Germinating Great Ideas!

AG CENTENNIAL 2006
THE UNIVERSITY OF MANITOBA

PLANT SCIENCE GRADUATE STUDENT SYMPOSIUM

•MARCH 17-18, 2006•

SYMPOSIUM PROGRAM

The University of Manitoba
Winnipeg, Manitoba, Canada

UNIVERSITY OF MANITOBA

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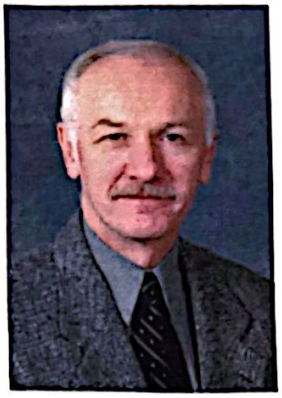
GREETINGS FROM THE DEPARTMENT HEAD



March 17, 2006

To Participants of the 22nd Annual Plant Science Symposium;

On behalf of the Department of Plant Science and the University of Manitoba, I extend to you a warm welcome to Winnipeg. Richard Cuthbert and his committee have been working diligently to make this another successful meeting, continuing a long series of previous meeting successes. The continuation of this meeting is a tribute to the founding organizers, to the annual participation of individuals such as yourselves, and to respective organizing committees from the three participating universities - North Dakota State University, the University of Saskatchewan and the University of Manitoba. The first four years of these meetings involved only students from the University of Manitoba. In 1985 both NDSU and the U of S were invited and came to actively participate. In 1986 NDSU hosted the meeting and from that point on this international meeting has rotated among the three universities. My congratulations to you on being part of this long tradition.

In 2006 the Faculty of Agricultural and Food Sciences at the University of Manitoba will be celebrating its centenary – 100 years of teaching, research and service to the community. We are proud of our record! Agriculture as a whole should be proud of its achievements! However, the challenges which lie ahead are significant. Supplying tomorrow's food, feed and fibers will need to be done more sustainably for the farmer, for the community, and for the environment. Your meeting has some friendly competition; there is some institutional pride, but I encourage you to get to know each other, for you are all on the same team for the challenges that lie ahead.

Have fun, enjoy Winnipeg, and I look forward to meeting some of you during the breaks.

Murray Ballance
Professor and Head
Department of Plant Science

GREETINGS FROM THE ORGANIZING COMMITTEE CHAIR

On behalf of the organizing committee, I welcome you to the Plant Science Graduate Student Symposium. We are happy that you are able to take part in the symposium and participate in the celebration of our Ag Centennial.

We believe this opportunity to present your research will not only help you to perfect your presentation skills, but also bring you new friends and contacts that you will find invaluable throughout your career. The symposium is an excellent place to share your thoughts and open your mind to new exciting ideas in the field of Plant Science.

The funding received by the Plant Science Graduate Student Symposium is the catalyst that makes this event happen. We thank our sponsors for their vote of confidence and look forward to their continued support.

Thank you for attending the symposium. The organizing committee and sponsors have made an extra effort this centennial year to ensure that you enjoy your participation in this important event. We hope that you take home many good memories.

Sincerely,

Richard Cuthbert
President
Plant Science Graduate Student Association

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Program at a Glance

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Friday, March 17, 2006

PRE-SYMPOSIUM TOUR
3:00 p.m. – 5:30 p.m.

Fort Garry Brewing Company Ltd. is Manitoba's largest brewer and distributor of premium beers. Having successfully completed an Initial Public Offering in January 1999, the company has recently undergone an expansion of operations. Proceeds from the Offering were invested in a new 25,000 square foot facility that houses the most modern and efficient brewing and packaging equipment available to today's regional brewery. Fort Garry's beers are presently available throughout Winnipeg, rural Manitoba and Alberta.

OPENING RECEPTION AND WELCOMING DINNER
VESUVIOS
5:30 p.m. – 7:00 p.m.

The city's most densely populated neighbourhood, "The Village" was created in the late 60's with an entrepreneurial spirit that lives today in a colourful mix of owner-operated shops, restaurants, salons and unique services. Today, merchants offer a variety of goods from coffee to cookware, books to home furnishings, giftware to gold, music to pottery. Contemporary fashions suited to every style are offered in many fine stores. Tempting delicacies are served in a variety of exceptional restaurants offering the cuisine of five continents, from fast food to fine dining. Unique attractions such as the Stradbrook Square Bell Tower add to the warm, welcoming ambience of this unique community.

MANITOBA MOOSE HOCKEY GAME
MTS CENTRE
7:30 p.m. – 9:30 p.m.

Last season over 380,000 fans cheered on the Moose to a North Division Championship and helped usher in a new era of hockey with the opening of the state-of-the-art MTS Centre. Join the Moose as they celebrate their 10th season and declare the MTS Centre "The Home of Hockey".

Websites:
www.moosehockey.com
www.mtscentre.ca

For more information on events and attractions in Winnipeg please visit the Destination Winnipeg website at:
www.destinationwinnipeg.ca

Program at a Glance

Saturday, March 18, 2006

BREAKFAST
7:00 a.m. – 8:00 a.m.

LOCATION: Agriculture Atrium

Sponsored by:

syngenta

SYMPOSIUM OPENING REMARKS
8:00 a.m. – 8:15 a.m.

