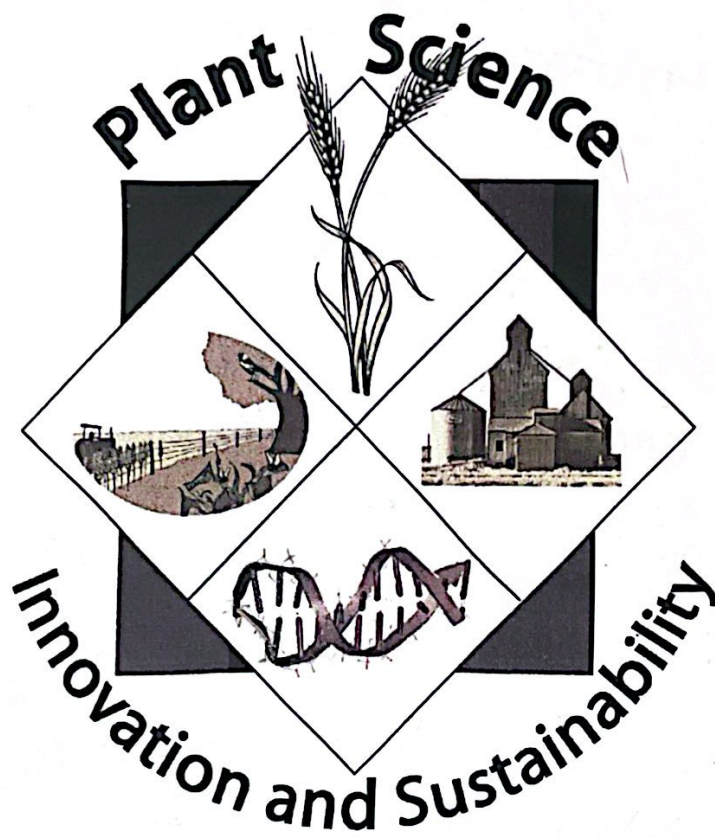


# 19<sup>th</sup> Annual Plant Science Graduate Student Symposium

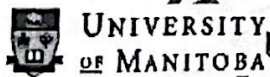


UNIVERSITY  
OF MANITOBA

**March 14-15, 2003**  
**University of Manitoba**  
**Winnipeg, MB**

## The 19<sup>th</sup> Annual Plant Science Graduate Student Symposium

The Plant Science Graduate Student Symposium was started in an effort to bring graduate students from different universities together and have them present their research in an informal atmosphere. This symposium provides the opportunity for graduate students to exchange ideas and introduces them to the research work of fellow graduate students. This event also provides an opportunity for graduate students to develop and improve their public speaking skills and to gain experience in the development and use of various visual aids, as a means of making a polished presentation. The location of the symposium rotates among the University of Manitoba, the University of Saskatchewan and North Dakota State University. Graduate students in the general area of Plant Science from other universities are also invited to attend and participate in the symposium.



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# The 19<sup>th</sup> Annual Plant Science Graduate Student Symposium

9:45 am Coffee Break

10:00 am **Haley Catton**, An Evaluation of Bur Oak (*Quercus macrocarpa*) Decline in the Urban Forest of Winnipeg, Manitoba

10:15 am **Sreedhar Alwala**, Studies on Slow Rate of Dry Matter Disappearance of Barley in Ruminants

10:30 am **Anthony R. Szumigalski**, A Comparison of Annual Monoculture versus Polyculture Cropping Systems in Manitoba.

Session II: **Plant Protection**  
**Chair: Rob Duncan**  
**Judges: Dr. Lakhdar Lamari**  
**Dr. Dilantha Fernando**  
**Dr. Fouad Daayf**  
**Rajesh Ramarathnam**

10:45 am Judge Introductions

11:00 am **Nadejda Krasheninnik**, Spike Morphology and FHB Reaction in Barley.

11:15 am **Quinn A. Holtslag**, Environmental Conditions Required for Stimulating Release of *Entomospodium mespili* Conidia.

11:30 am **Guotai Yu**, Evaluation of Some American and East Asian Varieties for Resistance to Fusarium Head Blight.

11:45 am **Yu Chen**, Interaction Between Weakly and Highly Virulent Strains of *Leptosphaeria maculans* Leading to Induced Resistance in Canola.

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# The 19<sup>th</sup> Annual Plant Science Graduate Student Symposium

12:00 am **Karl Schreiber**, Evaluation of the Role of a Protein Disulfide Isomerase in Plant Defense Responses.

12:15 am **Gayin L. Graham**, Effects of Spore Concentration and Plant Growth Stage on the Synergy of a Fungal Pathogen and Herbicides for Improved Control of Scentless Chamomile.

12:30 pm **Lunch**

**Session III: Plant Breeding and Genetics**

**Chair: Sharla Cowling**

**Judges: Dr. Murray Ballance**

**Dr. Rachel Scarth**

**Dr. Anita Brulé Babel**

**Darren Plett**

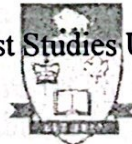
1:30 pm **Judge Introduction**

1:45 pm **Lisa L. Bergh**, Validation of Marker-Assisted Selection for Fusarium Head Blight Resistance QTL in Six-Rowed Barley.

2:00 pm **Suresh Bhamidimarri**, Efficiency of Marker-Assisted Selection over Phenotypic Selection for FHB Resistance in Durum Wheat.

2:15 pm **Yadeta Anbessa**, Genetic Analysis of Early Flowering, Short Internode Length and Double Podding Traits as Bases of Early Maturity in Chickpea.

2:30 pm **Juan Caffarel**, Leaf Rust Studies Using Bowman Backcross-Derived Lines.



2:45 pm **Bryan L. Gebhard**, Backcross Reciprocal Monosomic Analysis of FHB Resistance in Frontana Wheat.

