, fibre and flour were successfully incorporated. The addition of pea flours generally resulted in more golden fish nuggets with better product quality retention during heat lamp holding. Nutritional analysis showed that pea fibre could be successfully added to increase total dietary fibre to 6 g per 125 g of fish nuggets allowing for a “very high source of fibre” claim according to Canadian regulations. The finished product cost increased 0.6-cent/lb to use pea starch, pea flour and pea fibre in the fish nugget breading system. In the glazed chicken breast application, cook-up corn starch was successfully replaced (100%) with pea starch (wet and dry milled). Dry milled pea starch was slightly preferred over wet milled because it performed more like corn starch. Pre-gelatinized (instant) corn starch and gums were successfully replaced with pea fibre in glazes. Pea fibre was preferred over starch due to fibre’s ability to thicken at higher usage levels, increase cooking yields, and its potential health benefits. Generally treatments containing pea fractions had similar sensory qualities to the control and better product quality during freeze/thaw stress; however, they lacked the traditional glossy appearance of glazed breast fillets. This study has shown that pea fractions cannot only replace traditional corn and wheat ingredients in pre-dust, batter, and glaze coatings, but also can produce products that address consumers’ nutritional and health concerns.

ORAL – 20

Feeding value of peas - An update from the feed evaluation/NIRS project. M.L. Swift, Field Crop Development Center, Alberta Agriculture and Rural Development, Lacombe, Alberta.

Pulses are an important feedstock, particularly for swine and poultry. As such, determination of feeding value is important. The Feed Evaluation/NIRS project, was designed to ascertain the feeding value of barley, wheat, triticale, peas, dried distillers grains and wheat by products for poultry, swine and ruminants. A second goal of the project is to use near infrared reflectance spectroscopy (NIRS) to rapidly and accurately predict these feed values. To date, 100 samples of yellow and green peas grown in Alberta and Saskatchewan have been analysed. All samples were scanned in whole form on each of two NIRSystems, a NIRSystems 6500 scanning monochromator (Foss North America, Eden Prairie MN), and a Unity Scientific Spectra Star 2500 RTW machine.

Chemical composition (dry matter, crude protein, ash, lipid, starch, gross energy, acid and neutral detergent fiber) were determined for each sample. Energy digestibility and content (DE, AME) were determined for 8 of the samples using swine and poultry bioassay methods (fecal collection). Ruminal digestion was also determined for these 8 samples. Work to date shows little variation in the feeding value of peas for swine and ruminants but some variation for poultry. Ongoing work under the Feed Evaluation/NIRS research program will focus on the development of an in-vitro assay which can estimate DE/AME content (replacing animal bioassays) of pulses.

ORAL – 21

Genotype by environment analysis of the performance of two low phytate pea lines. T.

Delgerjav, G. Arganosa, A. Rehman, K.E. Bett, and T.D. Warkentin. Crop Development Centre, Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan.

Low phytate concentration in pea (*Pisum sativum* L.) seed would improve the bioavailability of phosphorus and micronutrients in humans and non-ruminant animals. Two low phytate pea lines (1-2347-144 and 1-150-81) were developed at the Crop Development Centre, University of Saskatchewan using chemical mutagenesis. These lines were grown in field trials at three diverse locations in Saskatchewan in 2009 and 2010. CDC Bronco, the parent cultivar from which they were derived and 2 other widely grown cultivars were also grown. Agronomic characteristics, total phosphorus and inorganic phosphorus content of all lines were determined. The low phytate lines had similar seedling emergence counts, days to flowering, days to maturity, vine length, lodging score, powdery mildew score, and mycosphaerella blight score and grain yield compared to CDC Bronco. Harvested seeds of the low phytate lines had substantially higher inorganic phosphorus (1.00-1.08 mg/g) concentration than CDC Bronco (0.29-0.31 mg/g) and the other normal phytate cultivars. The total phosphorus content was similar in all lines ranging from 3.28-3.56 mg/g. The phytate content of all lines will be evaluated using HPLC.

ORAL – 22

Quantitative trait loci analysis of folate content in common beans (*Phaseolus vulgaris* L.). S. Khanal¹, C. Shi², J. Xue³, J. Shi³, I. Rajcan¹, K.P. Pauls¹, and A. Navabi⁴. ¹Department of Plant Agriculture, University of Guelph, Guelph, Ontario, N1G 2W1; ² Agriculture and Agri-Food Canada (AAFC)-Greenhouse and Processing Crops Research Centre, Canada, Harrow, Ontario, N0R 1G0; ³AAFC-Guelph Food Research Centre, 93 Stone Rd. W, Guelph, Ontario, N1G 5C9; ⁴ AAFC/University of Guelph Bean Breeding Program, Department of Plant Agriculture, University of Guelph, Guelph, Ontario, N1G

Folates are among the essential vitamins needed during rapid cell division and take part in the synthesis of DNA, RNA and proteins. Folate deficiency is known to be linked with a number of health problems, including neural tube defects in newborns, heart diseases and many types of cancers in adults. Common bean (*Phaseolus vulgaris* L.) contain high levels of folate, yet the level of folate may vary significantly among bean genotypes. Folate is the general term for different chemical forms of vitamin B. Naturally occurring forms include tetrahydrofolate, 5-methyl tetrahydrofolate (5MTHF), 5-formyltetrahydrofolate and 10-formyltetrahydrofolate. Among them, 5MTHF occupies more than 80% of total folate content in common bean. The objectives of this study were to examine the mode of inheritance of folate content in dry bean and identify quantitative trait loci (QTLs) associated with folate content. Four varieties of common bean, including three large-seeded varieties (Taylor Hort, AC Elk, and Red Hawk), selected from the Andean gene-pool and a medium-seeded pinto variety (Othello) from the Mesoamerican gene-pool were inter-crossed in a one-way diallel mating design. The four parents, F₁ hybrids, and F₂ populations were grown in the field at the University of Guelph Elora Research Station in the summer of 2009. Total folate and 5MTHF content in dry whole seeds of each single plant was measured using high pressure liquid chromatography (HPLC) twice after extraction, with a one

hour interval. Significant variation in folate content was observed among the parental genotypes, F₁ hybrids, and F₂ individuals, ranging from 101 to 354 µg/100 g. The F₂ population of the cross between Red Hawk and Othello was genotyped with 72 informative SNP markers. Single marker QTL analysis identified a total of five markers, significantly associated with folate content. A QTL on linkage group B2, flanked with SNP markers g457_B and g2581, accounted for 10% of the phenotypic variance with significant additive and dominance effects on folate. This QTL effect will be further validated in other populations before applying QTL-linked markers in marker-assisted selection.

ORAL – 23

Genetic improvement of lentil in Canada – the next 10 years. A. Vandenberg¹, A. Tullu¹, M. Lulsdorf¹, K. Bett¹, D. Thavarajah², P. Thavarajah², M. Bandara³, and S. Banniza¹. ¹Department of Plant Sciences/Crop Development Centre, University of Saskatchewan, Saskatoon, Saskatchewan, ²Department of Cereal and Food Sciences, School of Food Systems, North Dakota State University, Fargo, North Dakota, ³Crop Diversification Centre South, Brooks, Alberta.

Lentil production will continue to expand in Canada, primarily driven by increasing consumer demand in South Asia and the Middle East and by declining reliability of production in key production and exporting regions. Genetic improvement strategies for lentil are determined by a mosaic of objectives influenced by production concerns, market factors, and genetic technologies. Yield, resistance to diseases and herbicide tolerance will continue to be core objectives. Other genetic improvement goals include widening the genetic base, increasing product diversification through market-linked diversification and specialization of lentil market classes, and improving the nutritional potential of lentils through biofortification. As production continues to expand we expect to see shifts in the spectrum of abiotic and biotic stresses that affect lentil production. Genetic improvement strategies will increasingly integrate genomic technologies.

ORAL - 24

Health benefits associated with consumption of dry beans and other pulses. M. Bennink. Food Science and Human Nutrition, Michigan State University, East Lansing, MI 48824-1224, USA.

Eating pulses is a low cost, sustainable approach to improving and maintaining good health. The contribution of essential nutrients by pulses has been long known, but we are now learning that the nutritional value of pulses goes far beyond the provision of essential nutrients. Eating dry beans can help prevent major causes of premature deaths in North America (Type 2 diabetes, cardiovascular diseases, and cancer at several sites in the body). Part of the beneficial effects can be explained by maintenance of normal blood glucose levels. Beans (and probably other pulses) are the perfect food to improve and/or promote glycemic control. Other beneficial effects resulting from pulse consumption are likely due to the wide variety of phytochemicals contained within pulses. Feeding beans reduces chemically induced colon and breast cancer in rodents and epidemiologic studies support the concept that eating beans helps to reduce colon and breast cancer incidence. Two pilot studies in Africa indicate that eating beans can help improve the nutritional and immunological status of children that are infected with the human immunodeficiency virus. While eating pulses will not guarantee good health, eating pulses on a daily basis will result in better health than if pulses are not consumed.

ORAL– 25

Consumption of a pulse-based diet reduces cardiovascular disease risk factors in older adults. G.A. Zello¹, S. Abeysekara², H. Vatanparast¹, and P.D Chilibeck². Colleges of ¹Pharmacy and Nutrition, and ²Kinesiology, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5C9.

Metabolic syndrome, type II diabetes and cardiovascular disease risk factors include hyperglycemia, hyperlipidemia, insulin resistance, and obesity which may be modifiable by diet. Our purpose was to determine the effects of a pulse-based diet in individuals 50 years or older for reducing these risk factors. Ninety participants (36 males, 54 females, age 60±7 y, body weight 77±20 kg) were randomized to receive a pulse-based diet (a diet supplemented with 2 servings per day of beans, chickpeas, peas, or lentils; ~230 g per day dry weight) or their regular diet for 2 months. Following a wash-out period of one month, the subjects were crossed-over to the opposite dietary intervention for an additional two months. Anthropometric measures, physical measures (body composition by dual energy X-ray absorptiometry), and biochemical markers (i.e. serum glucose, insulin, C-reactive protein and lipids) were assessed before and after each diet phase. Compared to the regular diet, the pulse-based diet decreased total cholesterol by 7% ($p<0.05$), and fasting blood glucose by 40% ($p<0.05$) and showed a trend to decreasing low density lipoprotein cholesterol (by 6%; $p=0.07$). A pulse-based diet is effective for reducing fasting blood glucose and cholesterol in older adults and, therefore, reduces the risk of type II diabetes, and cardiovascular disease.

ORAL – 26

Identification, quantification, and localization of proanthocyanidins in pea (*Pisum sativum* L.) seed coats. A. Jin, J. Ozga, and D. Reinecke, Plant BioSystems Group, Department of Agriculture, Food, and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada

Proanthocyanidins, also known as condensed tannins, are oligomeric and polymeric flavonoids. Historically, proanthocyanidins were considered as antinutritional compounds in pulse nutritional studies because they can precipitate proteins and reduce bioavailability of some minerals. However, recent research on the roles of proanthocyanidins as plant-based health-beneficial components in the human diet has led to renewed interest in this class of flavonoids in food crops. The objective of this study was to identify, quantify (using high performance liquid chromatography-photodiode array detector and liquid chromatography-mass spectrometry techniques), and localize (using histological techniques) proanthocyanidins in the seed coats of various pea cultivars. The proanthocyanidin composition and concentration in seed coats varied among the cultivars studied. For example, pea seed coats of 'Courier' contained proanthocyanidins (435.9 mg/100 g dry seed weight) almost exclusively consisting of prodelphinidin-type subunits. However, seed coats of 'Lan3017' contained lower levels of proanthocyanidins (43.2 mg/100 g dry seed weight) that mainly consisted of procyanidin-type subunits. Proanthocyanidins in these cultivars were mainly localized in the ground parenchyma layer and epidermal layer of pea seed coats. These data show that pea seed coats can be a good dietary source of proanthocyanidins.

ORAL – 27

Isolated yellow pea protein, but not fiber, suppresses short-term energy intake and postprandial glycemia in young healthy males. C. E. Smith, R. C. Mollard, B. L. Luhovyy, and G. H. Anderson, Department of Nutritional Sciences, Faculty of Medicine, University of Toronto, Toronto, Ontario M5S 3E2.

Canada is the world's largest producer of yellow peas, but less than 1% of domestic production is consumed by Canadians, with the rest being exported or used for livestock feed. Pulses are

healthy low-glycemic foods rich in protein (20-25%), resistant starch, and soluble and insoluble fiber. Thus, it is important to investigate the health benefits of pulses and promote their consumption in order to better the health of the Canada's population as well as its economy. However, the health benefits of pulses are largely unexplored. Previously, we found that pulses (1.5-2 cups) consumed two hours prior to a pizza meal reduced blood glucose (BG) before (premeal) and after (postmeal) the meal compared to white bread. Pulses also reduced appetite compared to white bread; however, this did not lead to changes in food intake (FI). The objective of the following studies was to elucidate the component(s) of pulses responsible for their benefits and assess their efficacy as a value-added food ingredient. We conducted 2 experiments investigating the effects of 10 or 20 g of commercially available isolated yellow pea protein (P10 and P20) or fiber (F10 and F20) on FI at an *ad libitum* pizza meal served at 30 min (experiment 1, n = 19) or 120 min (experiment 2, n = 20) and BG and appetite in young healthy males (20-30 y). In experiment 1, P20 led to lower FI than control (1180 ± 120 vs. 1346 ± 111 kcal) and all other treatments ($p = 0.0008$). Cumulative FI (pizza meal kcal + treatment kcal; CFI) was significantly lower following P20 compared to F10 (1305 ± 119 vs. 1454 ± 108 kcal, $p = 0.033$). Premeal (0 – 30 min) BG was significantly lower following both protein treatments compared to control (5% reduction, $p < 0.05$). Postmeal (50 – 120 min) BG was significantly lower following P20 compared to control and F10 (7% reduction, $p < 0.01$). There was no effect of treatment on premeal appetite ($p = 0.423$), but postmeal appetite was significantly higher following F20 and P20 compared to control (31.8 ± 1.6 , 29.4 ± 1.6 and 27.2 ± 1.7 mm, respectively, $p < 0.05$). However, there was no effect of treatment on change from baseline appetite ($p = 0.768$). In experiment 2, there was no effect of treatment on FI, CFI, or pre- or postmeal BG or appetite. In conclusion, protein is the component responsible for the short-term beneficial effects of yellow peas on the regulation of glycemia and FI, but its second-meal effects diminish by 2 hours post-consumption. Therefore, yellow pea protein may be an important value-added ingredient in functional foods aimed at improving glycemic control, decreasing FI, and reducing the risk of obesity and related morbidities.

ORAL – 28

Exploiting natural variation in legume Bowman-Birk inhibitors to dissect their potential role in human health-promoting programmes. A. Clemente¹, M.C. Marín-Manzano¹, and C. Domoney². ¹Department of Physiology and Biochemistry of Nutrition, Estación Experimental del Zaidín (CSIC), Profesor Albareda 1, 18008 Granada, Spain; ²Department of Metabolic Biology, John Innes Centre, Norwich Research Park, Norwich NR4 7UH, U.K.

Recent studies reveal that Bowman-Birk inhibitors (BBI) from legumes, such as soybean, pea, lentil and chickpea, may be exploited for therapeutic applications, pending elucidation of the molecular basis for the variation in biological activity. We have investigated the effect of sequence variation within the chymotrypsin inhibitory domain of BBI from pea on the inhibition of mammalian digestive enzymes as well as on the ability to inhibit the growth of human colorectal adenocarcinoma cells. More recently, the positive contribution of the trypsin inhibitory domain to the anti-proliferative properties of BBI was revealed by evaluation of the double-headed trypsin inhibitor, IBBD2, from soybean. A better understanding of the action mechanism of these dietary proteins on cell proliferation, together with the identification of their potential therapeutic targets, may be expected to open up possibilities for the future benefit of human health. These data can be exploited in breeding programmes, based on genomic and genetic knowledge of the relevant genes.

ORAL - 29

The effect of pulses on satiety, glycemia and food intake. B.L. Luhovyy, R.C. Mollard, A. Zykus, M.F. Nunez, C.L. Wong, and GH Anderson. Department of Nutritional Sciences, University of Toronto, Toronto, Ontario, Canada M5S 3E2.