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# The 19<sup>th</sup> Annual Plant Science Graduate Student Symposium

- 3:00 pm** Coffee Break
- 3:15 pm** **Zhang Chunzhen**, Implementation of Marker-Assisted Selection for Lodging Resistance in Pea Breeding
- 3:30 pm** **Clarissa de S. Barata**, SSR Polymorphisms and Heterosis Among Early Maize Inbred Lines.
- 3:45 pm** **Kenneth E. Lamb**, Mapping Genes Conferring Fusarium Head Blight Resistance in a Midwest Barley Accession C93-320-24.
- 4:00 pm** **Lasantha W.C. Ubayasena**, Evaluation of Genetic Diversity in the Genus *Echinacea* (Asteraceae) Using Genomic and Chloroplast DNA.
- 4:15 pm** **Ju Wang**, Analyzing SNP for Potato EST Data By Using StackPACK.
- 5:30 pm** Cocktails. Location: University Club
- 6:30 pm** Banquet. Location: University Club
- 7:30 pm** Awards Presentation
- 7:45 pm** Keynote Speaker: Mr. Paul Westdal
- 9:00 pm** Social at "Wise Guys on Campus"



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**Session I: Agronomy, Horticulture, and Plant Physiology**

**Nitrogen, Weed Control, and Moisture Conservation Benefits of Alfalfa Mulch Applied to Organically Grown Wheat.** Matthew Wiens and Martin Entz. Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2. Email: umwiens@cc.umanitoba.ca

Organic farming is best done in the context of mixed farming where soil building legume hay crops (i.e. alfalfa) are fed to livestock, and manure from livestock provides nutrients for crops. However, the time and labor requirements of animal husbandry may deter some farmers from attempting organic agriculture. An alternative may be a strip farming system where strips of annual crops are grown between strips of alfalfa. Instead of harvesting the alfalfa as hay, the alfalfa would be spread as mulch on the adjacent annual crops. The alfalfa mulch would provide nitrogen to the crop as it breaks down over the growing season. Other benefits of the mulch would be weed suppression and moisture conservation. After 3 years, the strips of land in alfalfa would be broken and annual crops would be planted, thereby exploiting the nitrogen fixation and other soil building contributions of the alfalfa. The annually cropped strips of land would be converted to alfalfa. The feasibility of such a system depends on how much benefit can be derived from the alfalfa mulch. This project is investigating the amount of nitrogen provided by alfalfa mulch to an organically grown wheat crop. Alfalfa mulch is applied to the wheat crop after seeding and nitrogen uptake into the crop is measured throughout the growing season. The mulch treatments are being compared to chemical fertilizer treatments in terms of nitrogen uptake, yield, protein, weed growth, and soil moisture content. Previous studies done by Dr. Martin Entz's lab on the nitrogen benefits of alfalfa to subsequent crops will be used together with information from the mulch project to derive a nitrogen budget for the proposed alfalfa/annual crop strip farming system.

**Physiological and Molecular Responses of Winter and Spring Canola During Cold Acclimation.** Brian Schilling and Larry Gusta. University of Saskatchewan. Department of Plant Sciences, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada bss539@mail.usask.ca

Many plant species show an increase in freezing tolerance due to exposure to low, non-freezing temperatures. This response is known as cold acclimation and occurs due to biochemical adjustments in cells that result in numerous molecular and physiological responses. Not all plants have the ability to cold acclimate or they only acclimate slightly. Spring and winter canola, *Brassica napus*, were acclimated to -14.0 °C and -15.5 °C respectively, after 23 days of exposure to decreasing day / night temperatures and photoperiod. Spring and winter canola were then deacclimated to -6.0 °C and -9.0 °C respectively, after a 10 day exposure to 20 °C / 16 °C under a 16 hour photoperiod.

During deacclimation, winter canola continued vegetative growth due to incomplete vernalization and spring canola began to elongate and flower. Canola types were then reacclimated for 23 days to levels measured previously during acclimation. Deacclimation was fully reversible for both types. The cotyledons harvested from canola did not acclimate or acclimated slightly compared to the leaves. Molecular and carbohydrate analysis showed differences do exist with regards to gene regulation between the leaves and cotyledons of spring and winter canola. Transcript expression of previously characterized cold responsive genes was expressed at different levels, in both cotyledons and leaves harvested from spring and winter canola. Western analysis, using antibodies raised against various stress-induced proteins, showed the proteins of interest accumulated at different times during acclimation, deacclimation and reacclimation

**The Effect of Tillage versus Planting Dates on Weed Seedling Emergence.** Anastasie Kabanyana and Rene Van Acker. Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2 E-mail: anastakaba@hotmail.com

Knowing how tillage and planting dates affect weed seedling emergence can assist producers to employ better timing of management practices and therefore increase the effectiveness of weed control. The objective of this study was to determine the effect of various combinations of tillage systems and time of planting on weed seedling emergence quantity and periodicity. The study was conducted in the spring of 2002 at two sites (Carman and Winnipeg) at the University of Manitoba Research Stations. The emergence of the most dominant weed species was monitored in barley under four tillage regimes and two planting dates (early and late plantings). Weed seedling densities and volumetric soil moisture data were collected twice a week at each site and hourly temperatures were recorded using Tidbits. Preliminary data analysis shows that tillage did not affect total weed densities at one of the sites. However, significant differences were observed between treatments for foxtail spp. Fall no tillage-spring tillage (FNTST) tended to increase weed densities, whereas fall tillage-spring no tillage (FTSNT) reduced foxtail densities. The effect of seeding dates on weed emergence was only evaluated at the Carman site. Seeding dates did not significantly affect densities of total weed emergence. Even though there were no major differences between early and late plantings, late seeding seemed to increase total weed densities. Management periods significantly influenced weed emergence. Total weed biomass was not influenced by tillage and planting dates. Treatments did not affect the periodicity of weed emergence. Cumulative emergence increased with growing degree days (GDD, base 0). The preliminary results suggest that tillage and planting dates did not affect weed emergence. The next step is to investigate further how tillage and planting dates affect soil moisture and temperature in order to better understand and explain the lack of significant differences among treatments.

### **Germination Modeling and its Regulation Mechanism of Winterfat Seeds.**

Ruojing Wang and Yuguang Bai. Department of Plant Science, University of Saskatchewan, 51 Campus Drive, University of Saskatchewan, Saskatoon, SK S7N 5A8. Email: ruw819@mail.usask.ca

The timing of seed germination plays a critical role in the survival of plants in a nature ecosystem. Plants adapted to their local habitats have mechanisms for optimum germinating time to ensure survival. Since the seedling stage usually shows the highest mortality rates, the mechanisms of delaying germination and spreading germination time can be found in native plants for better seedling establishment. Thus the successful prediction of seed germination is fundamental to the control and the restoration of native vegetation, therefore the productivity and conservation of native grassland. Population-based modeling approaches to predict germination as the functions of temperature and/or water potential have been well developed in last two decades as thermal time ( $\theta_T$ ) and hydrothermal time ( $\theta_{HT}$ ) concepts. The accuracy of  $\theta_{HT}$  model, however, depends on  $\Psi$  range to which seeds are exposed, and the assumptions of  $\theta_{HT}$  model were found not always valid. Determining water and temperature threshold and their physiological determinants for germination will increase predictability of seedling establishment under field condition. Winterfat (*Ceratoides lanata* Pursh) is nutritious forage with superior quality and an important structural and diversity component of the native grassland of Saskatchewan. The preliminary results show that temperature threshold for winterfat seeds are varied with seed size and collection, the further study will focus on physiological base of the modeling approach

**Inheritance of Multiple Herbicide Resistance in Wild Oat (*Avena fatua*).** Jocelyn Karlowsky, Anita Brule-Babel, Rene Van Acker and Lyle Friesen. Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2. Email: jocelynk36@hotmail.com

Three wild oat populations comprised of individuals with multiple herbicide resistance to imazamethabenz, flumetrop, and fenoxaprop-P are currently being studied to determine the mode of inheritance and interaction of resistance traits in these populations. Populations originated from the Swan River region of Manitoba, Canada. All three populations were characterized by Friesen et al. (Weed Science 2000 48:532-540). Parents used to make the initial crosses were self-pollinated and resulting seedlings were screened with the three herbicides. This step was taken to ensure that only progeny from parents that were homozygous for the resistance trait were advanced to the next generation. Reciprocal crosses were made between the three resistant populations and a known susceptible population (UM5). F1 plants were self-pollinated to produce the F2 generation. F2 seedlings are being screened to determine the mode of inheritance of resistance to the three herbicides. F2 plants are also being self-pollinated to produce F3 families, which will be screened to confirm F2 results. Initial results suggest that



resistance to imazamethabenz is controlled by one dominant, nuclear gene in the three populations.

**Genomics of Cold Acclimation and Freezing Tolerance in *Brassicaceae*.** Nirmala Sharma<sup>1,2</sup>, Derek Lydiate<sup>1</sup> and Isobel Parkin<sup>1</sup>, <sup>1</sup>Agriculture and Agri-Food Canada, Saskatoon Research Center, 107 Science Place, SK, S7N 0X2. <sup>2</sup>Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, S7N 5A8.  
E-mail: sharmani@agr.gc.ca

Freezing stress is a major environmental constraint limiting crop productivity and distribution of plant species. Understanding the molecular mechanisms of freezing tolerance is important for developing strategies to improve crop plant response to the stress. Many temperate plants acquire freezing tolerance through an adaptive process called cold acclimation, in response to a period of low, non-freezing temperatures. Cold acclimation is associated with numerous physiological, biochemical and molecular changes, including alterations in gene expression, accumulation of compatible osmolytes and protective proteins. However, the contribution of each of these changes to the attainment of freezing tolerance remains to be fully understood. *Arabidopsis thaliana* has been employed as the model system to explore the mechanisms of cold acclimation. One of *Arabidopsis*'s relatives, *Thlaspi arvense*, exhibits a higher level of freezing tolerance and is capable of over wintering in Canadian Prairies, thus making it a good candidate for studying the mechanisms of cold tolerance and potentially a useful source of genes for cruciferous plants, including the agriculturally important *Brassica* species. The aim of this study is to uncover the biochemical and molecular mechanisms of cold acclimation and freezing tolerance in *T arvense*, and to compare the low temperature responses of *T arvense* with the model *Arabidopsis* and cultivated *Brassica napus*. A range of physiological and biochemical parameters will be studied to identify key processes and /or genes involved in cold acclimation and to correlate them with the acquisition of freezing tolerance. DNA microarrays will be used to monitor and compare global gene expression within and among these species. The expression pattern of candidate genes will be further confirmed using northern hybridization. Once confirmed, mutations in these candidate genes will be identified to further aid in their functional characterization.

**An Evaluation of Bur Oak (*Quercus macrocarpa*) Decline in the Urban Forest of Winnipeg, Manitoba.** Haley Catton and Bill Remphrey. Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2. Email: umcatton@umanitoba.ca

Winnipeg is the only major city in Western Canada to have a large, indigenous population of mature Bur Oak (*Quercus macrocarpa*) trees in its urban forest. However, in 1986, it was noticed that a substantial number of the city's oaks were showing signs of suffering, which continue today. A preliminary investigation revealed that not one single primary pathogen is causing major damage to the trees, but that a more complex problem

involving both abiotic and biotic factors, otherwise known as oak decline, is to blame. This disease is caused by a combination of chronic and acute factors that may be highly region-specific, meaning a local study of oak decline is needed. In an effort to find factors associated with oak decline in Winnipeg, individual tree characteristics and environmental conditions surrounding 190 oaks of various health classes within the city will be recorded and analyzed.