Pulses have potential to be positioned as a food for body weight and metabolic control based on their composition, rate of digestion and absorption of fat and carbohydrates, and effects on the feeling of hunger. Since recently, the Canadian Food Inspection Agency accepts satiety claims on food that have been previously regulated as a drug claims. Therefore, the objective of our study was to determine the effects of ad libitum consumption of pulse meals (treatments) on meal size, post-meal appetite and blood glucose for 4 h prior to an ad libitum pizza meal. Food intake and post meal appetite and blood glucose was measured. Males ($n = 24$, 24.3 ± 3.6 y, 72.4 ± 7.8 kg and 22.8 ± 1.4 kg/m²) received each of the 4 treatments or control in random order. The pulse treatments contained pasta and tomato sauce and 44% of energy from: chickpeas, lentils, navy beans, or yellow peas. The control was pasta and tomato sauce (pasta and sauce) without pulses. Food intake was measured at the treatment meal (0-20 min) and pizza meal (260-280 min). Blood glucose and appetite were measured frequently from 0-340 min. The lentil meal resulted in lower food intake at the meal compared to the chickpea and pasta and sauce meals, while the navy bean treatment resulted in lower food intake compared to the chickpea meal ($P < 0.05$). The lentil treatment led to lower cumulative food intake (pulse meal + pizza meal) compared to pasta and sauce plus pizza meals ($P < 0.05$), but food intake at the pizza meal was not affected by the treatment meals 4 h earlier. All treatment meals lowered subjective appetite equally. All pulse treatments led to a lower peak blood glucose following consumption. The chickpea, lentil and navy bean meals reduced pre-pizza meal blood glucose area under the curve (0-260 min) relative to pasta and sauce. The chickpea treatment meal led to lower post-pizza meal blood glucose area under the curve (280-340 min) compared to the navy bean and yellow pea treatments ($P < 0.05$). Pulse type determines the effect of meals with pulses on food intake at a pulse meal, post-meal blood glucose, and blood glucose responses at a later meal. Obesity and diabetes are highly prevalent among the Canadian population. Because incorporation of some pulses in meals lowers meal-time energy intake, lower post-meal glycemia and reduce appetite, further studies of the benefits of frequent consumption of pulses in meals on appetite, food intake, and glucose regulation are merited. Furthermore such research is required for a health claim that may be permitted under ongoing regulatory change by Health Canada.

ORAL – 30

North Dakota State University Pulse Quality Program- a potential whole food solution to the global human malnutrition. D. Thavarajah, P. Thavarajah, K. McPhee. School of Food Systems and Department of Plant Sciences, North Dakota State University (NDSU), Fargo, ND 58108-6050, USA.

One third of global human populations are suffering from health problems associated with iron (Fe), zinc (Zn), selenium (Se) and vitamin deficiencies. Past attempts to reduce micronutrient deficiencies through food fortification and supplementation had limited success. Our research has shown lentils grown in North America are a good source of micronutrients. Cell culture, animal and human nutrition studies have shown most micronutrients in lentil are highly bioavailable. This presentation will provide an overview of the NDSU pulse quality program, latest nutrition study findings, and the results of existing breeding efforts. Anticipated impacts of the USA pulses to alleviate global micronutrient deficiencies will also be discussed.

ORAL -31

Present status and prospects of transgenic grain legumes. H.-J. Jacobsen. Institute of Plant Genetics, Leibniz Universität Hannover, Herrenhäuserstr. 2, D-30419 Hannover.

Upcoming constraints like climate change, population growth, increasing demands for “green energy”, require sustainable intensification of crop production, namely to grow more on less land and less inputs in fertilizer and pesticides. Pulses offer a number of advantages in that aspect as they not only provide healthy protein and calories but also play an eminent role in crop rotation programs. On the other hand, however, grain legumes with their limited gene pools require sophisticated breeding strategies, which, in the case that specific traits are not available in the respective gene pools, require genetic engineering. As the recalcitrance for gene transfer is history for most pulses, the *Agrobacterium*-based systems are ready to be applied for solving coming problems. Present transformation efficiencies are around 1-2% (number of fertile transgenic plants/number of initial explants). We have developed transgenic pea lines expressing 4 different antifungal genes (as single insertions or as stacked events), and weevil resistance using a B.t.-approach is on the way. Pea seeds can also be used to express antimicrobial compounds like resveratrol or lysozyme or vaccines as cheap alternatives to antibiotic application in animal feed. In faba beans we have interesting results regarding drought tolerance using a transgene approach. We also have now dicistronic vectors available allowing the expression of two or more transgenes under one promoter. A number of transgenic events are standing on the shelves in our labs, awaiting field trials to elucidate their respective performances.

ORAL – 32

Leveraging legume genomic resources for lentil genetic improvement. K.E. Bett^{1,2}, S. Vail^{1,2}, V. Penmetsa², A. Farmer³, G. May³, A. Vandenberg¹ and D. Cook², ¹Department of Plant Sciences, University of Saskatchewan, Saskatchewan, Canada; ²Department of Plant Pathology, University of California-Davis, CA, USA; ³National Center for Genome Resources, NM, USA.

Genomic information for lentil (*Lens culinaris*) and its wild relatives is relatively limited compared to other crop legume species such as soybean, chickpea, dry bean, pea and alfalfa. One strategy to develop molecular markers for use in genetic mapping projects has been to identify SNPs in a set of orthologous genes already mapped in other food legumes. We sequenced intron-spanning regions of 1369 gene orthologues from two *L. culinaris* and two *L. ervoides* mapping parents and identified SNPs that can be mapped in both species, as well as in populations derived from crosses between these two related species. The genetic mapping of these orthologues allows us to ascertain the extent of conserved genome organization between *Lens* and the reference legume *Medicago truncatula* and to other crop legume genomes. In addition, it enables the leveraging of extensive genome information available in *M. truncatula* for the development of additional molecular markers for lentil breeding. Moreover, these SNP-based molecular markers are being evaluated in sets of minicore germplasm collections of *Lens* accessions, to determine the extent of recurrence of these SNPs beyond the source genotypes, and to allow molecular marker based characterization of these germplasm collections.

ORAL – 33

454 Transcript profiling for SNP discovery in pulse crops. A. Sharpe¹, W. Clarke^{2,3}, R. Li¹, C. Sidebottom¹, S. Qiu¹, L. Sanderson⁴, P. Vijayan⁴, B. Taran⁵, T. Warkentin⁵, R. Datla¹, G. Selvaraj¹, K. Bett⁴, A. Vandenberg⁵, F. Bekkaoui¹, D. Murrell⁵, and W. Keller^{1,6}. ¹NRC-PBI, Saskatoon, Saskatchewan, ²Department of Computer Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, ³AAFC Saskatoon Research Centre, ⁴Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, ⁵Crop Development Centre, University of Saskatchewan, Saskatoon, Saskatchewan, ⁶Genome Prairie, 101-111 Research Drive, Saskatoon, Saskatchewan, S7N 3R2, Canada.

Pulse crops are of increasing importance to the agricultural economy and efforts to produce improved varieties better adapted to new markets and a changing environment are vital. The development of genomic resources to assist these goals is now the target of multiple research organizations in Saskatoon. This effort includes the development of targeted transcriptome resources in major pulse crops as well as the utilization of deep sequencing approaches for SNP discovery with the Roche 454 FLX instrument at NRC-PBI. The 454 strategy has utilized 3'-transcript profiling in eight different genotypes of lentil, chickpea and pea. Five kinds of tissue samples were collected for each genotype including: leaf (2-week old), stem (before flowering), etiolated seedling (1-week old), flower (mixed stages), and developing seed (mixed stages). For each genotype, equal amounts of the total RNA from each tissue were pooled, used for library construction and then 454 Titanium sequencing. The identification of unigene sets was carried out in all genotypes in the targeted species and is represented in the form of contigs of aligned 454 reads in different size ranges. The identification of robust SNPs has now been undertaken using data from each genotype against the reference genotype and is being used for the selection of an optimal subset of SNPs for high throughput marker development in each species. An analysis of these results will be presented and discussed.

ORAL– 34

Sequence comparison of the major resistance QTLs for common bacterial blight in OAC Rex and HR67. G.E. Perry, Y. Reinprecht, N. Singh, J. Chan, K. Yu and K. P. Pauls. University of Guelph, Department of Plant Agriculture, Guelph, Ontario.

Common bacterial blight (CBB), caused by the bacterium *Xanthomonas axonopodis* pv. *phaseoli*, is a significant pathogen in dry bean (*Phaseolus vulgaris*) that is endemic in most regions where dry beans are grown. To date, the genes responsible for this resistance have not been identified, although several resistant lines have been developed using interspecific crosses between *P. vulgaris* and *P. acutifolius*. To aid in the identification of CBB-resistance genes, a binary-bacterial artificial chromosome (BiBAC) library was created from HR67 and OAC Rex, CBB-resistant varieties of white bean derived from crosses with different accessions of *P. acutifolius*, with depths of 8.4 and 5.6, respectively. The libraries were screened with CBB resistance-associated molecular markers identified by previous studies, and the identified clones were analyzed and assembled into contigs covering approximately 400Kb in HR67 and 650Kb in OAC Rex. Selected clones from each contig were sequenced using a Roche 454 sequencing platform and the data assembled into contigs. The sequences from HR67 and OAC Rex were compared to each other, and to HR45, a sister line to HR67, which has had the major resistance QTL partially sequenced. Over the 65Kb region examined, HR67, HR45 and OAC Rex possess approximately 10Kb of homologous sequence clustered in 4 major regions surrounding the UBC-420 marker, which is only present in HR67 and HR45. Two of these regions share homology with putative resistance proteins, and may represent potential CBB resistance genes. The assembled sequences were also compared with *Glycine max* to identify syntenic regions between the two species. In both OAC Rex and HR67, several conserved regions were identified. OAC Rex showed high levels of homology to *G. max* chromosome 19, with NBS-LRR homologues found clustered at

approximately 700Kb in *G. max*, corresponding with the NBS-LRR gene cluster found in the end-sequences from the BiBAC library clones. Additional genetic homology was identified between *G. max* and the assembled contigs with a glucose-6-phosphatase isomerase gene, an ATP-dependant RNA helicase gene and the g2467 marker from *P. vulgaris* chromosome 4. The overall orientation and order of genetic elements appears to be homologous between the two species, with the position of the clones in the contig closely matching their order in *G. max*. HR67 showed strong homology for *G. max* chromosome 7, which has been shown to have homology to *P. vulgaris* chromosome 6.

ORAL – 35

Association mapping of common bacterial blight resistance QTL in Ontario bean breeding populations. C. Shi¹, A. Navabi², and K. Yu¹. Agriculture and Agri-Food Canada, ¹Greenhouse and Processing Crops Research Centre, Harrow, Ontario, Canada N0R 1G0; ²Agriculture and Agri-Food Canada/University of Guelph Bean Breeding Program, Department of Plant agriculture, Crop Science Building, University of Guelph, Guelph, Ontario, N1G 2W1.

Common bacterial blight (CBB), incited by *Xanthomonas axonopodis* pv. *phaseoli* (*Xap*), is a major yield-limiting factor of common bean (*Phaseolus vulgaris* L.) production around the world. Host resistance is practically the most effective and environmentally-sound approach to control CBB. Application of association mapping in QTL discovery in plant breeding programs is a promising approach to overcome some of the limitations with conventional QTL mapping strategies. The objectives of this research were to 1) apply association mapping to identify CBB resistance QTL in Ontario bean breeding materials and 2) evaluate whether association mapping can be used effectively to discover CBB resistance QTLs using SNP genotyping of plant materials, routinely developed in a bean breeding program. A population of 469 dry bean lines of different market classes representing plant materials routinely developed in a bean breeding program were used. Of them, 395 lines were evaluated for CBB resistance at 14 and 21 DAI (Days After Inoculation) in the summer of 2009, in an artificially inoculated CBB nursery in south-western Ontario. All lines were genotyped using 132 SNPs (Single Nucleotide Polymorphisms) evenly distributed in the genome. Of the 132 SNPs, 26 SNPs had more than 20% missing data, 12 SNPs were monomorphic, and 17 SNPs had a MAF (Minor Allelic Frequency) of less than 0.20, therefore, only 75 SNPs were used for association study, based on one SNP per locus. Marker data collected from all lines were used to construct population structure and kinship relationship matrices. The best possible population structure was to assign 36% and 64% of the lines into Andean and Mesoamerican subgroups, respectively. Kinship analysis also revealed complex familial relationships among all lines, which corresponds with the known pedigree history. Mixed Linear Model (MLM) analysis, including population structure and kinship, was used to discover marker/trait associations. Eighteen and 22 markers were significantly associated with CBB rating at 14 and 21 DAI, respectively. Fourteen markers were significant for both dates and the markers UBC420, SU91, g321, g471, and g796 were highly significant ($p \leq 0.001$). Meanwhile, g471 on LG (Linkage Group) 6 and g796 on LG 8 corroborate that both chromosome 8 and the distal region of the chromosome 6 are carrying major CBB resistance QTLs. Furthermore, 15 significant SNP markers were co-localized with or close to the CBB-QTLs identified previously by bi-parental QTL mapping. This study demonstrated that association mapping using a reasonable number of markers, distributed across the genome and with application of plant materials that are routinely developed in a plant breeding program can detect significant QTLs for traits of interest. Unlike conventional QTL discovery strategies, in which limited number of bi-parental populations (F_2 , RIL, or DH) are used, association mapping-based strategies can use diverse plant breeding populations derived from several bi-parental and/or complex crosses. This may address some of the concerns with conventional QTL mapping that the bi-parental mapping populations rarely give rise to new cultivars, the identified QTLs may not

be effective in multiple genetic backgrounds and that the QTL-linked markers are not immediately available for marker-assisted selection.

ORAL – 36

Investigation of relationships of yield, seed size, seed protein and starch content and development of varieties with improved protein content of field pea (*Pisum sativum* L.). D.J. Bing¹ and Qiang Liu². ¹Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C & E Trail, Lacombe, Alberta, Canada T4L 1W1, ²AAFC, Guelph Food Research Centre, 93 Stone Road W., Guelph, Ontario, Canada N1G 5C9.

Field pea (*Pisum sativum* L.) seed contains approximately 23% crude protein and 45% starch. Both constituents have been widely used in food and industrial products. Germplasm lines containing approximately 30% crude protein were identified in our germplasm collections. Unfortunately, these high protein germplasm lines have low yield, lodge, and are susceptible to a number of diseases. High protein germplasm lines were crossed with elite commercial varieties to develop breeding lines with improved seed yield, disease resistance, lodging resistance and seed size. It is essential for breeders to understand the relationships of seed yield, seed size, protein and starch content in order to develop varieties with either improved protein or starch content and/or quality. The objective of this study is to investigate the relationship among these four characters. Sixteen breeding lines with good potential for variety development were selected from the F₅ progenies developed from the crosses with the high protein germplasm lines and elite field pea varieties. These lines were grown in a 2 location x 2 replication RCBD experiment in 2009 along with four checks (one high protein germplasm line and three elite varieties or breeding lines). The excessive moisture severely damaged the trial at one location. Therefore, the information presented here is from the second location. Seed yield, seed size measured as seed weight, percent of seed protein (by weight) and percent of seed starch (by weight) contents were determined, and the relationships of these four characters were analyzed using SAS 9.2. The results showed that seed yield was highly positively correlated with seed weight ($r=0.74$, $p<0.01$) and seed starch content ($r=0.85$, $p<0.01$), but highly negatively correlated with seed protein content ($r=-0.75$, $p<0.01$). Seed starch content was highly positively correlated with seed weight ($r=0.73$, $p<0.01$), but highly negatively correlated with the seed protein content ($r=-0.90$, $p<0.01$). Seed weight was positively correlated with the seed starch content ($r=0.73$, $p<0.01$), but negatively correlated with seed protein content ($r=-0.58$, $p<0.01$). Some breeding lines developed from the crosses with the high protein germplasm (i.e. 30% of crude protein) have a 20% higher protein content compared to the highest yielding check variety, but the yield of these lines is 40% lower than the check variety. The study shows that varieties containing approximately 30% protein and superior agronomic characteristics can be developed with one or more cycles of crosses and selections, and they will likely have lower starch content than current commercial varieties.

ORAL – 37

Interaction of herbicide applications with reaction to ascochyta blight and phenology of several chickpea varieties. B. Taran, S. Banniza, T. Warkentin, A. Vandenberg, and F.A. Holm, Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, S7N 5A8.

Weed control is one of the major constraints of chickpea production in western Canada. The experiments were conducted to examine the interaction between herbicide treatments and ascochyta blight disease severity, phenological traits and yield of several chickpea varieties. Results of 2008 and 2009 experiments at Saskatoon and Elrose showed that under specific conditions, pre-emergent application of low rate imazethapyr slightly increased the severity of ascochyta blight infection but only caused minor effects on plant injury, days to flowering, days to maturity, plant height and yield of chickpea, whereas, post-emergent applications of

imazamox, imazethapyr and metribuzin caused increased ascochyta blight severity, delayed flowering and maturity, and reduced yield. The pre-emergent application of low rate imazethapyr may be acceptable to growers. Sulfentrazone was a safer option for broadleaf weed control in chickpea across locations and years. Efforts to further improve the tolerance to the imidazolinone class of herbicides in chickpea are underway. The information generated in the experiment is essential for producers to optimize weed management practices in chickpea while minimizing the risk of ascochyta infection.

ORAL – 38

***In vitro* micropropagation in chickpeas (*Cicer arietinum* L.) – a recalcitrant crop.** A. Yadav, Department of Botany, Maitreyi College, University of Delhi, Delhi, India.