**Studies on Slow Rate of Dry Matter Disappearance of Barley in Ruminants.** S. Alwala, B. G. Rossnagel and T. Zatorski, Dept. of Plant Sciences, University of Saskatchewan, 51, Campus Drive, Saskatoon, S7N 1A8, SK. Email: sra581@mail.usask.ca

Barley grain, as feed, has one drawback versus corn in that it digests very rapidly in ruminants leading to metabolic disorders such as acidosis and bloat. Our research focuses on evaluation of barley germplasm exhibiting a slow rate of dry matter disappearance (DMD) (digestibility over time) based on single kernel characterization system (SKCS), acid extract viscosity (AEV), gross particle size, in situ digestibility studies and other methods which would screen the grain textural differences. The inheritance of the slow DMD trait would also be studied in the two RIL populations and DH lines generated at Crop Development Centre involving Valier (slow DMD) as a parent. In addition, molecular markers for the trait under study would be screened and the importance of hordoinoline proteins with gross particle size and slow DMD would be addressed. Till date, the results from SKCS and AEV didn't show up considerable variability among the entries studied. Further studies to address the slow DMD trait are underway.

**A Comparison of Annual Monoculture vs. Polyculture Cropping Systems in Manitoba.** Anthony R. Szumigalski and Rene Van Acker. University of Manitoba, Winnipeg, MB R3T 2N2. Email: umszumig@cc.umanitoba.ca

It is generally accepted that polycultures (intercrops) tend to have greater yields (i.e., over-yielding) than monocultures because of enhanced pest/weed control and complementary use of resources between component crops. In this field experiment we investigated a wheat-canola-pea intercrop system, including the three species mix, all pair combinations of the three crops and the sole crops at two sites in Manitoba, Canada in 2001 and 2002. All crop treatments were planted at the same total density (144 seeds/m<sup>2</sup>). The effects of the different crop combinations on weed emergence and biomass were studied. To determine microsite effects and possible mechanisms of resource use, soil temperature, soil water content, soil inorganic N levels and photosynthetically active radiation (PAR) at the soil surface were measured. We hypothesize that the most diverse cropping system (i.e., the three-crop intercrop) will have the lowest weed biomass because crops will occupy more niche space that would have been available to weeds.

Therefore, we also predict that the three-crop system will have the greatest overall use of resources. With the exception of the pea sole crop, the monocultures tended to have higher weed biomasses than the polycultures. The three-crop system had the lowest weed biomass of all the polycultures. The pea sole crop had the lowest weed biomass of all cropping systems, possibly due to greater canopy interception of light. In most cases the intercrops resulted in over-yielding (land equivalent ratio > 1) when compared to component sole crops.

## Session II: Plant Protection

**Spike Morphology and FHB Reaction in Barley.** Nadejda Krasheninnik and Jerome D. Franckowiak. Department of Plant Sciences, Loftsgard Hall, North Dakota State University, Fargo, ND 58102. Email: Nadejda.Krasheninnik@ndsu.nodak.edu

Spike morphology in barley, controlled by the six-rowed spike 1 (*vrs1*) locus located in 2HL, is associated with Fusarium head blight (FHB) severity, which is generally lower for most two-rowed genotypes than for six-rowed genotypes. The *vrs1.a* allele is present in most six-rowed cultivars and produces well-developed lateral spikelets, the *Vrs1.b* allele in two-rowed cultivars reduces lateral spikelets to sterile bracts with a rounded tip, and the *Vrs1.t* (*deficiens*) allele causes an extreme reduction in the size of lateral spikelets. Disease occurrence and severity were thought to be determined in part by the spike morphology, because reduced air-movement and higher humidity in case of six-rowed spikes were considered favorable for FHB onset. FHB resistance QTLs were mapped to the centromeric region of chromosome 2, close to the *vrs1* locus, suggesting that a genetic association between spike morphology and FHB reaction might exist. To test this hypothesis thirty-six cultivars and experimental lines, containing spike morphology variants *Vrs1.t*, *Vrs1.b*, and *vrs1.a*, were inoculated and screened for FHB resistance. The results suggest that barley spike morphology and FHB reaction may be independent traits associated only by linkage.

**Environmental Conditions Required for Stimulating Release of *Entomosporium mespili* Conidia.** Quinn Holtslag<sup>1</sup>, W.R. Remphrey<sup>1</sup>, W.G.D. Fernando<sup>1</sup>, R.G. St-Pierre<sup>2</sup>, R. Dill-Macky<sup>3</sup>. <sup>1</sup>Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2. <sup>2</sup>Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, S7N 5A8. <sup>3</sup>Department of Plant Pathology, University of Minnesota, St. Paul Minnesota, USA 55108-6030. Email: agiefever@hotmail.com

*Amelanchier alnifolia* Nutt., commonly known as saskatoon, is a native fruit bearing plant that has excellent potential as a diversification crop in Canada. Currently,

production is limited by the fungal pathogen *Entomosporium mespili*. A prototype splash-dispersed spore trap was used to trap water-splashed *E. mespili* conidia as they are moved in rainwater during precipitation events. Analysis of data from the spore trap showed that the number of conidia per ml of rainwater collected is not dependent upon the amount of rainfall during a precipitation event, or on the percent of infected leaf area in the field. However, the start of conidia trapping is associated with the start of exponential infected leaf area increase. The first disease symptoms appeared 5 d after the first precipitation event that occurred 3 d from the date of flowering, which suggests that initial conidia release from over-wintering acervuli, occurred before it was first observed in our study. We also found that conidia are primarily released during the first 2 h during a precipitation event. A mechanistic disease-forecasting model is currently being constructed to incorporate the results from this study with temperature and leaf wetness durations required for *E. mespili* conidia to infect saskatoon leaves.

**Evaluation of Some American and East Asian Varieties for Resistance to Fusarium Head Blight.** Guotai Yu. Department of Plant Sciences, North Dakota State University, Fargo, ND 58105-5051. E mail: Guotai.Yu@ndsu.nodak.edu

Fusarium head blight (FHB), caused by a number of *Fusarium* species (principally *Fusarium graminearum*), has been the most destructive disease of barley (*Hordeum vulgare*) in North America. The major damage in barley from FHB is reduction in grain quality caused by the presence of the toxin deoxynivalenol (DON). The barley grain that has more than 0.5 mg/kg DON will not be accepted by American malting and brewing industry. It has been one of the major goals of barley breeding programs to develop barley cultivars resistant to FHB. However, it has not been very successful so far. This likely is because the level of resistance to FHB was not high in the donor. No single barley cultivar or accession is being used on a wide scale as a source of FHB resistance. More resistant resources are needed for developing barley cultivars resistant to FHB. The objective of this study is to screen for more resistant introductions by comparing the severities of FHB among the American and East Asian varieties. Over 40 varieties were evaluated in mist-irrigated FHB nurseries. Barley plants were artificially inoculated with infected corn grains. Preliminary results suggest that some East Asian varieties have a desirable level of resistance to FHB, which might be used as a source of FHB resistance in breeding program.