Chickpea has been recognized as one of the most important crops all over the world mainly because of its seeds, which are used as rich source of dietary protein. Unfortunately, its productivity has been severely hampered due to several constraints like its cultivation on marginal lands, impacts of biotic and abiotic stresses, low research and management efforts. Improvement of this crop through conventional breeding is not successful due to non-existence of the insect lepidopteron resistant germplasm. Incidentally, improvement of the crop by employing the technique of genetic engineering too, poses difficulty due to non-availability of efficient tissue culture protocols. Protocol development for each genotype, as well as, selection of the best genotype has been well documented in light of the urgent need for the crop improvement all over the globe, employing techniques of genetic engineering. The presentation reports on: (i) multiple shoot induction through seed explants, (ii) somatic embryogenesis through leaflet explants, and (iii) successful plantlet regeneration through seed explants of six chickpea genotypes (five drought tolerant and one normal, namely BG362, BG391, BG256, BG1101, BGD72 and BG1003, respectively) for improving the crop through biotechnological manipulations. Influence of several growth regulators such as N⁶-benzyladenine (BA), kinetin (Kn), 2,4-D (2,4-dichlorophenoxyacetic acid), α -naphthaleneacetic acid (NAA), indole-3-butyric acid (IBA) and indole-3-acetic acid (IAA) alone or in combinations has been studied on seed and leaflet explants. The seed explants elicited best morphogenic response in terms of multiple shoot production. Of the various growth regulators BA at 5 μ M proved optimum for eliciting morphogenic response in seed and 20 μ M 2,4-D proved optimum for eliciting 100% embryogenic response employing leaflet explants in all the genotypes. For induction of roots, MS (1/2) + IBA proved best where 72.5% of the shoots developed an average of 18.10 ± 1.37 roots within 20 d. The plantlets have been hardened and transferred to soil. Based on the above intensive and extensive investigations it has been concluded that BG256 proved best for differentiating somatic embryos and BG1101 may prove best for average shoot production and use for further improvement of crop using genetic manipulations.

ORAL – 39

Improving chickpea productivity under drought using physiological and molecular approaches.

A.U. Rehman¹, R. S. Malhotra², K. Bett¹, R. Bueckert¹, B. Tar'an¹, and T.D. Warkentin¹. ¹Department of Plant Sciences/Crop Development Center, University of Saskatchewan, Saskatoon, Saskatchewan, Canada. ²International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria.

Drought is the most important stress throughout chickpea growing areas and occasionally severe drought conditions lead to complete crop failure. The present research was thus conducted to characterize a chickpea mapping population of a cross between drought tolerant and susceptible genotypes. A population consisting of 155 recombinant inbred lines (RILs) was studied under drought conditions in the field in Syria for various morpho-physiological traits. SSR markers were used to tag quantitative trait loci (QTL) linked to important drought related traits. Results showed that high harvest index, early flowering, early maturity and higher 100-grain weight were the important attributes contributing to higher grain yield under drought. Similarly, data for canopy traits revealed that higher stomatal conductance and cooler canopies can lead to better performance under drought in Mediterranean environments. Analysis of the molecular mapping data revealed a significant QTL on Linkage Group 3 associated with harvest index, flowering time, maturity time and 100-grain weight. Information generated from this study can be utilized to identify drought related markers to aid in the development of more productive cultivars for western Canada.

POSTER – 1

Management of fusarium root rot of field peas with new disease control strategies.

D.L. McLaren¹, R.L. Conner², M.A. Monreal¹, S.F. Hwang³, K.F. Chang⁴, B.D. Gossen⁵, and R.M. Mohr¹. ¹Agriculture and Agri-Food Canada (AAFC), Brandon, Manitoba, R7A 5Y3, ²AAFC-Morden, Manitoba R6M 1Y5, ³Alberta Agriculture and Rural Development (AARD), Edmonton, Alberta T5Y 6H3, ⁴AARD-Lacombe, Alberta T4L 1W1, ⁵AAFC-Saskatoon, Saskatchewan S7N 0X2.

Fusarium root rot is the most common root disease of field peas in Manitoba. Research conducted outside of Canada indicates that the use of oats as a green-manure crop can reduce the level of certain diseases in subsequent crops. Plant inoculations with arbuscular mycorrhizal fungi (AMF) and residue management have been used to reduce yield losses caused by root diseases in other crops. Such alternative disease control methods may provide more stable and sustainable disease management in the long term. The objective of this study was to evaluate the efficacy of different tillage regimes and crop rotations in combination with residue management and seed inoculation with AMF in reducing pea yield losses caused by fusarium root rot. A two year, multi-location study was carried out to evaluate the treatments of oats harvested for grain with: a) straw removed (soil tilled vs. untilled), b) straw removed with fungicide applied to peas in year two of the study (soil tilled vs. untilled) and c) straw chopped and returned (soil tilled vs. untilled). A treatment of oats incorporated into the soil as green manure was also included as was a treatment of pea monoculture. Four additional treatments were: AMF inoculum with oat seed (+/- AMF application to peas in following year), and AMF inoculum with pea seed (single vs. double rate of inoculation). Results from the Manitoba sites showed there was considerable variability among site-years in the effect of different cultural treatments on severity of root rot. Repeated AMF inoculation often improved root nodulation. Highest yields in one site-year occurred with oats as a preceding crop and fall tillage, with the double rate of AMF inoculum in one year, and with the application of AMF over two consecutive years. Continuous field pea production usually adversely affected seed yields.

POSTER – 2

Esterase activity produced by conidia of *Peronospora viciae* f. sp. *pisi*.

J. Feng¹, K.F. Chang², S.F. Hwang¹, S.E. Strelkov³, B.D. Gossen⁴, R.L. Conner⁵, and D.L. McLaren⁶. ¹Crop Diversification Centre North, Alberta Agriculture and Rural Development (AARD), Edmonton, Alberta, T5Y 6H3, ²Crop Development Centre, AARD, Lacombe, Alberta, T4L 1W1, ³Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, T6G 2P5, ⁴Agriculture and Agri-Food Canada (AAFC), Saskatoon, Saskatchewan, S7N 0X2, ⁵AAFC, Morden, Manitoba, R6M 1Y5, ⁶AAFC, Brandon, Manitoba, R7A 5Y3.

Downy mildew caused by *Peronospora viciae* f. sp. *pisi* is a common foliar disease of the pea crop (*Pisum sativum*) in Canada. Cool, damp spring conditions in central Alberta, in recent years have caused an upswing in the prevalence of this disease. To better understand the pathogenesis, esterase activity secreted by conidia of *P. viciae* f. sp. *pisi* was assayed using indoxyl acetate hydrolysis, which generates indigo blue crystals. When conidia were incubated on artificial media in the presence of indoxyl acetate, blue

crystals were observed around the conidia. In contrast, no such crystals were produced on the conidia after surface washing with a buffer, indicating that the esterase activity was extracellular or weakly bound to the conidia surface. Activity of these esterases was inhibited by diisopropyl fluorophosphate, which is selective for serine esterases. These observations indicate that *P. viciae* f. sp. *pisi* can produce extracellular serine esterases during conidia germination. The importance of these serine esterases for the fungal pathogenesis is under investigation.

POSTER – 3

Characterization of mycosphaerella blight resistance, lodging resistance, and selenium concentration in a pea recombinant inbred line population. Y. Liu, B. Tar'an, S. Banniza, and T. Warkentin. Crop Development Centre, University of Saskatchewan, Saskatoon, Saskatchewan, S7N 5A8.

Moderate variation for adult plant resistance to mycosphaerella blight, pre-harvest lodging and selenium accumulation has been identified in field pea. In order to map the quantitative trait loci (QTL) associated with these traits, a population of 142 F₉ recombinant inbred lines (RILs) derived from a cross between Carrera (susceptible to mycosphaerella blight and lodging) and CDC Striker (moderately resistant to mycosphaerella blight and lodging) was phenotyped in Saskatoon and Rosthern, Saskatchewan in 2010, and will be again grown and phenotyped in 2011. Mycosphaerella blight development was measured as area under the disease progress curve (AUDPC). At Saskatoon, AUDPC ranged from 139 to 270 among RILs, while at Rosthern it ranged from 141 to 269. Lodging was rated at two week intervals beginning at mid-flowering stage. At physiological maturity, lodging ratings of the RILs ranged from 4 to 9 at Saskatoon and 1 to 9 at Rosthern. The total Se concentration in each line will be determined using an atomic absorption spectrophotometer. A total of 350 simple sequence repeat (SSR) primers are being screened on the parents using polyacrylamide gel electrophoresis. Polymorphic primers will be tested on all of the RILs. QTL analysis will be conducted to detect associations between phenotype and genotype.

POSTER – 4

Developing a breeding strategy for stemphylium blight resistance in lentil. R. Podder, S. Banniza and A. Vandenberg. Department of Plant Sciences/Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan S7N 5A8.

Stemphylium blight (SB), caused by *Stemphylium botryosum* Wallr. is a major biotic constraint in many lentil production regions of the world, particularly the northeastern lentil growing area of South Asia. The disease causes defoliation, stem deformation and yield loss. It is increasing in importance in western Canada as the lentil crop expands into new production areas. To date, there have only been a few investigations into the genetics of SB resistance. Research studies have been initiated to develop appropriate field and indoor techniques for phenotyping SB reactions in lentil with the objective to study the inheritance of resistance in lentil. As a starting point, we will screen genetic resources from the CDC breeding program and from selected gene banks around the world using

representative germplasm from cultivated and wild species. The results of these studies will play an integral role in developing a long term strategy for resistance breeding to SB.

POSTER – 5

Anthracnose resistance breeding in lentil. L.E. Zadeh, A. Tullu, S. Banniza, and A. Vandenberg. Department of Plant Sciences, Crop Development Centre, University of Saskatchewan, Saskatoon, Saskatchewan, S7N 5A8.

Colletotrichum truncatum causes anthracnose of lentil, leading to yield and quality reduction. This is one of the major biotic stresses of Canadian lentil crops. Breeding resistant varieties of the crop is the most effective way of dealing with this problem. The wild lentil species *Lens nigricans* has shown resistance to both races of *C. truncatum*. It may be possible to transfer resistance genes from *L. nigricans* to the cultivated lentil using embryo rescue techniques. Faba bean, *Vicia faba*, will be used as a rootstock for grafted scions of interspecific F₁ plants. We will develop and use single nucleotide Polymorphism (SNP) markers to track the transfer of the resistance genes in the segregating populations. Ideally, this should enable us to optimize a potential strategy for introgression of resistance genes using marker-assisted selection (MAS).

POSTER – 6

SNP based genotyping of *Ascochyta lentis* resistance genes in lentil. E. Sari, A. Tullu, S. Banniza, and A. Vandenberg. Crop Development Center, University of Saskatchewan, 51 Campus Dr., Saskatoon, Saskatchewan, S7N 5A8.

Ascochyta blight caused by the fungus *Ascochyta lentis* Vassilievsky is one of the most destructive diseases of lentil in Canada. The disease affects both seed yield and seed quality. The use of resistant cultivars is advantageous over chemical and cultural practices having no negative impact on the environment and being the most economical method of controlling the disease. Efforts have been made to improve ascochyta blight resistance in lentil in the Crop Development Center, University of Saskatchewan, but as the pathogen is capable of shifting in aggressiveness, efforts made to introduce single resistance genes may be undermined. Many sources of genetic resistance are available, both in *Lens culinaris* and wild species, and molecular markers for use in resistance breeding have already been developed. However, it is still ambiguous if the available resistance genes are unique. The objective of the study is to develop and use marker technology based on single nucleotide polymorphisms (SNPs) to unravel the genetic control of resistance in the different sources of resistance available in lentil. Recombinant inbred lines (RILs) will be evaluated for resistance to ascochyta blight under greenhouse conditions using an aggressive isolate of the fungus. Analysis of segregation data will then be performed followed by genotyping of the material using SNPs and mapping of the resistance genes of each source. Ultimately, pyramiding different resistance genes in an individual cultivar will contribute to sustainable resistance to the disease and support the productivity of the lentil industry.

POSTER - 7

Anthracnose resistance in lentil – genetic inheritance and molecular markers under development. R. Shaikh¹ and L. Buchwaldt². ¹Agriculture and Agri-Food Canada, Morden Research Station, Morden, Manitoba, R6M 1Y5; ²Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, Saskatchewan, S7N 0X2.

Anthracnose, caused by *Colletotrichum truncatum*, is one of the most damaging diseases of lentil (*Lens culinaris*) in western Canada. The first disease symptoms generally appear at early flower when tan, necrotic lesions develop on leaflets which cause premature defoliation. Deep penetrating lesions develop on stems and cause the entire plant to wilt. Pinhead sized black microsclerotia develop on infected plant material that can survive in the field for several years. Two races of *C. truncatum*, Ct1 and Ct0, have been identified. A few lentil lines are resistant to race Ct1 and cultivars have been developed from these. One line, VIR 421, has partial resistance to race Ct0. Sources of resistance have also been found in wild lentil species. This study was undertaken to determine the number of resistance genes effective against race Ct1 in three accessions, PI 320937 (Germany), Indianhead (Czechoslovakia) and PI 345629 (former Soviet Union), their allelism and dominance. Populations of F₁, F₂, BC₁R and BC₁S were generated from crosses between each resistant parent and a susceptible cultivar Eston, and from back crosses of F₁ to each parent. Plants were grown in a greenhouse. At early flower they were spray-inoculated with race Ct1 isolate 95B36 at 10⁵ conidia per ml and incubated at 100% RH for 24 hours. Stem symptoms were rated 7 and 14 days after inoculation using a qualitative scale based on the number of lesions and depth of penetration into the stem. Results showed a single dominant gene governs resistance to race Ct1 since progenies segregated 3 R : 1 S in F₂ and 1 R : 1 S in BC₁S; while all F₁ and BC₁R plants were resistant. To examine the allelic relationships, the three resistant parents were inter-crossed. All F₁ and F₂ plants were resistant thereby demonstrating the presence of a single allelic gene. We designate this dominant resistance gene *CtIR1* in PI 320937, Indianhead and PI 345629. A single source of Ct1 resistance emphasizes the need to search for non-allelic resistance genes in case the effect of *CtIR1* breaks down in the field. After screening of 244 accessions (Vavilov Research Institute of Plant Industry, Russia) from 23 countries, 12 new accessions were identified with resistance to race Ct1 and 14 had partial resistance to race Ct0. We are also constructing a molecular linkage map in lentil based on simple sequence repeat (SSR) markers which are developed from genomic DNA and EST libraries. Around 120 polymorphic SSRs will be mapped in recombinant inbred lines developed from Eston x Indianhead. QTL analysis will identify loci associated with anthracnose and ascochyta blight resistance both present in Indianhead. The SSR markers will be a new addition to the world lentil genomic resource for molecular research.

POSTER – 8

Innovations in pulse crop research and field techniques. B. Barlow, D. de Silva, S. Ife, J. Horner, M. Thompson, M. Parada, T. Prado, S. Wagenhoffer, A. Vandenberg, T. Warkentin, and B. Tar'an. University of Saskatchewan, Plant Sciences Department, Crop Development Center, 51 Campus Drive, Saskatoon, Saskatchewan, S7N 5A8.

Agriculture research is all about change - adopting new technologies and inventing new techniques. Research groups face some common and some unique challenges depending

on the direction of their research, their resources and their environment. Challenges include material handling, seed storage, seed drying, different soil conditions and labelling. We have recently developed a new zero-till air plot seeder, GPS and auto-steer applications for seeding, modifications to a combine for better bean harvest, and new techniques in the greenhouse and growth chamber. Ongoing work includes a one acre high-tunnel green house, a double plot seeder and auto trip seeding. We intend to hold a conference for pulse crop technical support staff in 2011.

POSTER – 9

Searching for a herbicide to control group 2 (ALS) resistant cleavers (*Galium aparine*) in pulse crops. K.L. Sapsford¹, F.A. Holm¹, E.N. Johnson², and H.J. Beckie³.

¹Dept of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan,

²Agriculture and Agri-Food Canada, Scott, Saskatchewan, ³Agriculture and Agri-Food Canada, Saskatoon Saskatchewan.

Cleavers, *Galium aparine*, have increased in frequency in Western Canada over the past 4 decades, from the 43rd most abundant weed in the 1970's surveys to the 9th most abundant weed in the 2000's surveys. The 2001 Alberta survey for herbicide-resistant weeds found no Group 2-resistant cleavers. In the 2007 survey, 17% of the cleavers fields were found to have Group 2-resistant cleavers. Most herbicides that are registered to control broad-leaved weeds in pulse crops are Group 2 (ALS inhibitors). Therefore they will not control Group 2-resistant cleavers. The non-Group 2 herbicides that are registered on pulse crops are not effective against cleavers or, at best, only suppress this species. Trials in Saskatchewan were started in Saskatoon, Scott, Melfort and Choiceland in 2010 to look at alternative products to control Group 2-resistant cleavers. These included sulfentrazone (Group 14), linuron (Group 7), ARY-ALS7HPPS (Group 15) plus other non-registered herbicides that may be available to Western Canadian pulse crop producers in the future. All of these herbicides were applied with and without the addition of bentazon (Group 6). In the fall of 2010, trials will be initiated to evaluate these herbicides in combination with ethalfluralin (Group 3) to determine if the combination of products and modes of action will be the best strategy to control Group 2-resistant cleavers. Initial trial results from 2010 have shown good cleavers control with sulfentrazone; however, the rate may have to vary depending on soil organic matter level. Linuron did not control cleavers; ARY-ALS7HPPS showed some activity, but did not control this weed. The addition of bentazone did not significantly increase cleaver control. These trials will continue over the next few years. Hopefully, we will have an answer to a growing problem for pulse crop producers in Western Canada in the not-too-distant future.