**Interaction Between Weakly and Highly Virulent Strains of *Leptosphaeria maculans* Leading to Induced Resistance in Canola.** Yu Chen and Dilantha Fernando. Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2. E-mail: ychen89@hotmail.com

Blackleg, caused by *Leptosphaeria maculans* (anamorph = *Phoma lingam*), is a fungal disease of *Brassica* species worldwide and can cause devastating losses in canola. The pathogen occurs as weakly and highly virulent strains, which can be classified into four Pathogenicity Groups (PG) based on the phenotype interaction on cv. Westar, Glacier and Quinta. Strains in PG1 are weakly virulent (WV), whereas strains in PG2, PG3, and PG4 are highly virulent (HV). The goal of this experiment is to understand the interaction between weakly virulent and virulent strains and to investigate interactions leading to induced resistance. The trial consists of three strain combinations, i.e. PG1+PG2, PG1+PG3 and PG1+PG4. For each combination, three-inoculation treatments i.e. mixture of WV and HV strains, WV strain first and HV strain after, HV strain first and WV strain after, were conducted on the canola cotyledons of cv. Westar and Liberty Link cv. LG21S3. Each treatment has three replicates. Four time intervals (0, 12, 24 and 48 hrs) were set for each WV and HV inoculation combination series. Wound inoculation method was applied with a *L. maculans* pycnidial suspension ( $2 \times 10^7$  pycnidiospore/ml, 10  $\mu$ l/wound site). Lesion size was measured 12 days after the last inoculation. HV strains produced larger lesions than the WV strain. However, the lesion size was significantly reduced in all treatments when the WV strain was inoculated first, followed by a HV strain. The result was the same when WV and HV strains were co-inoculated. Treatments with inoculations of a HV strain first, followed by the WV strain indicated that lesion size was similar to HV strains inoculated alone. This study showed that the WV strain might induce resistance against a HV strain *in vivo*, which has significant implications to the control of blackleg of canola. The mechanism of induced resistance is being investigated at the present time.

**Evaluation of the Role of a Protein Disulfide Isomerase in Plant Defense Responses**  
Karl Schreiber. Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK. S7N 5A8 Email: schreiber@sask.usask.ca

Protein disulfide isomerase (PDI) acts as an important mediator of protein folding by catalyzing the oxidation, reduction, and isomerization of disulfide bonds. This activity may facilitate the response of plants to pathogen infection, specifically in terms of meeting the increased demand for correctly folded defense-related polypeptides. With this in mind, attempts were made to assess the role of PDI in plant defense, using *Arabidopsis thaliana* and *Brassica carinata* as model systems. Expression of the PDI gene was examined in *B. carinata* leaves exposed to defense-associated molecules such as methyl salicylate, methyl jasmonate, and copper chloride. Although the degree of induction varied, each compound did upregulate PDI transcription over a similar timeframe. As a more direct evaluation of PDI function, *A. thaliana* was transformed with an expression construct bearing PDI in the antisense orientation. Consequent reductions in PDI transcript levels were associated with increased levels of infection by various strains of *Pseudomonas syringae*.

**Effects of Spore Concentration and Plant Growth Stage on the Synergy of a Fungal Pathogen and Herbicides for Improved Control of Scentless Chamomile.** G.L. Graham<sup>1,2</sup>, G. Peng<sup>2</sup>, K.L. Bailey<sup>2</sup> and F.A. Holm<sup>1</sup>. <sup>1</sup>Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8. <sup>2</sup>Agriculture and Agri-Food Canada, Saskatoon Research Center, 107 Science Place, Saskatoon, SK S7N 0X2. Email: grahamg@agr.gc.ca

Scentless chamomile is a significant weed problem in western Canada, due in large part to its natural tolerance to herbicides. Field surveys have revealed a group of fungal pathogens that caused substantial damage to the weed when sprayed inundatively but the damage could be reduced substantially when low volumes were applied using conventional spray equipment, especially against the weed at more advanced growth stages. Based on extensive compatibility testing and synergy screening, a host-specific pathogen, *Colletotrichum* sp., was co-applied with selected herbicides to enhance the efficacy and reduce the rate of the pathogen. The herbicides utilized were 2,4-D ester and clopyralid plus MCPA ester at recommended label rates and treatments were applied to the weed at the 8- and 11-leaf stage. The pathogen was applied as conidia at  $2 \times 10^7$ ,  $7 \times 10^6$ ,  $7 \times 10^6$  and 0 spores  $\text{ml}^{-1}$  with or without herbicide present at 200 L  $\text{ha}^{-1}$  in a spray chamber. In general, as the pathogen dose increased, the fresh weight of treated plants decreased. When compared to chemical or pathogen treatments alone, the herbicide plus pathogen mixtures exhibited more effective weed control, especially at the 11-leaf stage with the highest dose of the pathogen. The benefit provided by the synergy varies depending on the pathogen/herbicide combination, pathogen dose and weed growth stage. Options for tank mixing this pathogen with 2,4-D ester or clopyralid plus MCPA ester are discussed.

### **Session III: Plant Breeding and Genetics**

**Validation of Marker-Assisted Selection for Fusarium Head Blight Resistance QTL in Six-Rowed Barley.** L.L. Bergh and R.D. Horsley, Department of Plant Sciences, North Dakota State University Fargo, ND 58105. Email: Lisa.l.Bergh@ndsu.nodak.edu

Fusarium head blight (FHB) of barley (*Hordeum vulgare* L.) has caused severe economic losses to growers in the upper Great Plains of the United States and the Prairie Provinces of Canada since 1993. Breeding of FHB resistant cultivars offers the best solution for growers since chemical and cultural control methods for FHB have been largely unsuccessful in barley. Several breeding populations segregating for FHB resistance will be screened using microsatellite markers found to be associated with FHB resistance in several mapping populations. It is our hope that these previously identified markers can be successfully used for marker-assisted selection in our breeding populations. In a separate study, we will screen new six-rowed sources of FHB resistance using the same

microsatellite markers previously mentioned. QTL for FHB resistance in barley mapping populations with Zhedar 1, Zhedar 2, Clho 4196, and Chevron as resistant parents have been found in similar chromosomal regions. If similar QTL for FHB resistance are found in the new sources of resistance, the time-consuming process of developing and screening a mapping population may not be needed.

**Efficiency of Marker-Assisted Selection over Phenotypic selection for FHB Resistance in Durum Wheat.** B. Suresh, E.M. Elias and S.F. Kianian, Department of Plant Sciences, Loftsgard Hall, NDSU, Fargo, ND 58105.  
E-mail: suresh.bhamidimarri@ndsu.nodak.edu

We are studying the efficiency of Marker Assisted Selection (MAS) for type II Fusarium Head Blight (FHB) resistance caused by *Fusarium graminearum* in two durum wheat populations derived from a Chinese hexaploid bread wheat source 'Sumai 3'. This study is based on the hypothesis that for a trait such as FHB, the use of molecular markers for MAS would reduce the time involved in selection and reduce in costs. The first population consisted of 1814 F<sub>2:4</sub> lines that were developed from crossing a durum cultivar Ben to Sumai3/Sceptre//D88816 line. The second population consisted of 320 F<sub>2:5</sub> that were derived from backcrossing cultivar Lebsock to the experimental line Lebsock//Sumai3/Lebsock. These two populations were screened for FHB resistance in the greenhouse in spring 2002 by inoculating the heads with *Fusarium graminearum* and later scoring the diseased heads for type II disease severity. Screening for the resistance QTL located on the chromosome 3BS was done using the microsatellite locus *Xgwm533*. In the greenhouse evaluation, 1124 lines in the first population and 180 lines from the second population were found resistant with FHB severity rating of less than 21%. Microsatellite marker identified the resistant QTL in 524 lines from population I and 131 lines from population II. We calculated the efficiency of each selection process so far and found that, it took us 44 working days with MAS to screen the two populations with an approximate cost of \$ 1.43 per data point and it took 141 days with an approximate cost of \$ 0.99 per data point with phenotypic selection in the greenhouse. In our next step of study, we plan to advance the agronomically desirable lines for possible release as resistant cultivars or use as parents for repeated backcross to adapted durum elite germplasm.

**Genetic Analysis of Early Flowering, Short Internode Length and Double Podding Traits as Bases of Early Maturity in Chickpea.** Yadeta Anbessa, Tom Warkentin, Bert Vandenberg and Rosallind Ball. University of Saskatchewan, Department of Plant Sciences, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada. Email: anbessa@sask.usask.ca.

Late maturity is a major production constraint and partly responsible for low and unstable grain yield in chickpea (*Cicer areitinum* L.) in the Prairies. The crop is often killed by frost while pod filling is yet in progress. It was hypothesized that incorporating early flowering, short internode length and double podding traits into high yielding genotypes would induce early maturity and ensure high and stable grain yield in this crop. On an assessment of the time (days) to flowering, six selected genotypes were grown under 18 and 12 hours of photoperiod in phytotron. Genotypes flowered 12 to 21 days earlier under the long day. 298T-9 and 272-2 flowered as early as 25 days after planting under this inducing condition. The former was also least sensitive to photoperiod. Insensitivity to photoperiod (day-neutral response) is a means of ensuring consistent early flowering irrespective of the day length that should subsequently reduce the time taken to maturity. Average length of internode was only about 0.5cm in E100Ym, though it exceeded 2cm in other genotypes. As a result, this genotype produced flowers/pods at faster rate and close to one another. Average seed weight to the maximum seed size was 86% in E100Ym as compared to a range of 50-70% in other genotypes at harvest. This indicates that short internoded genotypes with enhanced rate of pod development tended to reach maturity stage earlier. On the top of this, double podding increased number of pods per reproductive nodes and efficiency of grain formation. Partitioning coefficient for the seed, the ratio of seed growth rate to crop growth rate, was significantly ( $P \leq 0.05$ ) higher in the double podded genotype (272-2). The work is in progress to further incorporate early flowering, short internode length and double podding traits into high yielding genotypes and examine the effects on maturity duration of chickpea. As the traits seem to complement each other, such that early and nearly simultaneous flower/pod development is possible, it is anticipated that combination of these traits would ensure the desired earliness in maturity duration of chickpea.

**Leaf Rust Studies Using Bowman Backcross-Derived Lines.** Juan Caffarel and Jerome Franckowiak. Plant Sciences Department. North Dakota State University. Fargo. North Dakota. Email: [juan.caffarel@ndsu.nodak.edu](mailto:juan.caffarel@ndsu.nodak.edu)

Several sources of genetic resistance to barley (*Hordeum vulgare* L.) leaf rust (incited by *Puccinia hordei* Otth) have been identified in barley cultivars as well as related wild species. These accessions differ in flowering time, photoperiod response and plant height and some hybridize poorly with cultivated barley. This makes their use in crosses for breeding purposes and genetic studies difficult. A common genetic background differing in just one of the resistance *Rph* genes would make the previously mentioned studies easier. Efforts have been made to transfer different genes into the two-rowed barley cultivar Bowman. Bowman was crossed to each source of resistance, and resistant offspring were backcrossed with Bowman, up to six times. This study will be conducted using leaf rust resistant backcross-derived lines from about 100 different sources. The lines will be tested to confirm that the source of resistance was transferred. Also, their reactions to different pathogen isolates will be compared to the reactions of the donors



parents. Studies will be conducted to test allelism among new sources of *Rph* resistance with those already known.