POSTER – 10

Post-emergence rotary hoeing for weed control in pulse crops. E.N. Johnson.

Agriculture and Agri-Food Canada, Scott Research Farm, Box 10, Scott, Saskatchewan, S0K 4A0.

Mechanical alternatives to herbicides are required for organic production but they may also provide some solutions for managing herbicide resistant weeds. Mechanical weed control is generally not compatible with no-till systems which have been widely adapted by Canadian Prairie producers; however, the min-till rotary hoe may be an exception.

Two experiments were conducted at the Scott Research Farm to investigate the performance of a min-till rotary hoe in pulse crops. The first experiment was conducted in 2004 to 2006 and investigated the tolerance of field pea (*Pisum sativum* L.) and lentil (*Lens culinaris* L.) to rotary hoeing at various growth stages, as well as the effect of hoeing on crop residues. Field pea and lentil were direct seeded into standing cereal stubble and one to six passes of the rotary hoe were conducted at pre-emergence, ground-crack, 5-node, 8-node, and the 11-node stage of the crop. Surface residues were maintained on the soil surface even with 6 passes of the rotary hoe. Field peas and lentils exhibited the ability to tolerate rotary hoeing based on plant counts conducted 3 to 4 weeks after harrowing. There was less plant mortality when rotary hoeing was conducted at later crop stages, indicating a higher ability to resist injury at later growth stages. The number of passes had a significant effect on field pea and lentil yield which was independent of crop stage. Under weed-free conditions, field pea yields declined by 5 to 10% after 2 passes were conducted at all crop stages tested. This indicates that the crop's ability to recover from post-emergence harrowing was similar at all growth stages. The second experiment was conducted in 2007 and 2008 to evaluate the weed control efficacy of rotary hoeing in field pea. Single, double, and triple passes with the hoe were conducted sequentially at the ground-crack, 3-node, and 5-node stage of field pea. Most of the weed control benefit and yield increases resulted from hoeing at the ground crack stage. Two to three passes at the ground-crack stage reduced weed biomass and improved field pea yield; however, hoeing had a higher impact on weed biomass and crop yield in 2007 when wild mustard (*Sinapis arvensis* L.) and green foxtail (*Setaria viridis* L.) were the predominate weeds compared to 2008 when wild oat (*Avena fatua* L.) was predominate. Pre- and post-emergence rotary hoeing has potential to manage broadleaf weeds in organic pulse production and it may be an option for controlling herbicide resistant broadleaf weeds such as wild mustard (*Sinapis alba* L.), kochia (*Kochia scoparia* L.), and cleavers (*Galium aparine* L.) in conventional pulse crop production. A min-till rotary hoe may also incorporate soil applied herbicides without burying much surface residue. This may resurrect some older herbicide chemistries such as dinitroanilines and provide an alternative mode of action for managing weed resistance.

POSTER – 11

Field pea effects on subsequent crops and economics of various crop combinations in southeast peace area of Alberta. K.S. Gill. Smoky Applied Research & Demonstration Association (SARDA), Box 90, Falher, Alberta, T0H 1M0.

Most farmers in the Southeast Peace area of Alberta do not include field peas in their crop rotations mainly because of the economic considerations. The objective of the field trials was to compare the crop performance after peas relative to other crops and economics of various crop combinations. A field trial was done to compare the effects of 2007 peas and canola on the 2008 wheat grown under four nitrogen fertilizer rates (0, 20, 40 and 60 lb N/ac) and compare the economics of these 2 combinations (Study 1). Nutrient soil probe data in 2008 wheat showed higher nitrogen flow in the peas than canola stubble. Wheat yield tended to be greater after peas than canola, with significant differences at the 40 lb N/ac. Canola sale provided \$30/ac more than peas, but the pea-wheat combination was \$96/ac more profitable than the canola-wheat combination. In two field trials, 2010 wheat was grown under half and full rates of soil test based

recommended nitrogen fertilizer rates where peas, canola and barley had been grown in 2009 (Study 2). Results will be used to compare the seed yield of 2010 wheat and economics of these combinations. From a crop rotation field trial, the data on 2010 canola and wheat crops grown subsequent to the 2009 peas, canola, flax, wheat and barley crops will be selected (Study 3). Results will be used to compare the yield and economics of various 2009-2010 crop combinations.

POSTER – 12

An overview of PURENet field studies at Scott. Saskatchewan. M. Sather¹, R. Lemke², R.E. Farrell¹, A. Bedard-Haughn¹, F.L. Walley¹, and J.D. Knight¹ ¹Department of Soil Science, University of Saskatchewan, Saskatoon, Canada. S7N 5A8; ²Agriculture and Agricultural Food Canada, Saskatoon, Saskatchewan, Canada, S7N 0X2.

The inclusion of pulses in crop rotations provides an important environmental benefit by reducing the energy and greenhouse gas intensity of the entire cropping system. Nevertheless, previous work has highlighted a number of knowledge gaps that limit confidence in this assessment. The gaps identified include a lack of knowledge about the amount of below-ground C and N contributed by pulses and the impact that pulse residues may have on nitrous oxide emissions. Under the umbrella of the Pulse Research Network (PURENet), a medium-term pulse rotation (12 years) study located at Scott, Saskatchewan is being used to investigate changes to soil quality, particularly soil organic carbon and nitrogen, due to the presence of pulse crops in rotation - with field-based activities being complimented with more targeted, process-level studies. The Scott site has been cropped under various wheat, canola, and pea rotations since 1998. In 2008, the site became one of the cornerstones for a broad range of studies looking at the impact of pulses on soil and environmental parameters. Every year for the past three years, graduate students and researchers have collected a suite of soil and plant samples and measured greenhouse gas emissions from rotations with and without pulse crops and/or increasing pulse crop frequency to develop a better understanding of the role that pulses play in soil and environmental quality. Soil measurements that have been collected over the past 3 years include soil organic C and N, light fraction C and N, and available N and phosphorous distribution within the soil. Greenhouse gas emissions, specifically N₂O, CH₄ and CO₂ also have been collected from spring melt to freeze-up since 2008. Crop yield, crop residue C and N concentrations and meteorological data also have been collected throughout the course of this study. Numerous graduate projects also have been undertaken in order to look at more specific rhizosphere-scale contributions to soil C and N. The scale of the research at Scott is difficult to grasp when only looking at the results from one specific study. The objective of this poster is to provide a broad overview of the numerous projects that have been undertaken at Scott and link them to one another.

POSTER – 13

Nitrogen cycling in pulse vs. non-pulse rotations: gross mineralization and nitrification. L.P. Comeau, A.R. Sangster, A. Bedard-Haughn, R. Lemke and J.D.Knight. Department of Soil Science, University of Saskatchewan, Saskatoon, Saskatchewan, S7N 5A8.

Pulse crops in rotation are known to improve the sustainability of cropping systems through biological N fixation, however studies indicate there may be additional benefits, particularly with respect to the influence of pulse crops on the overall N cycle in both the pulse and non-pulse years. To quantify these additional benefits, soil processes and properties related to N cycling were examined using soils from long-term rotation studies established at two Agriculture and Agri-Food Canada Experimental Farms: five crop rotations in the Dark Brown soil zone (with and without field pea) at Scott, Saskatchewan and four crop rotations in the Brown soil zone (with and without lentil) at Swift Current, Saskatchewan. Stable ^{15}N isotope dilution techniques were used to quantify gross mineralization (2008, 2009, and 2010) and nitrification (2008 and 2010 only) rates. In-field incubations were repeated three times in each growing season: pre-seeding, anthesis and at or near harvest. In 2008, ^{15}N tracer techniques were also used to estimate the proportion of N_2O emissions derived from nitrification-related processes rather than denitrification processes. Results will be presented and implications discussed.

POSTER – 14

Does the frequency of pea in long-term rotations impact nitrogen fixation? J.D. Knight¹, J. Guerin², and M. Sather¹. ¹Department of Soil Science, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8; ²Centre de recherche sur les grains inc., Saint-Mathieu-de-Beloeil, QC, Canada, J3G 0E2.

Long-term plots at the Agriculture Agri-Food Canada Research Station located at Scott, Saskatchewan provide an opportunity to evaluate the frequency with which pea (*Pisum sativum*) is included in rotation on biological nitrogen fixation (BNF), and other nitrogen acquisition parameters in the pea crop. Rotations that included pea every year (continuous pea), every second year (pea-wheat), every third year (pea-canola-wheat) and every fourth year (canola- wheat-pea-wheat) were evaluated in 2008 and 2009 for BNF using the enriched isotope dilution technique. Wheat microplots were established within each pea plot to serve as non-nitrogen fixing reference crops. Amounts of nitrogen from BNF in the seed and straw of the crop were determined, as well as total nitrogen in these plant parts and additional yield parameters and soil nutrient parameters. Not surprisingly seed and straw yield in the continuous pea was always the lowest of all rotation treatments. Pea grown in continuous rotation also acquired less of its nitrogen from BNF. In general, as the diversity of the crop rotation increased, the percentage nitrogen derived from atmosphere and the amount of nitrogen in seed and straw derived from the atmosphere increased. Including pea every other year in rotation with wheat decreased the percentage of nitrogen from fixation compared to the two more diverse rotations.

POSTER – 15

Soybean production potential in southern Alberta. M. Bandara and A. Kruger. Alberta Agriculture and Rural Development, Crop Diversification Centre South, 301 Horticultural Station Road East, Brooks, Alberta, Canada T1R 1E6.

In Canada, soybean, *Glycine max* (L.) Merr, production is mainly confined to relatively warm growing regions in the provinces of Ontario, Quebec and Manitoba. Interest in growing soybean on the Canadian Prairies is increasing, but limited research information is available on its production in this region. During the past six years, several cultivars/lines were planted and agronomic evaluations were conducted to select the most adaptable soybean genotypes with high productivity under rainfed and partially-irrigated conditions in southern Alberta. Results showed that maturation of the tested genotypes varied from 123 to 131 days, with a seed yield ranging from 1714 to 2537 kg ha⁻¹. Increasing seed density from 30 to 90 seeds m⁻² resulted in a quadratic increase in seed yield of soybean. Based on performance, several early maturing, high-yielding conventional cultivars/lines, as well as 'Roundup Ready' soybean genotypes, were selected for seed production in southern Alberta.

POSTER – 16

Partial field resistance and partial physiological resistance to white mould in dry bean. P.M. Balasubramanian¹, R.L. Conner², D.L. McLaren³, and A. Hou². Agriculture and Agri-Food Canada, ¹Lethbridge, Alberta, T1J 4B1, ²Morden, Manitoba, R6M 1Y5, ³Brandon, Manitoba, R7A 5Y3.

White mould is a severe constraint to both irrigated and dryland bean production systems across Canada. The pathogen, *Sclerotinia sclerotiorum*, has a broad host range and causes loss of seed yield and quality in dry bean. Dry bean cultivars with both partial field resistance (avoidance) and partial physiological resistance would be preferred by producers in order to reduce disease risk and production costs. The objective of this study was to characterize select dry bean cultivars and bean germplasm lines for partial field resistance and partial physiological resistance to white mould. Partial field resistance to white mould was assessed by growing bean genotypes in inoculated disease nurseries at Lethbridge, Alberta, and Winkler and Brandon, Manitoba. Disease incidence and severity were determined for each dry bean genotype. Partial physiological resistance to white mould was evaluated by growing bean genotypes in a controlled environment at Lethbridge. Cut ends of the actively growing plants were inoculated with a mycelial culture of *S. sclerotiorum* and partial physiological resistance was assessed based on lesion size and development. Partial field resistance was confirmed in several dry bean cultivars and in germplasm lines based on one year's (2009) data. The field disease nursery was repeated in 2010 and will be grown in 2011 and 2012. Partial physiological resistance was observed primarily in dry bean germplasm lines and not in dry bean cultivars. Bean germplasm lines with both partial field resistance and partial physiological resistance were identified. These lines may be used as parents to pyramid resistance genes into dry bean cultivars for enhanced resistance to white mould.

POSTER – 17

Inheritance of CBB resistance in a resistant-intercross population of common bean.

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Common bacterial blight (CBB), caused by *Xanthomonas axonopodis* pv. *Phaseoli*, is a damaging widespread disease of common bean (*Phaseolus vulgaris* L.). Genetic resistance to CBB in common bean is limited, but has been introgressed by inter-specific crossing with tepary bean (*P. acutifolius*). In Canadian common bean germplasm, CBB resistance is derived from two distinct tepary bean sources, i.e., PI440795, from which OAC Rex was developed and PI319443, from which HR67 and HR45 germplasm lines were developed. A recombinant inbred line (RIL) population (n=225) of a cross between the resistant genotypes OAC Rex and HR45, known to carry different resistance QTL, was evaluated for resistance to CBB in the field (Field-2009) and in the growth room (GR-2010). RILs were selected for the growth room experiment based on the Area Under Disease Progress Curve (AUDPC) Field-2009 data. A subset of high, moderate and low AUDPC RILs (n=60) was selected and artificially inoculated in the growth room and evaluated for resistance. After the final growth room rating, the inoculated leaves were photographed and analysed using Assess 2.0 Image Analysis Software for Plant Disease Quantification. RILs were also genotyped with the SCAR marker UBC420 and the microsatellite marker pvCTT001, known to be associated with resistance QTLs on chromosomes B6 and B4 in HR45 and OAC Rex, respectively. RILs were also genotyped with other markers developed based on sequence information from genomic regions associated with CBB resistance. The frequency distribution of AUDPC from Field-2009 had a continuous variation with population mean shifted toward resistance. Final growth room rating from GR-2010 had a trimodal distribution which reflected low, moderate and high AUDPC. The QTL associated with the SCAR marker UBC420 and the marker SSR6 on B6 explained up to 34.6% and 59% of variation in CBB resistance in Field-2009 and GR-2010, respectively. UBC420 and SSR6 had significant epistatic interactions with pvCTT001 on chromosome B4 for Field-2009 but not GR-2010. UBC420 had a negative interaction effect with pvCTT001, whereas SSR6 had a positive interaction effect.

POSTER – 18

Image analysis for accurate quantification of common bacterial blight severity in common bean.

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Common bacterial blight (CBB), caused by *Xanthomonas axonopodis* pv. *Phaseoli* (*Xap*), is a damaging disease of common bean (*Phaseolus vulgaris* L.) throughout the world. Accurate, precise, and reproducible assessment of CBB severity (phenotyping) is important for quantitative genetic studies and for selection in bean breeding programs. The objectives of this study were to: 1) quantify CBB severity using image analysis as compared with the commonly-practiced visual disease assessments and 2) examine the

potential of image analysis in marker-QTL association studies involving CBB resistance. Segregating populations ($n = 21 \times 4$), derived from four different BC₁F₁ crosses were employed. Each F₁ was derived from the backcross of a susceptible genotype (AC Compass or Nautica) with the three-way cross progeny of the susceptible genotypes crossed with resistant intercross F₁s. Digital images of unifoliate leaves were taken 18 days after inoculation with common isolates of *Xap* in a growth room. Image analysis assessments of CBB percent infected area were performed using the software Assess[®] 2.0 to collect three sets of data (two replications of automatic assessments by two individuals and one round of manual assessment). Infected leaves were also visually rated for CBB severity by three individuals, using a 0 to 5 scale. Each plant was also genotyped with the previously known CBB-associated SCAR marker, SU91. Both image analysis and visual assessments were found to be highly repeatable with correlation coefficients $r = 0.95-0.99$ ($P < 0.001$) for three image analysis assessments, and $r = 0.90-0.92$ ($P < 0.001$) for three visual assessments. Image analysis had a positive, but non-linear association with visual rating. Image analysis provided significantly greater differentiation between the phenotypic values of the two SU91 genotypic groups. The difference between the two SU91 genotypes was between 4.9 to 11 folds for image analysis assessments, but only 2.2 to 3.1 folds for visual assessments. The proportion of the CBB resistance phenotypic variance accounted for by the marker SU91 was 75% for visual assessment, but only 40% for assessment using image analysis. This suggests that the visual assessment of CBB severity may result in overestimation of the effect of quantitative trait loci. These results indicate that while visual assessment of CBB severity is a reliable tool for selection in breeding programs, assessments using image analysis may be more suitable for phenotypic evaluations in quantitative genetic studies.

POSTER – 19

Sensitivity of *Ascochyta pinodes* populations to prothioconazole. J.A. Delgado¹, T. Stoppler¹, B. Gossen², K.F. Chang³, F. Dugan⁴, S. Markell¹, and R.S. Goswami¹.

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Ascochyta blight of field peas is a yield-limiting disease and affects field pea growing areas of North America. It is mainly caused by the fungal pathogen *Ascochyta pinodes* (*Mycosphaerella pinodes*). Two QoI fungicides and one triazole fungicide are currently labeled as foliar sprays for management of *Ascochyta* blight of field peas in North Dakota. Fungicide sensitivities of *A. pinodes* to the triazole prothioconazole were determined to implement a baseline that would help the monitoring of sensitivity shifts of *A. pinodes* populations in North Dakota. A total of 52 isolates of *A. pinodes* collected prior to the use of prothioconazole on field peas were tested. Among these, 29 isolates were collected from the Pacific Northwestern part of US and 23 were collected from the Central part of Canada. All the isolates were screened in vitro by assessing the mycelial growth at five concentrations of the prothioconazole added to half strength CV8 agar and the effective concentration at which 50% of the growth was inhibited (EC50) was

determined for each isolate. Prothioconazole EC50 values ranged from 0.6950 to 9.3402 µg/ml with a mean of 2.2379 µg/ml. The EC value frequency showed that *A. pinodes* isolates exhibited a bimodal behavior. The fourteen most sensitive isolates ranged from 0.6950 to 0.9854 µg/ml with a mean of 0.8617 µg/ml. Prothioconazole sensitivity for the remaining isolates ranged from 1.1007 to 9.3402 µg/ml with a mean of 2.7449 µg/ml. Additional studies to improve and facilitate the monitoring of prothioconazole sensitivity of *A. pinodes* populations and assessment of current sensitivity levels are in progress.

POSTER – 20 NOTE: ABSTRACT WILL NOT BE PUBLISHED IN CJPS

Effect of downy mildew on growth and yield of field pea. K.F. Chang¹, S.F. Hwang², S.E. Strelkov³, B.D. Gossen⁴, G.D. Turnbull², and D.J. Bing⁵. ¹Alberta Agriculture and Rural Development (AARD), Lacombe, Alberta T4L 1W8; ²AARD, Edmonton, Alberta T5Y 6H3; ³University of Alberta, Edmonton, Alberta T6G 2P5; ⁴Agriculture and Agri-Food Canada (AAFC), Saskatoon, Saskatchewan S7N 0X2; ⁵AAFC, Lacombe, Alberta T4L 1W1.

Downy mildew, caused by *Peronospora viciae* f.sp. *pisi*, has caused substantial damage to field pea crops in Alberta, particularly under the cool, wet conditions experienced in 2010. A total of 150 healthy and diseased plants were sampled in a W-pattern from an infested field in central Alberta on July 27, 2010. Plant height and pod length and width were recorded to evaluate the impact of downy mildew on vegetative and reproductive development in pea plants. Plant growth and pod size were reduced in the diseased plants. Just prior to harvest in 2010, over 300 plants in four infested commercial fields of pea were sampled in a W-pattern. Disease severity, pod numbers and yield per plant were recorded to assess the impact of downy mildew on yield. Pod numbers decreased and yield losses increased with increasing severity. These results indicate that moderately severe downy mildew can reduce pod size, number of pods and yield by 50-75%.

POSTER – 21

Effect of seeding depth, seeding date and seed treatment on downy mildew of field pea in Alberta. K.F. Chang¹, S.F. Hwang², S.E. Strelkov³, B.D. Gossen⁴, G.D. Turnbull², and D.J. Bing⁵. ¹Alberta Agriculture and Rural Development (AARD), Lacombe, Alberta T4L 1W8; ²AARD, Edmonton, Alberta T5Y 6H3; ³University of Alberta, Edmonton, Alberta T6G 2P5; ⁴Agriculture and Agri-Food Canada (AAFC), Saskatoon, Saskatchewan S7N 0X2; ⁵AAFC, Lacombe, Alberta T4L 1W1.

Downy mildew, caused by *Peronospora viciae* f. sp. *pisi*, can cause substantial damage to field pea crops in Alberta. Trials were conducted in commercial fields near Gibbons and Mannville, Alberta, where the soil was infested with downy mildew. Each trial was laid out in a randomized complete block design with four replicates and seeded to field pea cv. Midas in May of 2009 and 2010. The objective was to assess the effect of seeding date, seeding depth, and fungicide treatment on the severity of downy mildew. To assess the impact of seeding depth, seed was sown at 2, 5, and 7 cm depth. No differences in downy mildew incidence or severity, plant mortality or seed yield were detected, except that mortality was higher at 7-cm relative to 5-cm depth at Mannville in 2009. To assess the impact of seeding date, the treatments at Mannville were seeded on 5, 13, 30 May in 2009 and 10, 20 May and 13 June in 2010. At Gibbons, the seeding dates were 5, 15, 30

May in 2009 and 10, 20 May and 4 June in 2010. Plant mortality caused by downy mildew was higher in the early-seeded treatment at Mannville in 2009 than in those seeded in mid to late May. In 2010, the incidence and severity of downy mildew declined as seeding date was delayed at both sites, but yield was lowest for the final seeding date. To assess the efficacy of fungicide seed treatments, application of Allegiance, Apron Maxx, DCT, Reason, and Reason + Allegiance were examined. All treatments reduced plant mortality caused by downy mildew in 2009, but had no effect on seed yield. To assess the efficacy of foliar fungicides, Bravo, Curzate, Headline, Quadris, Ridomil Gold and Reason were examined. On 5 August, 2008, the selected foliar fungicides were applied to a naturally infested field. The experiment was also conducted at both study sites in 2009. Quadris, Reason and Headline improved yield in 2008. In contrast, all of the fungicides reduced plant mortality in 2009 but did not affect yield.

POSTER – 22

Assessing the potential for clubroot spore contamination of field pea seed. R.J. Howard¹, D.A. Burke¹, S.L.I. Lisowski¹, S.E. Strelkov², D.C. Rennie², S.F. Hwang³, G.D. Turnbull³, L.M. Kawchuk⁴, and M.W. Harding⁵. ¹Alberta Agriculture and Rural Development, Crop Diversification Centre South, Brooks, Alberta T1R 1E6; ²University of Alberta, Department of Agriculture, Food and Nutritional Science, Edmonton, Alberta T6G 2P5; ³Alberta Agriculture and Rural Development, Crop Diversification Centre North, Edmonton, Alberta T5Y 6H3; ⁴Agriculture and Agri-Food Canada, Research Centre, Lethbridge, Alberta T1J 4B1; ⁵Innovotech Inc., Crop Diversification Centre South, Brooks, Alberta T1R 1E6.

Clubroot, caused by the soilborne pathogen *Plasmodiophora brassicae*, is an important disease of crucifers worldwide and has become an economical problem in canola, in Alberta. Pathogen resting spores are disseminated in infested soil carried on machinery and equipment, and recent research has demonstrated that seed of canola, pea and wheat, as well as potato tubers, harvested from clubroot-infested fields may also be contaminated with resting spores. Studies were conducted in 2009-10 to determine the potential predisposition of field pea seed to resting spore contamination in fields naturally infested with the clubroot pathogen near Bassano and Leduc, Alberta. Replicated experimental plots of yellow peas were exposed to four harvesting regimes, i.e. 1) Hand-harvested, 2) Direct-combined, 3) Swathed and combined, and 4) Swathed, rained-on and combined, to assess the relative risk of spore infestation via dust and earth tag. In 2009 at Bassano, the order of treatments from least to most contaminated as determined by quantitative polymerase chain reaction (qPCR) was 1, 2, 3 and 4 (range 0-75 spores/10g seed), while at Edmonton they were 3, 4, 1 and 2 (228-688 spores/10g seed). This trial was repeated at the trial site near Bassano in 2010 and results are pending.

POSTER – 23

Field pea response to phosphorus (P) fertilizer in Southeast Peace area of Alberta. K.S. Gill, Smoky Applied Research & Demonstration Association (SARDA), Box 90, Falher, Alberta T0H 1M0.

Field pea response to P fertilizer has been documented. However, an informal survey of the farmers in the Southeast Peace area of Alberta indicated that fertilization of peas with

P was not considered economical and was generally not practiced. The objective of field trials during the 2008, 2009 and 2010 growing seasons was to study the response of peas to P fertilization based on the soil test results. Two field trials were done in 2008 to monitor the response of peas to half and full rates of soil test based P recommendation (Study 1). At the Smoky River site, both the seed yield and contribution margin were increased due to P fertilization. Lack of adequate rainfall during the growing season was considered responsible for the lack of pea yield response at the Greenview site. The response of peas to different P rates (0, 60, 80, 100, 120 and 140% of soil test based P recommendation) was monitored during the 2009 and 2010 growing seasons (Study 2). Yield response to fertilizer was observed in both years. Again the magnitude of pea yield response was reduced by drought stress during both years of the study. Based on the results from two studies, P fertilization is recommended for growing peas in the Southeast Peace area and the yield response to P fertilization depends on the availability of soil moisture during the growing season.

POSTER – 24

Quantification of glomalin-related soil protein using the Bradford and ELISA methods. M. Sather, I. Moolecki, F.L. Walley, R. Lemke, J.D.Knight, and R.E. Farrell. Department of Soil Science, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8.

Arbuscular mycorrhizal fungi (AMF) produce large amounts of glomalin, a glycoprotein that can sequester carbon. Glomalin contains 30-40% C incorporated in its protein and carbohydrate subunits and is a sticky substance that enhances soil structure, further promotes soil C storage and influences pore size and connectivity. Glomalin was first documented in 1996 and is thought to be important to soil carbon sequestration and N₂O emission cycles. However, glomalin is only operationally defined as the protein extracted from soil by autoclaving with a citric acid buffer. The assumption is that the harsh extraction procedure destroys most other proteins with the exception of glomalin. Because glomalin is operationally defined, the preferred terminology is glomalin-related soil protein (GRSP). Easily extractable GRSP is extracted from the soil by a single autoclave cycle. Total extractable GRSP is extracted from the soil through multiple autoclave cycles. The Bradford protein assay and the enzyme-linked immunosorbent assay (ELISA) are both used to quantify GRSP extracted from soil. A study was undertaken in 2009 to quantify GRSP, using the Bradford protein assay and the ELISA, in soils from two long-term pulse rotation studies. The objective of the study was to look at differences in GRSP between various rotations, with and without pulse crops. A secondary objective involved comparing the results obtained from the two different methods. Both methods required significant troubleshooting throughout the research process in order to obtain reproducible results. Rotational effects were observed at Swift Current, Saskatchewan; however, there were no rotational effects at the Scott, Saskatchewan. The effects will be discussed in the context of the strengths and weaknesses of the two methods.

POSTER – 25

Carbon fate in pulse vs. non-pulse rotations: A ^{13}C greenhouse study. L.P. Comeau, A.R. Sangster, A. Bedard-Haughn, R. Lemke, and J.D. Knight. Department of Soil Science, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8.

Both the quantity and quality of crop residues can impact soil properties and processes. Plants enriched with isotopic tracers can be used to trace crop residue decomposition to various C pools but only if the tracer is homogeneously distributed throughout the plant. In order to determine if repeat-pulse labeling could be used to trace crop residue decomposition, the method was used to expose plant material of field pea and canola plants to $^{13}\text{CO}_2$ in a controlled environment. Field pea and canola were grown in large intact soil cores were exposed weekly to pulses of 33 atom% $^{13}\text{CO}_2$ and grown to maturity. The label was not homogeneously distributed throughout the plant; in particular, the pod fractions were less enriched than other fractions. Nevertheless, root contributions to below-ground C were successfully determined from the enriched root material, as was ^{13}C enrichment of soil within the top 15 cm. In 2010, the weekly $^{13}\text{CO}_2$ labeling procedure was modified and repeated, growing pea, canola, lentil, and wheat in large intact soil cores from long-term rotation studies at two Agriculture and Agri-Food Canada Experimental Farms: Scott and Swift Current, Saskatchewan. The above- and below-ground fate of the ^{13}C was then traced, both within the labeling growth season and through a subsequent wheat phase. Results will be presented and implications discussed.

POSTER – 26

Temporal dynamics of nitrogen rhizodeposition of pea. M. Arcand, R. Farrell, and J. D. Knight. Department of Soil Science, University of Saskatchewan, Saskatoon, Saskatchewan, S7N 5A8.

Pulse crops can play an integral role in reducing the environmental impacts of traditional cereal-based crop rotations in the prairies by reducing reliance on N fertilizers and potentially improving soil C storage. Determining the impacts of pulse crops on N supply to subsequent crops and/or N and C dynamics from remaining crop residues requires better quantification of belowground residue contributions of N to soil, including those from rhizodeposits. This greenhouse study used the cotton-wick method to label pea plants (*Pisum sativum*) continuously with 0.4% (w/v) ^{15}N -enriched urea (99 atom %) to determine N rhizodeposition at nine leaves fully expanded (vegetative stage), early flowering, and maturity of pea. The aboveground plant parts were preferentially enriched with ^{15}N , which is expected since ^{15}N urea solution is fed directly to the stem. Enrichment of rhizosphere soil with ^{15}N decreased as plants matured with a concomitant increase in rhizodeposits recovered in the bulk soil with time, suggesting translocation of root derived N outside of the rhizosphere. Belowground plant N (roots, nodules, and rhizodeposits) comprised 46, 26, and 14% of total plant N at vegetative, flowering, and maturity, respectively. At each growth stage, rhizodeposition comprised a higher proportion of belowground N than roots and nodules. Moreover, in this study 80% of total plant N was removed in the pea grain at maturity, while 10% remained in straw, chaff and intact roots and 10% recovered in rhizodeposits, highlighting the importance of rhizodeposits to the total plant N balance.

POSTER – 27

Yellow pea, lentil, navy bean and pinto bean addition to wheat flour cookies and their effect on physical and nutritional properties. F. Zucco¹, Y. Borsuk², and S.D. Arntfield². ¹Federal University of Santa Catarina, Florianópolis, Brazil, ²Department of Food Science, University of Manitoba, Winnipeg, Manitoba, R3T 2N2.

Nutritionally enhanced cookies were prepared from the blends containing different proportions (25%, 50%, 75% and 100%) of navy bean, pinto bean, green lentil and commercial yellow pea flours. The influence of the replacement of wheat flour by pulse flours on the quality characteristics of the cookies was analyzed. The effects of degrees of milling (fine and coarse) of the non-commercial flours were also considered. The supplementation with pulse flours significantly affected the physical and chemical parameters of the cookies. Fine flour incorporation remarkably increased cookies' hardness and decreased spread factor while coarse flours marginally altered both parameters. The replacement of wheat flour by green lentil flour showed the greatest impact on the physical characteristics and the cookies from its coarse degree of milling were of unacceptable structure and poor handling properties. Significant differences were observed for the colour parameters, but less evident alterations were reported for pinto bean addition. Regardless of flour type, the protein content and antioxidant activity of the cookies baked with pulse flours were remarkably higher than the control. The increase was up to 68% for protein level and up to 207% for antioxidant activity. Best results regarding antioxidant activity were achieved by incorporation of coarsely ground pinto beans. Despite significant differences detected between control and pulse flours, overall analysis indicated that cookies with acceptable physical characteristics and improved nutritional profile could be produced by partial or complete replacement of the wheat flour.

POSTER – 28

The capacity of symbiotic N fixation of pulse crops grown on the Canadian prairie. X.Y. Wang¹, Y.T. Gan¹, C. Hamel¹, and R.L. Lemke². ¹Semiarid Prairie Agriculture Research Centre, Agriculture and Agri-Food Canada, Gate #3, Airport Road East, Swift Current, Saskatchewan, S9H 3X2. ²Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, Saskatchewan, S7N 0X2.

Annual pulse crops play an important role in improving N supply power of the soil and increasing the productivity of subsequent crops. A field study was conducted at Swift Current, Saskatchewan in 2008 and 2009 to quantify N fixing capacity of various annual pulses based on the N¹⁵ enriched isotope dilution technique. The test included 6 pea cultivars (Venture, CDC striker, Cooper, CDC Meadow, CDC Golden and CDC Handel), 11 lentils (CDC Sedley, CDC Glamis, Laird, CDC Viceroy, CDC Richlea, CDC Meteor, CDC Robin, CDC Blaze, CDC Rouleau, CDC Imperial and CDC Impact), 6 chickpeas (CDC Vanguard, CDC Anna, CDC Nika, Amit, CDC Frontier and CDC Luna), along with fababean (Blitz), lupin (Arabella) and drybean (Pintium). In 2008, the amount of biological N₂ fixed from the atmosphere by pea, fababean, lentil, chickpea and lupin (drybean in 2009) was estimated at 58, 50, 38, 33 and -7 kg N ha⁻¹, respectively, and the corresponding values were 37, 45, 23, 22 and 15 kg N ha⁻¹ in 2009. There were significant interactions between year and crop species (P<0.05), primarily due to greater

N₂ fixation of fababean compared to pea in 2009, and the extremely lower N fixation value of lupin (2008) compared to drybean (2009). Cultivars did not differ in N fixation and their interaction with year was not significant. Averaged across cultivars, N fixation of pea, lentil and chickpea ranged from 40-65, 22-41 and 19-34 kg N ha⁻¹, respectively. The results illustrated that pea and fababean fixed a consistently greater amount of N₂ from the atmosphere than the other species and lupin fixed 0 N. No differences in N fixing capacity among cultivars within a crop species suggested that there is lack of genetic advancement in cultivar development for the improvement of symbiosis.