**Backcross Reciprocal Monosomic Analysis of FHB Resistance in Frontana Wheat.**

\*B.L. Gebhard and W.A. Berzonsky. Department of Plant Sciences, North Dakota State University, Fargo, ND 58105. Email: Bryan.Gebhard@ndsu.nodak.edu

Fusarium Head Blight (FHB), commonly known as scab, is a widespread disease of wheat (*Triticum aestivum* L.) and other small grain cereals grown in warm and humid regions around the world. Scab is a devastating disease that reduces the yield, quality, and economic value of wheat. Developing host resistance to FHB is very important since resistant cultivars will augment fungicide treatments and other control strategies. The FHB resistance found in the Brazilian cultivar Frontana (Type I) is thought to be different than the commonly used FHB resistance source, Sumai-3 (Type II). Substituting chromosomes of wheat as a technique for studying quantitative inheritance was first reported in 1957. This technique, based on the use of aneuploids, enables the analysis of the effects of individual chromosomes on agronomic characters. In the 1970's, the monosomic condition (2n-1) found in *T. aestivum* cultivar Chinese Spring was transferred to the *T. aestivum* cultivar Chris. The Chris monosomics (2n-1) and Frontana (2n) have already been crossed according to the backcross reciprocal monosomic analysis method. Two reciprocally derived series of monosomic families are being developed which, on average, have genetically identical backgrounds, but also have different hemizygous chromosomes (chromosome of interest). One family's hemizygous chromosome will be derived from resistant Frontana while the other family will come from susceptible Chris. The resulting population will be spray inoculated with *Fusarium graminearum* in the greenhouse, germinated in deoxynivalenol (DON) media, and examined for differences in head morphology. We hope to identify chromosomes that contain genes for FHB resistance.

**Implementation of Marker-Assisted Selection For Lodging Resistance in Pea Breeding.** Zhang Chunzhen, Tar'an B., and Warkentin T. Department of Plant Sciences, University of Saskatchewan, 51 Campus Dr. Saskatoon, SK, S7N 5A8. Email: zhangc@sask.usask.ca

Lodging resistance is a key criterion in pea breeding programs. In traditional breeding, a large number of lines are discarded in F<sub>3</sub> or later generations, because of susceptibility to lodging and much labor and other costs are wasted. Implementation of selection using molecular markers for lodging resistance at earlier generations will significantly enhance the efficiency of the pea breeding process. Ten F<sub>2</sub> populations consisting of a total of 869 plants were grown in the field in Saskatoon in the summer of 2002. These 10 populations were derived from crosses between the lodging susceptible cultivar Carrera, crossed with

ten other lodging resistant lines. DNA samples were extracted from each individual plant. Each plant was scored for the presence of coupling phase linked SCAR markers A001 and A002, as well as a repulsion phase linked SCAR marker A004. The results showed that the frequency of marker presence is similar to the estimated frequency, obeying the rule of independent single gene segregation. Chi-Square analysis showed that the combination of A001 and A004 markers also followed a two gene model ( $P > 0.05$ ) in 8 populations. Due to linkage between A001 and A002 markers, population No. 3 and No. 4 did not follow the two or three independent gene segregation model. F<sub>3</sub> populations will be planted in the field in 2003 to evaluate the effectiveness of Marker-Assisted Selection for lodging resistance in pea.

**SSR Polymorphisms and Heterosis Among Early Maize Inbred Lines.** Clarissa de S. Barata. Department of Plant Sciences, North Dakota State University, Fargo, ND 58105. Email: clabarata@hotmail.com

The development of successful corn hybrids requires establishment of heterotic patterns, defined as the cross between known genotypes that expresses a high level of heterosis. The advancement in molecular markers technology has been very useful helping to define heterotic patterns. The use of this technology has also helped to study genetic divergence among cultivars, which plays an important role in heterosis. Therefore, the integration of molecular markers in conventional corn-breeding programs might increase its efficiency. Since simple sequence repeat (SSR) markers demonstrated to be the best technique to study different genotypes of corn, the objective of the present research is to determine whether this type of marker can predict hybrid cross performance among ND inbred lines, and also to assess if heterotic groups could be identified with the same type of molecular markers. Twelve ND released inbred lines, representing diverse background, and one ND unreleased inbred line will be used in a diallel mating. The crosses and 10 checks will be evaluated in experiments with two replicates arranged in a randomized completed block design (RCBD) at four North Dakota environments including the years 2001 and 2002. Data will be collected on stand counts, days of anthesis and days of silking, emergence percentage, root lodging, stalk lodging, dropped ears and grain yield. DNA will be extracted from 10-12 days old leaves and tested with about 100 SSR markers. Observed heterosis will be compared with genetic diversity values generated by SSR markers.

**Mapping Genes Conferring Fusarium Head Blight Resistance in a Midwest Barley Accession C93-320-24.** K.E. Lamb, M.J. Green, R.D. Horsley. Department of Plant Sciences, North Dakota State University, Fargo, ND 58105. Email: Kenneth.Lamb@ndsu.nodak.edu

*Fusarium* head blight (FHB), incited primarily by *Fusarium graminearum*, adversely affected the quality of barley grown in eastern North Dakota and northwestern Minnesota over the last decade. Quality of harvested grain was reduced because of blighted kernels and the presence of deoxynivalenol (DON), a mycotoxin produced by the pathogen. A line currently used by U.S. Midwestern barley breeding programs as sources of genes for FHB resistance is C93-3230-24. This six-rowed line from the cross B2912\*2/Hietpas 5 was identified by researchers at Busch Agricultural Resources, Inc. (BARI) to have FHB resistance similar to Chevron, and better FHB resistance than either of its parents in a greenhouse test. Field tests conducted the last five summers in mist-irrigated FHB nurseries in North Dakota confirmed that C93-3230-24 has FHB resistance approaching Chevron. The genetic background of C93-3230-24 appears to be completely different than that of any of the FHB resistant accessions identified by Prom et al. (1996). Thus, this line may have alleles for FHB resistance and DON accumulation not currently identified.