POSTER – 29

Barley crop response to preceding cool season pulses in Alberta. C.M. Williams¹, J.R. King¹, S.M. Ross¹, M.A. Olson², C.F. Hoy², K.J. Lopetinsky³. ¹Department of Agricultural, Food and Nutritional Science, University of Alberta, 4-10 Agriculture-Forestry Centre, Edmonton, Alberta T6G 2P5; ²Alberta Agriculture and Rural Development; ³Pulse Research Consultant.

Pulse crops in rotation impact the nitrogen (N) balance of the cropping system and affect the yield of the subsequent crop. Producers have identified a need for more information on the effects of integrating cool season pulse crops into current rotations. In 2008, a two year rotational study was initiated to investigate the effects of 'Canstar' field pea (*Pisum sativum* L.), 'Snowbird' tannin-free faba bean (*Vicia faba* L.), and 'Arabella' narrow-leafed lupin (*Lupinus angustifolius* L.), on the yield and quality of a subsequent barley crop, at two sites in central Alberta – Barrhead and St. Albert. In year 1 of the rotation (YR1), pea, faba bean, lupin, barley (with and without N fertilizer), and canola (with and without N fertilizer) were grown. The following year barley was produced across all YR1 treatments. In YR1, N fixation, removal and return were assessed for each pulse crop. In YR2, yield and N content of barley was measured at grain maturity. In 2008 and 2009, YR1 pulse crop N fixation in above-ground biomass averaged 52% Ndfa (N derived from the atmosphere) for faba bean, 45% for pea, and 31% for lupin. At Barrhead in 2008 and 2009, the N fixed in the above-ground biomass of pulses averaged 55 kg N ha⁻¹, and the N exported in harvested pulse seed averaged 117 kg N ha⁻¹. At St. Albert, the N fixed in pulse biomass averaged 122 kg N ha⁻¹, and the N exported in harvested seed averaged 179 kg N ha⁻¹. In 2009, mean YR2 barley grain yields were 2.13 Mg ha⁻¹ at Barrhead and 4.61 Mg ha⁻¹ at St. Albert. Barley grain yields following peas and faba bean were equal to or better than treatments with added N fertilizer. Barley seed protein content was higher in Barrhead than St. Albert because of lower available moisture at the Barrhead site. Following a pulse in rotation, barley seed % protein averaged 15% at Barrhead and 13% at St. Albert, and the mean kernel weight (g per 1000 seeds) was 46 g at Barrhead and 42 g at St. Albert. The YR2 barley that followed a pulse in rotation had quality characteristics equal to that following barley or canola with added N fertilizer. Preliminary results indicate that peas and faba beans in rotation maintain subsequent crop yield and quality without the addition of N fertilizer.

POSTER– 30

Effects of plant growth regulators on crop maturity, seed yield and seed quality of the Kabuli chickpea cultivar CDC Frontier in southern Alberta. P.P. Lokuruge¹, M.S. Bandara², A. Kruger², R.J. Howard², D.A. Burke², T. Harms², N. Chaudhary³ and B. Taran¹. ¹Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, S7N 5A8; ²Crop Diversification Centre South, 301 Horticultural Station Road East, Brooks, Alberta, T1R 1E6, ³Alberta Agriculture and Rural Development, 7000-113 Street, Edmonton, Alberta, T6H 5T6.

Late and uneven crop maturity in chickpea, caused mainly by an indeterminate growth habit, is as important as Ascochyta leaf blight, as a major impediment for the production of high quality chickpea production on the Canadian Prairies. While development of early maturing chickpea cultivars with determinant growth habit is a permanent solution for this production constraint, limited agronomic approaches have been tested to achieve the goal. Plant growth regulators (PGRs) with growth retarding properties have been successfully used to control excessive growth and attain uniform maturity of annual cereals and several pulses. A three-year field study was initiated in 2010 to examine the impact of three PGRs, Cycocel (cholomequate chloride = A), Apogee (pro-hexadione-Ca= B) and Palisade (trinexapac-ethyl = C), applied at four rates (1000, 2000, 4000 and 6000 ppm for A and C, and 750, 1500, 3000 and 4500 ppm for B), plus an untreated control, at three plant growth stages (10, 20 and 30 days after first flowering), on crop maturity, seed yield and quality of the Kabuli chickpea cultivar CDC Frontier grown under rainfed and partially-irrigated conditions at Brooks and Bow Island, Alberta. PGR treatments were applied either separately or as a mixture with a fungicide, and were arranged in a split-plot design with three replicates at each location. Data on plant height at different growth stages, seed yield components, green seed percentage, water use efficiency, disease incidence and severity, seed yield, and cost-effectiveness of production packages are being collected, and preliminary information on the experimental treatment effects on these traits will be presented.

POSTER – 31

Exploiting response to photoperiod to improve adaptation and yield of chickpea in the Canadian prairies. K. Daba, T. Warkentin, and B. Tar'an. Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, S7N 5A8.

Knowledge of the time required for the initiation of flowering is crucial for chickpea adaptation. Flowering is a major factor affecting variation in crop duration. The crop duration should be sufficiently long to allow the crop to accumulate enough photosynthate for adequate yield, but at the same time short enough to fit the available growing season. Genetic analysis of flowering time and its bearing on agronomic performance is fundamental for genetic improvement to develop suitable chickpea varieties for the prairies. A three year (2010-2012) study was initiated to characterize the response of selected chickpea genotypes for flowering response under different photothermal conditions, to evaluate if a photoperiod sensitive phase exists in chickpea and to map genes for early flowering, photoperiod insensitivity and reaction to ascochyta blight in chickpea. In the first phase of the study, chickpea collections from International

Center for Agricultural Research in Dry Areas (ICARDA), International Crop Research Institute for the Semi Arid Tropics (ICRISAT) and University of Saskatchewan totalling 100 genotypes will be screened under controlled environments for their response to temperature and photoperiod under either long day (16 h) or short day (10 h) and 22 °C and 16 °C day and night temperatures respectively. Screening under long day was completed in summer 2010. At present screening of the same genotypes under short day is under way. The second phase of the study will include screening of selected chickpea genotypes based on their response to photoperiod to determine the timing and duration of the photoperiod sensitive phase and the time of floral initiation. Third phase encompasses mapping genes for early flowering, photoperiod insensitivity and reaction to ascochyta blight using 92 RILs derived from a cross between ICCV96029 (early flowering, early maturing, susceptible to ascochyta blight) and CDC Frontier (late flowering, late maturing, moderately resistant to ascochyta blight). A replicated field experiment was conducted at Elrose, Saskatchewan in 2010. This experiment will be repeated in Saskatoon and Elrose in 2011 and 2012. Assessment of time to flowering under different photoperiod regimes (10 h and 16 h) will be conducted in growth chambers. DNA will be extracted from leaves of the parents and the RILs for genotyping using microsatellite and SNP markers followed by linkage mapping and QTL analysis.

POSTER – 32

Quality assessment of pulse crops grown in North Dakota. K. McPhee¹, P. Thavarajah¹, and D. Thavarajah². ¹Department of Plant Sciences, ²School of Food Systems, North Dakota State University, Fargo, North Dakota 58108, USA.

Pulse crop production has increased substantially in the upper Midwest region including North Dakota, eastern Montana and South Dakota and accounts for more than 80% of total US production. Quality of these crops has traditionally been based on visual assessment of size shape and color. Recent interest in understanding the nutritional benefits of pulse crops as whole foods has led to deeper inquiry into the nutritional composition of the seed. Thirty-eight breeding lines and check cultivars were evaluated for content of mineral nutrients and phytic acid. Genetic variation differed among the traits evaluated, but ranged from 30% to more than 15 fold for phytic acid. These results will provide the basis for further evaluation of available genetic variation and selection within the breeding program.

POSTER – 33

Anti-inflammatory activity of flavonoids isolated from the seed coat of coloured beans (*Phaseolus vulgaris* L.) on murine macrophages. K.M. Pitura and S.D. Arntfield, Department of Food Science, University of Manitoba, Winnipeg, Manitoba, R3T 2N2.

The common bean (*Phaseolus vulgaris* L.) or dry bean has played an important role in traditional diets worldwide. Dry beans are a significant source of nutritional and non-nutrient compounds. Non-nutrient plant substances, including flavonoid compounds, are mainly found in pigmented dry bean seed coats which may be removed and discarded. Bean extracts, particularly from the seed coats, are known to possess antioxidant activity. An understanding of the main flavonoid compounds in pigmented dry bean seed coats, as

well as their antioxidant and cellular anti-inflammatory activity will assist in their further utilization as flavonoid resource materials. The objective of this study was to identify and quantify the main flavonol glycosides in pigmented dry bean seed coat extracts and to determine their anti-inflammatory effects using a cell culture model. Flavonoid glycosides were identified from extracts of different pigmented seed coats of dry beans: black beans, pinto beans, and dark and light red kidney beans, representing nine varieties grown in Manitoba. Based on high performance liquid chromatography mass spectrometry-mass spectrometry (HPLC-MS-MS), black beans contained the 3-*O*-glucosides of kaempferol, quercetin, and myricetin. Pinto beans contained mainly kaempferol 3-*O*-glycosides, while dark and light red kidney beans contained quercetin 3-*O*-glucosides. Crude extracts were examined for cellular measures of antioxidant activity in lipopolysaccharide (LPS) stimulated murine macrophage RAW 264.7 cells. After a 24-hour incubation with the extracts, a pinto bean extract, Windbreaker, demonstrated anti-inflammatory activity by inhibiting the production of tumor necrosis factor alpha (TNF α), a pro-inflammatory cytokine. All other extracts generally induced TNF α production indicating pro-inflammatory properties. The results suggest the extract of a pinto bean, Windbreaker, has the potential to be used as functional food and nutraceutical that may provide protective effects against chronic inflammatory diseases.

POSTER – 34

Biochemical and molecular characterization of two low phytate pea lines. A.S.K. Shunmugam, B. Tar'an, K. Bett, and T. Warkentin, Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, S7N 5A8.

Phytate is the major storage form of phosphorus in crop seeds, but is not well digested by humans or non-ruminant animals. In addition, phytate chelates several essential micro nutrients which are also excreted contributing to phosphorus pollution in the environment. Environmental and nutritional concerns led to the development of cultivars with the low phytate trait. The present study is aimed at biochemical and molecular characterization of two low phytate pea mutant lines, 1-150-81 and 1-2347-144 developed at the Crop Development Center, University of Saskatchewan in collaboration with Dr. Victor Raboy, USDA, Idaho. Biochemical characterization will be done on the two mutants, their progenitor, CDC Bronco and CDC Meadow that were grown in a replicated trial in field at Saskatoon and Rosthern, Saskatchewan in 2010, and will be grown again at these locations in 2011. Flowers were tagged at the time of pollination and samples of developing seeds were collected 7 days after pollination and at weekly intervals thereafter until maturity. The concentrations of phytate-phosphorus, isomeric forms of phytate phosphorus and inorganic phosphorus in these developing cotyledons and seed coats will be assessed by using colorimetric and HPLC methods. The pattern of phytate-phosphorus and inorganic phosphorus accumulation will be determined in developing seeds. Molecular characterization will include cloning, sequencing and mapping of the gene(s) associated with the low phytate trait. Molecular markers will be developed based on the gene sequence(s). Recombinant inbred lines (RILs) are under development from crosses between the two mutant lines and CDC Meadow. The RILs will be evaluated in replicated field trials in Saskatchewan in 2011 and 2012 and will be genotyped using available microsatellite markers or SNP markers and phenotyped using

colorimetric and HPLC assays. These data will then be used to identify the molecular marker(s) for the trait. The study will help us to understand the nature of the low phytate mutation(s).

POSTER – 35

Understanding the genetic basis for carotenoid pigments in lentils. Z. Ye and A. Vandenberg. Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, S7N 5A8.

Cotyledon color is one of the main marketing characteristics of lentil (*Lens culinaris* Medik.). Cotyledons may be red, yellow, or green. Genetic and environmental effects determine the appearance of the cotyledons. Little information exists regarding the biochemical profile, concentration and heritability of the specific pigments in lentil cotyledons. Preliminary work indicated that β -carotene concentration in lentil cotyledons has considerable genetic variability. In future research, HPLC methods combined with a G \times E analysis will be used to determine the concentration of β -carotene and the family of carotenoid pigments from seed fractions derived from: (1) a subset of wild and cultivated lentil germplasm accessions; (2) a set of replicated lentil breeding lines grown at multiple locations in 2 years; and (3) selected RIL populations developed in the CDC lentil breeding program. Results of this research will allow us to determine: (1) if interspecific hybridization used for disease resistance gene transfer influences pigment profiles in lentil seeds; (2) the heritability of the pigments found in lentil seeds; and (3) whether breeding for increased concentration of β -carotene or related carotenoids is feasible for lentil.

POSTER – 36

Lactic acid assisted wet fractionation improved the purity and physicochemical properties of field pea (*Pisum sativum* L.) starches. S. Naguleswaran and T. Vasanthan. Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada, T6G 2P5.

The lactic acid (LA) assisted starch isolation is inherently less costly than chemicals like NaOH for protein solubilization, and also possess less concern to the food industry since LA naturally occurs in many foods such as dairy products. The use of LA in the isolation of starch from field pea (*Pisum sativum* L.) flour was investigated. The objectives of this study were: a) to compare the yield, purity and morphology of starches isolated from field pea flour with and without the use of lactic acid, and b) to evaluate how the use of lactic acid influences the physicochemical properties of the isolated field pea starches. The yield, purity, morphology and the physicochemical properties (color, swelling, gelatinization and pasting characteristics, x-ray diffraction pattern and crystallinity) of the starches isolated with and without LA were determined. When compared to the control (0% LA), addition of LA at concentrations ranging from 0.5 to 7.0% (v/v) significantly increased the purity of the isolated starches up to 4% (w/w) and reduced the residual protein content by 6% (w/w). The resistant starch and apparent amylose contents of the isolated starches using LA were significantly higher (up to 25% and 42.5%, w/w, respectively). Furthermore, the LA processed starches showed significantly lower swelling factor and pasting viscosities, but generally insignificant changes were observed

in the gelatinization parameters as compared to that of control. Marginal differences were observed in the x-ray diffractograms between control and the LA processed starches. However, the relative crystallinity of LA processed starches was significantly higher than the control. The present study revealed that the use of LA in field pea starch isolation show benefits in terms of starch purity, brightness, resistance to amylolysis and apparent amylose content.

POSTER – 37

Development of an oilseed pea. Ehasn Khodapanahi. Bioresearch Engineering Department, McGill University, Montreal, QC, H4B 1X7.

The growing global interest in bio-energy is a consequence of more environmental concern and increasing demand of renewable energy sources in recent decades. In warm temperate regions of Canada, protein and vegetable oil production is mainly achieved by growing soybean (*Glycine max*) as a dual purpose crop which is replaced by canola (*Brassica napus*) and field pea (*Pisum sativum*) in cooler regions. Field pea cultivated area has been expanding since 2006 but this crop has never been considered as a source of lipid. The aim of the project is to develop field pea to a novel oilseed crop that reflects soybean oil and protein production in less temperate areas of the country. Furthermore, the produced oil and fat is expected to be of interest to bio-fuel markets and cosmetic industries. The research objective is being accomplished by multiplication and screening of more than 170 different varieties of field peas for their total lipid content and initial breeding to improve the content. The methodology was developed by comparing eight different extraction methods (application of different solvents or apparatus) which were applied to canola and soybean samples as well for method validation. Moreover, the lipid content will be characterized by MS and HPLC for composition determination. So far the results show a range of 2-4 % lipid content in different varieties of field pea which is in agreement to the literature but this percentage is expected increase by selective breeding progress.

POSTER – 38

Linkage between genotype and phenotype in wild lentil. M. Fedoruk, A. Tullu, S. Vail, A. Vandenberg, and K.E. Bett, Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan.

Wild lentil species can be a source of traits that could help overcome production constraints in cultivated lentil (*Lens culinaris*). For this study, wild lentil genotypes will be characterized genotypically using Single Nucleotide Polymorphic (SNP) markers. They will also be grown in the field in order to observe and record their various phenotypes. Once this is complete, both the genotypic and phenotypic data will be analyzed to identify putative associations. This could aid in the development of molecular markers that would help plant breeders track the genes for a specific trait in an interspecific cross.

POSTER – 39

KnowPulse: a breeder-focused web portal that integrates genetics and genomics of pulse crops with model genomes. L.Sanderson, E. Barlow, P. Vijayan, A. Vandenberg, B. Tar'an, T. Warkentin, and K.E. Bett, Dept. of Plant Sciences, University of Saskatchewan, Saskatchewan, Canada.

Integrating phenotypic and genotypic data of germplasm collections and breeding lines is critical for the effective use of the vast quantities of genomic data being generated today. To this end, we have developed KnowPulse (knowpulse2.usask.ca), a web-based resource for use by breeders, geneticists and others involved in pulse crop research. As a first step, legume crop sequence data generated at the University of Saskatchewan, legume sequence datasets at NCBI and the DFCI gene indices have been stored in the KnowPulse database. Each sequence in this database has a detailed page view, which links to the original data source and a graphical view using GBrowse. The KnowPulse GBrowse implementation uses the *Medicago truncatula* 3.0 genome build (Medicago Genome Sequence Consortium) as a reference and facilitates comparisons of DNA sequences across multiple legume species. Plans for the future include the integration of genotypic, phenotypic and pedigree data and development of data entry and management modules. We also expect to add software tools that will enable breeders to associate phenotypes and marker genotypes with breeding materials, enhance crossing design and improve germplasm development strategies.

POSTER – 40

Characterization of *Phaseolus acutifolius* as a source for developing genetic variability in dry bean breeding. P.Vijayan¹, J. Martinez¹, Q. Lu¹, V. Gurusamy¹, I. Alahakoon¹, A.Vandenberg¹, D. Debouck², and K.Bett¹. ¹University of Saskatchewan, Department of Plant Sciences, 51 Campus Dr., Saskatoon, Saskatchewan, Canada S7N 5A8. ²CIAT, Km 17, Recta Cali-Palmira, Apartado Aéreo 6713, Cali, Colombia.

Several wild and cultivated accessions of tepary beans (*Phaseolus acutifolius*) were screened for tolerance to sub zero temperatures and other phenological traits in the laboratory and the field in Saskatoon. Physiological studies were also conducted to evaluate sub zero temperature tolerance, electrolyte leakage as well as super-cooling properties of detached leaves. A wild accession of *P. acutifolius* (W6 15578) and a cultivated tepary bean accession were found to be relatively tolerant to low temperature stress, based on these studies. Results also showed that a high degree of variability exists in tepary bean germplasm in germination, flowering and seed related traits. Although agronomic and seed quality traits of these genotypes are inferior, they are valuable sources of low temperature tolerance and potentially other agronomic traits like drought and disease tolerance in dry bean. *P. acutifolius* accessions have been crossed with cultivated bean and hybrid progeny generated using ovule/embryo rescue techniques. Results of these studies and evidence of introgression of stress tolerance, phenological and seed traits into the dry bean genome observed in 500 BC2F3 hybrid population derived from a cross between *P. vulgaris* and *P. acutifolius* W6 15578 will be presented.

POSTER – 41

Wilderness adventures: Using wild germplasm to sustain genetic improvement of cultivated lentil. A. Tullu¹, S. Vail², J. Fiala³, B. Haçikamiloğlu⁴, H. Yuan¹, M. Lulsdorf¹, K. Bett¹, and A. Vandenberg¹. ¹University of Saskatchewan, Saskatoon, Saskatchewan, Canada; ²Agriculture and Agri-Food Canada, Saskatoon, Saskatchewan, Canada; ³Bayer Crop Science, Saskatoon, Saskatchewan, Canada; ⁴Harran University, Sanliurfa, Turkey.

Plant breeding relies heavily on intensive use of favorable alleles present in cultivated germplasm. This can lead to narrowing of the genetic base in comparison to landraces or wild species. The phenotypic profiles of non-cultivated germplasm sources of lentil have been partially documented for potential use in germplasm improvement. These include the progenitor subspecies, *Lens culinaris* ssp. *orientalis* and other species for sources of resistance to major abiotic and biotic stresses including winter hardiness, drought tolerance, and resistance to rust, vascular wilt, ascochyta blight and the parasitic plant known as broomrape (*Orobanche* spp.). Comparisons across the set of 6 wild species suggest that a high frequency of favorable genes are available from *L. ervoides*. This variation can be accessed with the aid of embryo rescue. Interspecific crosses between *L. culinaris* and *L. orientalis*, *L. odemensis*, *L. tomentosus*, *L. lamottei* and *L. nigricans* have been obtained from different research groups around the world. At the Crop Development Centre, we have successfully developed interspecific recombinant line (RIL) populations between cultivated and wild species. These populations are characterized for resistance to anthracnose as well as variability for morphological characters such as branches per plant, flowering date, maturity, seed yield per plant, plant height, etc. in the field and under greenhouse conditions. We have targeted a breeding approach combining evaluation of interspecific RILs and repeated backcrosses of selected RILs to adapted cultivars to transfer desirable traits. Breeding lines are under evaluation in yield trials. Preliminary results indicated that 13% of multiple backcross breeding lines exceeded the mean yield of check cultivars. Further evaluation of the variability in the overall pool of germplasm, at the nucleotide level, has been initiated to further advance cultivar development. The NAPGEN EST project initiative and an Agricultural Development Fund project have been completed. These genomic resources together with intraspecific and interspecific genetic populations will accelerate the creation of genetic maps, association maps, QTLs and marker assisted selection (MAS) technologies for implementation in the lentil breeding program. The overall strategy is to use genotyping technologies to allow deployment of genes responsible for economic traits of interest to producers, exporters and consumers.

POSTER – 42

Techniques for quantifying nitrogen fixation of pulse crops on the Canadian prairie. X.Y. Wang¹, Y.T. Gan¹, C. Hamel¹, and R.L. Lemke². ¹Semiarid Prairie Agriculture Research Centre, Agriculture and Agri-Food Canada, Gate #3, Airport Road East, Swift Current, Saskatchewan, S9H 3X2. ²Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, Saskatchewan, S7N 0X2.

The estimated quantity of N fixed by a pulse crop can vary largely depending on the estimation methodology employed. This study determined the relative consistence of three techniques: N¹⁵ natural abundance with barley as reference crop (NAB), N¹⁵ natural

abundance with flax as reference crop (NAF), and N^{15} enriched isotope dilution (NID). The study was conducted in 2008 and 2009, at Swift Current, Saskatchewan, with various cultivars of pea, chickpea, lentil, fababean and lupin. Averaged across all crop species, the N fixation estimated using NAB, NAF and NID methodologies was 51, 64 and 40 kg N ha¹⁵ in 2008, respectively, and the corresponding values were 23, 21 and 26 kg N ha¹⁵ in 2009. Dry conditions in 2009 lowered N fixation. The growing season precipitation in 2009 was 65 mm, compared to 110 mm in 2008, and 80 mm of the long-term (1970-2009) average. In 2008, NAB and NAF estimation generated greater N fixation values than NID method. In the drier 2009, however, the NID method generated the similar value of N fixation as NAB and NAF. Significant effect of year \times method (<0.01) was primarily attributed to the relatively higher value of NID among the three techniques in 2009 compared to its lowest value among three techniques in 2008. Our results indicated that NID method is more consistent than NAB or NAF in estimating N fixation of pulse crops and is less affected by weather conditions.

POSTER – 43

Ureide concentrations in faba genotypes. R. Bueckert, J. Pritchard, and D. Broersma. Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, S7N 5A8.

Faba (*Vicia faba*) is classified as a cool season crop like pea and lentil, having amino acid metabolism where the main transport forms of N from N_2 fixation are typically the amides glutamine or asparagine, or amino acids aspartate and glutamate. But faba may have N_2 fixation metabolism in the shoot that appears to be intermediate between cool season pulses and warm season legumes like common bean (*Phaseolus*) and soybean. Warm season legumes use ureides, which are non-structural cyclic amino acids like allantoin and allantoate, as the major form of N arising from N_2 fixation. Ureides are an efficient means of supplying amino N to the shoot, and may play a role in more stress-tolerant N_2 fixation metabolism, making the crop better suited to dryland production. Our goal was to measure the ureide concentrations in a range of 15 genotypes (cultivars and breeding lines) of faba at various times during reproductive development at two locations in Saskatchewan, 2009. We measured ureides by a colorimetric assay for leaves, stem and pod material at flowering, mid pod fill, and close to physiological maturity. The presence and amount of ureides will be related to the N content of the various shoot organs. Ultimately, we would like to use ureides and the ratio of certain amide amino acids to screen wide ranges of genotypes for a more stress tolerant faba.

POSTER – 44

The feasibility of winter pulses grown in Alberta agro-ecological environments. M.A. Olson¹, B. Henriquez¹, C.F. Hoy¹, K. E. McPhee², R. H. McKenzie³, A. Middleton³, P. Pffiffner³, K. Coles⁴, M. Bandara⁵, A. Kruger⁵, D. J. Bing⁶, D. Beauchesne⁶, K.F. Chang⁷, and R. Bowness⁷. ¹Alberta Agriculture and Rural Development, 4709 - 44 Ave, Stony Plain, Alberta, T7Z 1N4; ²North Dakota State University, Fargo, North Dakota, USA; ³Alberta Agriculture and Rural Development, Lethbridge, Alberta; ⁴Southern Applied Research Association, Lethbridge, Alberta; ⁵Alberta Agriculture and Rural Development, Brooks, Alberta; ⁶Agriculture and Agri-Food Canada, Lacombe, Alberta; ⁷Alberta Agriculture and Rural Development, Lacombe, Alberta.

The objective of this study was to assess whether existing germplasm of selected winter pulse species, field pea, lentil and faba bean, is adapted to the climatic conditions of Alberta, Canada. The test sites were established at Lethbridge [N 49° 41' 39", W 112° 49' 58", elevation 910 m (2,986 ft)], Brooks [N 50° 33' 51", W 111° 53' 56", elevation 760 m (2,493 ft)], Lacombe [N 52° 28' 6", W 113° 44' 13", elevation 850 m (2,789 ft)] and Edmonton [N 53° 34', W 113° 31' 53", elevation 668 m (2,192 ft)]. Two yellow cotyledon winter pea cultivars, Specter and Windham, one winter red lentil cultivar Morton, one winter tannin-type faba bean cultivar Diva were seeded in the fall of 2008 using three seeding rates (1.0X (normal), 1.5X, 2.0X) and three seeding dates at 10 day intervals, and treatments were arranged in a randomized complete block design with four replicates. In the spring 2009, two spring pea cultivars Cutlass (yellow cotyledon) and Cooper (green cotyledon), one red spring lentil cultivar CDC Redberry, and one zero tannin spring faba bean cultivar Snowbird, were seeded in early spring at three seeding rates. Survivability of winter pulses varied with location, seeding date and seeding rate. The furthest north location, Edmonton, had 0% survivability regardless of winter specie. Winter faba bean did not survive at any of the locations. As well, winter lentil did not survive at Lacombe and survivability % was poor at Brooks (range 0.2 – 6.4%). The most southerly location, Lethbridge, faired much better with mean survivability for winter lentil (52-79 %). As for winter pea, the range for mean survivability % was: Lacombe (1-56%); Brooks (7-33%); Lethbridge (61-116%). These results indicate that winter pulses, particularly, winter pea has a production potential mainly in southern regions of Alberta.

POSTER – 45

Acidification, microbial growth, physical and rheological properties of yogurt supplemented with lentil flour. F. Zare¹, J.I. Boye², V. Orsat¹, C. Champagne², and B.K. Simpson³. ¹Bioresource Engineering Department, McGill University, QC; ²Agriculture and Agri-Food Canada, QC; ³Food Science & Agricultural Chemistry Department, McGill University, QC.

Prebiotic and probiotic yogurt were reported to be among the fastest growing food sub-sectors in 2009 according to the Canadian Dairy Commission due to their high nutritional benefits. Yogurt could be further enriched with prebiotics via supplementation with lentil ingredients containing high amounts of protein, fibre and vitamins. In this study yogurt and probiotic beverages were supplemented with 1-3% (w/v) lentil flour and compared to 1-3% (w/v) skim milk powder-supplemented and control yogurt in terms of acidification trend, microbial count (*Streptococcus thermophilus* and *Lactobacillus bulgaricus*) as well

as physical (pH, syneresis, and colour) and rheological (dynamic oscillation temperature sweep test at 4-50 °C) properties. Acidification measurement after 4 hours fermentation showed lower pH in supplemented samples in comparison with non-supplemented control ($p < 0.05$). Yogurt with 1-3% lentil flour was not significantly different from 1-3% skim milk supplemented yogurts in terms of microbial count (CFU) ($p < 0.05$). During storage pH decreased from ~4.5 to ~3.5 after 14 days in all samples, however pH reduction was significantly smaller in 2% and 3% lentil-supplemented samples after 28 days. Lentil supplementation reduced syneresis in comparison with non-supplemented samples. Colour values “a” and “L” were not significantly different in all samples and they remained constant after 28 days. The results are promising and suggest that lentil ingredients could potentially be considered for use in yogurt- and probiotic-type applications.

POSTER – 46

Angiotensin I-converting enzyme *in vitro* inhibitory activity of nine *Phaseolus vulgaris* legume tryptic hydrolysates. X. Rui^{1,2}, J.I. Boye², C. Barbana², B.K. Simpson³, and S.O. Prasher¹. ¹Bioresource Engineering Department, McGill University, QC; ²Agriculture and Agri-Food Canada, QC; ³Food Science & Agricultural Chemistry Department, McGill University, QC.

In the present study, *in vitro* angiotensin I-converting enzyme (ACE) inhibitory properties of 9 varieties of beans (*Phaseolus vulgaris*) namely white, pinto, pink, cranberry, black, great northern, light red kidney, dark red kidney and small red were investigated. Trypsin was employed to hydrolyze the protein isolates (PIs). The highest ACE inhibitory activities were found in white (IC₅₀ of 200 ± 11 µg/mL) and small red bean hydrolysates (IC₅₀ of 170 ± 10 µg/mL), whereas black bean hydrolysate presented the lowest activity (IC₅₀ of 406 ± 8 µg/mL). Bean tryptic hydrolysates were subsequently characterized by electrophoresis and reverse phase high performance liquid chromatography (RP-HPLC). Results showed that all investigated hydrolysates had predominant proteins/peptides with molecular mass (MM) of ~25K. Dissimilar profiles were obtained from cranberry and light red kidney hydrolysates which yielded extra bands with MM of ~16K. The RP-HPLC chromatograms for these two varieties also differed by having more intensive peaks. Protein hydrolysate from black bean had extensively associated peptides/proteins, whereas white and great northern bean hydrolysates presented fewer bands with high MM and larger number of peaks with lower retention times in the RP-HPLC chromatogram indicating higher susceptibility to trypsin. The results show that differences in the protein composition and peptide profiles of the nine *Phaseolus vulgaris* protein hydrolysates may affect their *in vitro* ACE inhibitory properties.

POSTER – 47

The feed value of field pea and five other annual crops harvested prior to seed fill. S.M. Ross¹, J.R. King¹, K.J. Lopetinsky², M.A. Olson³, and C.F. Hoy³. ¹Department of Agricultural, Food and Nutritional Science, University of Alberta, 4-10 Agriculture-Forestry Centre, Edmonton, Alberta, T6G 2P5; ²Pulse Research Consultant; ³Alberta Agriculture and Rural Development, Stony Plain, Alberta, T7Z 1N4.

Limited information is available about the feed value of annual crops that are salvaged for forage due to drought. In 2009, a cropping system study at 2 sites in central Alberta was used to assess the feed value of six annual crops prior to seed fill, at 10 weeks after seeding. The crops grown were field pea, barley, canola, flax, triticale and wheat. They followed field pea in the rotation and no N fertilizer was added. Spring rainfall was less than normal at both sites in 2009. Dry matter (DM) biomass yields averaged 3.29 Mg ha⁻¹ at Barrhead and 3.54 Mg ha⁻¹ at St. Albert. The N yields of biomass averaged 85 kg N ha⁻¹ at Barrhead and 106 kg N ha⁻¹ at St. Albert. Feed values were good, with mean protein content of 18% and mean relative feed value (RFV) of 128. Flax had lower DM yields than the other crops. Barley and triticale were among the higher yielding crops but had lower N content. Canola biomass had higher N yields (117 kg N ha⁻¹ at Barrhead and 162 kg N ha⁻¹ at St Albert) than the other crops. Forage quality indices ranged from: 28 to 56% for neutral detergent fibre (NDF), 20 to 31% for acid detergent fibre (ADF), and 2 to 7% for lignin. Dicot crops (pea, canola and flax) had lower NDF values (28 to 40%) than the monocot crops (barley, triticale and wheat) (48 to 56%). Lignin values were higher for the dicot crops (4 to 7%) than the monocot crops (2 to 3%). Field pea biomass yields were 3.2 to 3.4 Mg ha⁻¹ with protein content of 15 to 25%, N yields of 83 to 127 kg N ha⁻¹, NDF of 28 to 36%, ADF of 20 to 26%, lignin of 4 to 5%, and RFV of 159 to 189. Field pea had greater relative feed value than cereal crops due to lower concentrations of resistant fibre.

POSTER – 48

Physicochemical and functional properties of fiber fractions from pulses. N. Wang, R. Toews, and L. Maximiuk. Canadian Grain Commission, Grain Research Laboratory, Winnipeg, Manitoba, Canada.

This study was aimed to investigate the physicochemical and functional properties of fiber fractions from field pea (*Pisum sativum*), lentil (*Lens culinaris*) and chickpea (*Cicer arietinum* L.), and to determine the relationship between those properties. Fiber fractions from several varieties of field pea, lentil and chickpea were prepared using a laboratory wet milling procedure. Physicochemical and functional properties of those fiber fractions were determined according to published methods. The fiber fractions contained 663.2 to 804.6 g kg⁻¹ of total dietary fiber, 61.1 to 171.1 g kg⁻¹ of protein, 102.7 to 195.6 g kg⁻¹ of starch, and 2.5 to 10.5 g kg⁻¹ of fat. Fiber fractions from pea and Kabuli chickpea displayed significant higher fat absorption than that from lentil and Desi chickpea. Pulse fiber fractions exhibited significantly higher swelling capacities and water retention capacities in comparison to commercial pea cotyledon fiber. Fat absorption of pulse fiber fractions was positively correlated with specific surface area ($r=0.840$, $p<0.001$) but negatively correlated with mean particle size ($r=-0.916$, $p<0.001$). Pulse fibers would have potential in various food applications, such as bakery and meat products, due to their superior water hydration and retention properties.