**Evaluation of Genetic Diversity in the Genus *Echinacea* (Asteraceae) Using Genomic and Chloroplast DNA.** Lasantha W.C. Ubayasena, Branka Barl and Graham J. Scoles, University of Saskatchewan, Department of Plant Sciences, Saskatoon, SK, S7N 5A8. Email: lau956@duke.usask.ca

Fifty-six accessions representing eight of the nine recognized species of the genus *Echinacea* were used in this study along with two outgroup taxa to evaluate the genetic diversity and relationships using genomic and chloroplast DNA variations. The genomic DNA variations were investigated using 16 RAPD primers and 17 ISSR primers. The chloroplast genome variations were examined using the restriction enzyme digestion patterns of three intergenic spacer regions. The genetic diversity and relationships within and between these species are discussed based on cladistic analysis, UPGMA cluster analysis, and analysis of molecular variances (AMOVA). Ninety-two percent of the RAPD bands and 99% of the ISSR bands were found to be polymorphic within the genus. The cladistic analysis of both RAPD and ISSR markers has consistently revealed eight distinct clades, each corresponding to a different species, identified based on morphological characters. The apparent interspecific relationships were not supported by either bootstrap or decay values. The dendrograms based on UPGMA cluster analysis using Jaccard's similarity coefficients and AMOVA analysis for both marker systems confirmed the existence of eight distinct groups, each corresponding to a different species. Several subgroups within the major groups representing the accessions of different geographical origins, commercial cultivars and suspected interspecies hybrids were revealed. The AMOVA analysis of genetic variation among species indicated that the ISSR markers were more powerful than RAPD markers in detecting the intraspecific variations. Results of the chloroplast DNA variations clearly supported *E. angustifolia* as a distinct species in the genus. Furthermore, it proved that utilizing chloroplast DNA variations is a powerful tool in identification of interspecific hybrids of *E. angustifolia*.

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The recognized genetically distinct accessions of three commercially important species could be used in future breeding programs. The results of this study also highlighted some geographical areas that should be given special attention in planning conservation strategies in order to prevent further reduction of diversity in the genus *Echinacea*.

**Analyzing SNP for Potato EST Data By Using StackPACK.** Ju Wang, Department of Plant Sciences, North Dakota State University, Fargo, ND 58105. Email: Ju.Wang@ndsu.nodak.edu

Stackpack is an effective internet software for SNP (single nucleic polymorphism) analysis. This software was used to analyze the potato EST data from the USDA plant genomic database. In this study, the total 252 SNP have been counted in 150 clusters and 294 contigs. About 20% of total SNP occurred on the first and second bases in the ORF and all others occurred on the third base in the ORF. After checking the SNP in the third base it was found that about 72 out of 198 SNP could cause the mutants, but from the coding table only half of them could be counted. This means that about 36 SNP, which take 18% of the total SNP on the third base in the ORF would be unconservable changes. Thirty six SNP from third base, and 54 SNP from the first and second bases in ORF, which total to 90 out of the 252 SNP or 36% of SNP, could cause amino acid changes.



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**Paul Westdal**  
**BANQUET KEYNOTE SPEAKER**

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Paul Westdal is an agricultural consultant based in Winnipeg. He is presently coordinating a development project in China, is a founder of a technology company in Manitoba, and has patented several inventions in the field of biotechnology. Mr. Westdal is a director of Agri-Tec International; a consortium of prairie based grain construction and manufacturing companies, a director of Burcon NutraScience Incorporated and a protein technology company, as well as a project manager for the Canada Grain Council Post Farm Food Safety Program. During his career in the grain industry he has worked with the Canadian Wheat Board in Canada and Europe and with the United Nations World Food Program in Africa. He holds a Master of Science degree from the University of Manitoba. Mr. Westdal is married to Charlotte. They have three children and two grandchildren.

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## Student Presentation Evaluation Sheet

Speaker: \_\_\_\_\_ Session: \_\_\_\_\_ Agronomy/Horticulture/ PI.Physiology  
 \_\_\_\_\_ Plant Protection  
 \_\_\_\_\_ Plant Breeding/ Genetics

Topic	Score					Comments
<b>Subject Matter</b>						
<b>Introduction</b>	1	2	3	4	5	
Logic/Concise						
Interest/Relevance						
<b>Objectives</b>	1	2	3	4	5	
Clear						
<b>Methods</b>	1	2	3	4	5	
Clear/Simple						
<b>Results/Discussion</b>	1	2	3	4	5	
Adequate						
Comprehensive						
Clear						
<b>Summary/Conclusions</b>	1	2	3	4	5	
Clear/Adequate						
Justified						
<b>Presentation</b>						
<b>Clarity of Speech</b>	1	2	3	4	5	
Voice, English						
<b>Maintenance of Interest</b>	1	2	3	4	5	
Enthusiasm						
<b>Schedule</b>	1	2	3	4	5	
Timing						
<b>Visual Aids</b>						
<b>Quality/Quantity</b>	1	2	3	4	5	
<b>Discussion</b>						
<b>Questions</b>	1	2	3	4	5	
Stimulation/Answer						

**TOTAL (50):** \_\_\_\_\_

**Overall Comments:**

**The 19<sup>th</sup> Annual Plant Science Graduate Student Symposium Organizing Committee would like to express their sincere appreciation to the following:**

**Department of Plant Science**

**Sessions Judges:**

***Agronomy, Horticulture and Physiology* - Dr. Jane Froese, Dr. Bill Remphrey, Dr. Kevin Vessey**

***Plant Protection* - Dr. Lakhdar Lamari, Dr. Dilantha Fernando, Dr. Fouad Daayf**

***Plant Breeding and Genetics* - Dr. Murray Ballance, Dr. Rachel Scarth, Dr. Anita Brûlé Babel**

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Notes



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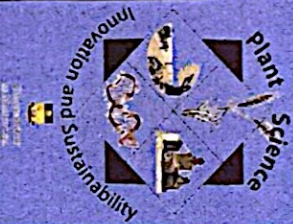
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