POSTER – 49

Comparison of protein films mechanical properties made from common dry bean (*Phaseolus vulgaris*) varieties and storage protein deficient lines. L.S. Chia¹, A. Jensen², L-T. Lim², C. Moresoli³, R.L. Legge³, and K.P. Pauls¹. ¹Department of Plant Agriculture, ²Department of Food Science, University of Guelph, Guelph, Ontario, ³Department of Chemical Engineering, University of Waterloo, Waterloo, Ontario.

Protein isolates from common dry bean can be cast with glycerol to produce films with good tensile strength and oxygen barrier properties that are suitable for packaging or other industrial applications. The protein isolates from normal dry beans (Hooter, AC Elk and OAC Rex) have similar protein profiles, but produced films of varying strength and elasticity. In particular, films from Hooter protein isolates had greater tensile strength and greater elongation than AC Elk and OAC Rex films. To further examine the influence of protein composition on the properties of the films, the storage protein deficient lines, SMARC1-PN1, SMARC1N-PN1 and SARC1 were used. SMARC1-PN1 and SARC1 have higher accumulations of arcelin protein, and SMARC1-PN1 is deficient in phaseolin. SMARC1N-PN1 lacks both arcelin and phaseolin protein but has a large accumulation of 54kDa protein and higher concentration of protein from 70 to 80 kDa. Films produced from SARC1 had weaker tensile strength as compared to the rest of the films. Films produced from SMARC1N-PN1 were very strong compared to the rest of the films tested. During 4 weeks of storage, the aging process had strong effects on the mechanical properties of the protein films made from Hooter, AC Elk, OAC Rex and the mutants SMARC1-PN1, SARC1 and Sanilac. However, aging had no significant effect on the mutant line SMARC1N-PN1 protein film. Therefore, it seems that the higher molecular weight bean proteins (70 to 80kDa) play significant roles in the mechanical properties of the films.

POSTER – 50

Low phytic acid lentil: An answer for micronutrient malnutrition? C.-T. See¹, P. Thavarajah^{1,2}, D. Thavarajah² and A. Vandenberg¹. ¹Department of Plant Sciences/Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, S7N 5A8; ²Department of Cereal & Food Sciences, School of Food Systems, North Dakota State University, Fargo, North Dakota, USA 58108-6050.

Zinc (Zn) and iron (Fe) deficiencies are the most common forms of micronutrient malnutrition in the world. Zn plays a role in immune function, protein synthesis, DNA synthesis, and catalytic activity of enzymes. Fe is an essential component of proteins involved in oxygen transport and the regulation of cell growth and differentiation. Approximately one-third of the world's population live in regions with high risk of Zn deficiency. Almost 50% of the population in developing countries has anemia caused by Fe deficiency. Phytic Acid (PA) is an antinutrient naturally present in seeds of all cereal and legumes crops. It plays three physiological roles in the seed: phosphorus storage, energy storage, and triggering cessation of metabolism to ensure seed dormancy. However, when consuming food that contains phytic acid along with micronutrient (e.g. Fe, Zn, Ca, Mg, K), it will form phytate salts, which cannot be broken down by monogastric animals including humans due to the lack of the digestive enzyme phytase. Our studies have shown that lentil has low PA. PA concentration increases when lentil

plants are exposed to rising temperature during seed filling. In contrary, lentils grown under cooler temperatures remained a good source of Fe and Zn and low PA concentrations. Lentil is a whole food rich in Zn and Fe and low in phytic acid and can play an important role in alleviating some forms of micronutrient malnutrition.

POSTER – 51

Cooking and canning quality of selected dry bean genotypes grown in Manitoba. G. Boux¹, A-S. Bellido¹, L. Malcolmson¹, P. Frohlich¹, P. Balasubramanian², A. Hou³, and R. Conner³. ¹Canadian International Grains Institute, 1000-303 Main St, Winnipeg, Manitoba, R3C 3G7, ²Agriculture and Agri-Food Canada Research Centre, Lethbridge, Alberta, T1J 4B1, ³Agriculture and Agri-Food Canada Research Centre, Morden, Manitoba, R6M 1Y5.

Canada exports 80% of its dry bean production, making it a very important cash crop in Manitoba. Beans grown in this region however, are recognized as having variable cooking and canning qualities which processors find undesirable. The objective of this study was to determine the effects of genotype, site (location x year combination), and the genotype x site interaction on the cooking and canning quality of dry beans grown in Manitoba. Selected dry bean genotypes (35) were comprised of 8 market classes and were grown in replicated trials in four locations over two crop years. Cooking quality was determined by measuring the cooking time of soaked beans using the automated Mattson bean cooker. Beans were canned using a modified laboratory canning protocol and quality was determined by measuring the hydration coefficient, clumping, percent washed drain weight and appearance of the canned beans. Significant differences were found among genotypes and sites and there was a significant genotype x site interaction for all quality attributes with the exception of the clumping characteristic. Overall, the Manitoba grown beans examined in this study demonstrated acceptable cooking and canning quality attributes.

POSTER - 52

Lentils (*Lens culinaris* L.) as an ingredient in emulsified ovo-vegetarian sausages: nutritional, sensory and physicochemical property evaluation. H. Tharangani¹, D. Amarakoon¹, J. Vidanarachchi¹, H.W. Cyril¹, K. Samarasinghe¹, A. Vandenberg², P. Thavarajah^{2,3}, and D. Thavarajah³. ¹Faculty of Agriculture, University of Peradeniya, Peradeniya, Sri Lanka; ²Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8; ³Department of Cereal & Food Sciences, School of Food Systems, North Dakota State University, Fargo North Dakota, USA 58108-6050.

More than 30% of the Sri Lankan population is deficient in selenium (Se), iron (Fe) and zinc (Zn). Lentil (*Lens culinaris* L.) is an excellent source of complex carbohydrates, protein (20-30%), dietary fibre, and a range of micronutrients (Se, Fe, and Zn) combined with low concentration of phytic acid. Therefore, incorporation of lentil may increase the micronutrient concentration in vegetable based sausages as a whole food ingredient to increase micronutrient intakes, especially for vegetarian populations. The current study was carried out to determine the micronutritional, sensory and physicochemical changes of ovo-vegetarian sausages using lentils as a substitute for textured vegetable proteins.

The Canadian and locally available lentils were added up to 17% to replace vegetable proteins. Addition of Canadian grown lentils significantly increased Se and Fe concentrations compared to locally (in Sri Lanka) purchased non-Canadian lentils (Se: 150 vs. 94 ppb and Fe: 44 vs. 41ppm). With increased percentage of lentil in ovo-vegetarian sausage, Se, Fe and Zn concentrations increased with both lentil types. Preliminary sensory quality and physicochemical data showed favourable results with addition of both lentil types. Therefore, lentils could be considered as a good protein substitute to increase Se, Fe and Zn micronutrients in sausage products.

POSTER – 53

Capturing market opportunities for Canadian pulses: Pulse flour milling and utilization project description. H. Maskus. Canadian International Grains Institute, 1000-303 Main Street, Winnipeg, Manitoba, Canada R3C 3G7.

The Canadian International Grains Institute (CIGI) will embark on a Pulse Flour Milling and Utilization project to explore the processing of pulses into flours for use in food products. Working together with Pulse Canada, industry partners, and other food development centres across Canada, the four-year project is funded through Agriculture and Agri-Food Canada's Canadian Agricultural Adaptation Program (CAAP) with financial support from the Saskatchewan Pulse Growers, the Alberta Pulse Growers and the Canadian Special Crops Association. The primary activities in this project are twofold, firstly to compare the composition and functional properties of flours made from various pulse market classes using a variety of milling technologies, and secondly to optimize the performance of pulses in the application of pulse flours in a range of food products. The project has been designed to enhance Canada's capacity to produce value-added, high-quality pulse flours and pulse-based foods. Several project deliverables have been identified to accomplish this. Technical knowledge and expertise related to the production of pulse flours will be investigated systematically to determine the impact of various milling technologies of physical and functional properties of the flours. This technical knowledge will be disseminated to the Canadian Pulse Processing Industry through various methods including webinars, technical bulletins and trade articles. Functional flour knowledge will then be transferred to product development applications to ensure that the optimal pulse ingredient is used to produce the highest quality food products. Interested food industry partners will be engaged from the onset of this product development phase to encourage their participation and the utilization of the pulse ingredients developed from this project. By creating commercial opportunities and developing a strong knowledge base this project will create an enhanced pulse milling industry in Canada.

POSTER – 54

Worldwide dry bean germplasm collections useful for cultivar development for production in Canada. A. Hou¹, R.L. Conner¹, V. Nguyen², Y. Cui², and P.

Balasubramanian³. Agriculture and Agri-Food Canada, ¹Morden Research Station, Morden, Manitoba, R6M 1Y5; ²Southern Crop Protection and Food Research Centre, London, Ontario, N5V 4T3; ³Lethbridge Research Centre, Lethbridge, Alberta, T1J 4B1.

Dry bean (*Phaseolus vulgaris* L.) genetic diversity in Canadian breeding programs is limited and cultivars especially black beans generally lack resistance to anthracnose. One hundred sixty black bean accessions originated from twenty countries were evaluated for agronomic traits, resistance to anthracnose races 73 and 105, and storage protein profiles. The collections were grown in the greenhouse and field in 2008 and 2009 at the Morden Research Station. Thirty five accessions were photoperiod-sensitive. Significant variation was observed in agronomic traits that included growth type, maturity, lodging resistance, pod colour, seed size, seed shape, seed coat pigmentation intensity, and yield potential. Artificial inoculation in growth chambers identified 47 accessions that were resistant to anthracnose race 73 and 46 accessions resistant to race 105. Forty three accessions were resistant to both races of 73 and 105. Three lines were resistant to race 105, but susceptible to race 73 which needs to be confirmed. Polyacrylamide gel electrophoresis (PAGE) revealed major seed storage proteins at approximately 42 KDa. Most banding variation was observed in peptides with size ranging 24-32 KDa. Germplasm collections with desirable agronomic traits, anthracnose resistance and unique protein profiles may provide diverse materials for dry bean cultivar development and genetic research.

POSTER – 55

Double, double, toil and trouble – New technologies for lentil. H.Y. Yuan, M.M.

Lulsdorf and A. Vandenberg, Crop Development Centre, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8.

Lentil is an economically important pulse crop for Saskatchewan and Alberta produced mainly for the export market. Double haploid (DH) technology can significantly reduce the time required for developing new cultivars through instant homozygosity and by increasing the selection efficiency due to the reduced population size required for screening. In our study, anther culture of CDC Maxim and CDC breeding line 3156-11 were used to develop DH technology for lentil. Our results showed that a combination of a 20/17°C day/night temperature regime for donor plant growth and a 7-day cold pretreatment of buds induced good symmetrical nuclei division. For buds harvested from the lower (10°/5°C) day/night temperature regime, a heat shock treatment at 32.5°C for 18 h could induce good symmetrical nuclei division. A combination of cold treatment with electroporation using three pulses of either 250 V or 500 V with 25 µF or centrifugation using 168g for 3 min, or a combination of heat shock with a 5 µM trifluralin treatment had no side effect on microspore viability. A modified Gamborg's B₅ medium with four organic supplements (riboflavin, calcium pantothenate, glycine, and glutamine) promoted callus production, but embryo-like-structures (ELS) or embryos were not generated. Extensive microscopic observations showed that microspore nuclei division ceased after the first symmetrical division and most of the microspores died. Further study showed that the anther somatic cells exerted a negative effect on

microspore viability under present culture conditions. Therefore, current experiments are focused on the continued division of microspore nuclei by using isolated microspore culture instead of anther culture.

POSTER – 56

Genetic diversity of selected chickpea elite lines and their progenitors based on microsatellite markers. Marwan¹, T. Warkentin¹, A. Sharpe², and B. Taran¹.

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Understanding the genetic variation of the germplasm pool and breeding lines of chickpea (*Cicer arietinum* L.) has a pre-eminent role in crop improvement for yield and adaptive potential to cope with changing environmental conditions. We tested 96 chickpea genotypes representing elite lines and their progenitors, to determine the Linkage Disequilibrium (LD) based on microsatellite polymorphisms. Two-hundred and twenty microsatellite markers will be tested to estimate the genetic relationship among those 96 chickpea genotypes. Analysis of the first 14 genomic microsatellite markers indicated that the average number of alleles per marker was 13.6 with a range from three to 29 and a mean gene diversity of 0.70. Principal Coordinate analysis was done by using genetic distance from GenAlEx Software (<http://www.anu.edu.au/BoZo/GenAlEx/>). Clustering individuals into populations (population structure) on the basis of multi-locus genotypic data was performed by simulating Markov chain Monte Carlo (MCMC) algorithm implemented in STRUCTURE program. Four populations (ΔK) were estimated based on the highest log probability of K. However, some individuals were found slightly interchanged between clusters. SSR allele diversity information generated in this study will be used to quantify the degree of relationship in chickpea germplasm more accurately.

POSTER – 57

Development of temperature-switch PCR (TS-PCR) markers for SNP genotyping in common bean. K. Yu¹, B. Zhang¹, C. Shi¹, and A. Navabi². ¹Agriculture and Agri-Food Canada, Greenhouse and Processing Crops Research Centre, Harrow, Ontario, N0R 1G0; ²Agriculture and Agri-Food Canada/University of Guelph Bean Breeding Program, Department of Plant Agriculture, Crop Science Building, University of Guelph, Guelph, Ontario, N1G 2W1.

Single nucleotide polymorphism (SNP) markers are by far the most common form of DNA polymorphism in a genome. It was estimated that common bean (*Phaseolus vulgaris* L.) has an average of one SNP in 88 base pairs. Based on an estimated common bean genome size of approximately 600 Mb, there would be 6 to 7 million SNPs available in the common bean genome. Currently, there are several platforms available for automatic analysis of SNPs, such as the KASPar SNP Genotyping System and the Illumina GoldenGate SNP Genotyping System. However, these systems require special equipment that is not affordable to the average molecular breeding lab. Therefore, a simpler marker system is required for effective use of SNPs in bean breeding. Temperature-switch Polymerase Chain Reaction (TS-PCR) has proven to be a robust

assay for reliable amplification and genotyping of SNPs. In this study, a number of TS-PCR markers have been developed for known SNPs present in common bean. Since TS-PCR is a biphasic three or four-primer PCR system with a universal primer design that permits amplification of the target locus, in the first phase of thermal cycling before switching to the detection of the alleles, it can simplify assay design for a range of commonly used single-marker SNP genotyping methods, and reduce the requirement for individual assay optimization and operator expertise in the deployment of SNP assays.

POSTER – 58

Development of SNP markers for lentil breeding. Q. Lu¹, P. Vijayan¹, L. Sanderson¹, A. Vandenberg¹, A. Sharpe², and K.E. Bett¹. ¹Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, ²NRC-PBI, Saskatoon, Saskatchewan.

The development of single nucleotide polymorphism (SNPs) markers linked to loci controlling key agronomic traits and seed characteristics is important for future crop improvement. The feasibility of such marker-assisted selection strategy in lentil breeding programs is severely constrained by the lack of robust markers linked to important traits. The objective of our research is to design lentil SNP primers and develop SNP-based genotypic markers. A large number of candidate SNPs were identified, and primers have been designed for KASPar assays (KBiosciences). A subset of 33 KASPar primers was tested on 11 lentil genotypes to ascertain which are polymorphic in key mapping populations. Polymorphic SNPs have been mapped in the recombinant inbred line populations LR18 (Robin x 964a) and LR39 (Eston x PI320937) along with microsatellite markers that will anchor the new maps to already published lentil maps. LR18 has been phenotyped for various disease resistance, agronomic and seed characteristics and LR39 has been chemotyped for micronutrient content. These genotypic and phenotypic data will be analysed to detect SNPs linked to relevant quantitative trait loci and identify potential molecular markers for these traits.

POSTER – 59

Genetic control of post-harvest darkening in pinto bean. H. Elsadr¹, Q. Lu¹, L. Wright², K.P. Pauls², and K.E. Bett¹. ¹Dept. of Plant Sciences, University of Saskatchewan, Saskatchewan; ²Dept. of Plant Agriculture, University of Guelph, Ontario.

Post harvest darkening of the seed coat is an undesirable characteristic in certain market classes of dry bean, particularly pinto, cranberry and carioca, and represents a problem for producers and consumers. There are at least three post harvest darkening phenotypes: non darkening (ND), slow darkening (SD) and regular darkening (RD). The gene *J* has been associated with after-darkening in beans and *jj* beans tend not to darken with age. The SD phenotype is also controlled by a single recessive gene. A cross between a SD pinto and a ND cranberry was developed and a population of F₂ individuals and associated F₃ families was phenotyped for darkening. DNA was obtained from the F₂ individuals and mapping of what appears to be two unlinked, but epistatic, genes is being carried out.