LOCATION: Carolyn Sifton Lecture Theatre
Dr. Micheal Trevan
Dean, Faculty of Agricultural & Food Sciences

AGRONOMY & PATHOLOGY SESSION
8:15 a.m. – 10:45 a.m.

LOCATION: Carolyn Sifton Lecture Theatre

SESSION CHAIR: Rajesh Ramarathnam

JUDGES:

- **Dr. Lakhdar Lamari**
- **Dr. Jane Froese**
- **Dr. Mario Tenuta**

8:15 a.m. **Jeremy Klassen**
University of Manitoba
"Is there genetic variation in *Fusarium oxysporum* f. sp *conglutinans* strains infecting canola?"

8:30 a.m. **Rebekah Oliver**
North Dakota State University
"Relatives of wheat: A novel source of resistance to Fusarium Head Blight"

8:45 a.m. **Anndrea Hermann**
University of Manitoba
"Hemp agronomy 101"

9:00 a.m. **Biligetu**
University of Saskatchewan
"Quantifying re-growth characteristics of brome grass species response to defoliation"

9:15 a.m. **Lee Kalcsits**
University of Saskatchewan
"The effect of different temperature regimes during autumn dormancy induction on subsequent spring deacclimation of hybrid poplar (*Populus x* spp.) clones"

9:30 a.m. **Marie-Soleil Turmel**
University of Manitoba
"The effect of cover crops on arbuscular mycorrhizal fungi mediated nutrient uptake"

9:45 a.m. **Xiaowei Guo**
University of Manitoba
"Relationships among previous cropping practices, fusarium inoculum of spring wheat and rainfall"

10:00 a.m. **Yu Chen**
University of Manitoba
"New pathogenicity groups (pgs) of *Leptosphaeria maculans* in Western Canada and North Dakota"

10:15 p.m. **Emma Gamotin**
North Dakota State University
"Pyramiding different sources of Fusarium Head Blight resistance into spring wheat"

10:30 a.m. **Kaveh Ghanbarnia**
University of Manitoba
"Map-based cloning of avirulence gene of *Leptosphaeria maculans*, fungal pathogen of *Brassica napus*"

Program at a Glance

Germinating Great Ideas!

CLASSICAL PLANT BREEDING CONCURRENT SESSION
9:30 a.m. – 10:45 a.m.

LOCATION: 134 Agriculture

SESSION CHAIR: Kevin Baron

JUDGES:
- **Dr. Anita Brûlé-Babel**
- **Dr. Carla Zelmer**
- **Janice Cuthbert**

9:30 a.m. **Adams Frimpong**
University of Saskatchewan
"Precocious seed color development in common bean (*Phaseolus vulgaris*)"

9:45 a.m. **Angela Sebelius**
North Dakota State University
"Inheritance of stem rust resistance in an Amagalon-derived oat line"

10:00 a.m. **Bandla Narasimha Rao**
University of Saskatchewan
"Baking quality of durum wheat cultivars: Studying the rheological properties and gluten protein components associated with enhanced baking"

10:15 a.m. **Jie Qiu**
University of Saskatchewan
"Genetic diversity in plains rough fescue as revealed from seed and tiller samplings using AFLP markers"

10:30 a.m. **Baojun Yang**
North Dakota State University
"Meiosis in the absence of chromosome pairing and recombination"

MORNING COFFEE
10:45 a.m. – 11:00 a.m.

LOCATION: Agriculture Atrium

Sponsored by:

CAN-OAT MILLING

CLASSICAL PLANT BREEDING SESSION
11:00 a.m. – 12:00 p.m.

LOCATION: Carolyn Sifton Lecture Theatre

11:00 a.m. **Sushmita Mitra**
University of Saskatchewan
"Elucidating the genetic basis of flax (*Linum usitatissimum* L.) fibre production"

11:15 a.m. **Juan Carlos Caffarel**
North Dakota State University
"Leaf rust studies in barley using Bowman backcross-derived lines"

11:30 a.m. **Jocepascual Martinez Rojo**
North Dakota State University
"Tepary bean as a potential source of frost tolerance for common bean"

11:45 p.m. **Benilda Sable**
University of Manitoba
"Flowering phenology and reproductive capability of volunteer and crop canola in Western Canada and potential gene flow"

Program at a Glance

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Program at a Glance

SYMPOSIUM LUNCHEON
12:00 p.m. – 12:45 p.m.

LOCATION: Agriculture Atrium

Sponsored by:

GenomePrairie

MOLECULAR PLANT BREEDING & PHYSIOLOGY SESSION I
12:45 p.m. – 2:45 p.m.

LOCATION: Carolyn Sifton Lecture Theatre

SESSION CHAIR: Christian Willenborg

JUDGES:

- **Dr. Murray Ballance**
- **Dr. Fouad Daayf**
- **Patricia Cuthbert**

12:45 p.m. **Chenggen Chu**
North Dakota State University
"Molecular mapping of hybrid necrosis genes Ne1 and Ne2 in hexaploid wheat using microsatellite markers"

1:00 p.m. **Derek Law**
University of Manitoba
"Molecular characterization of PgAGO, a novel conifer gene of the ARGONAUTE family expressed in the apical cells and required for somatic embryo development in *Picea glauca*"

1:15 p.m. **Dejun Cui**
University of Saskatchewan
"Isolation and mapping of novel proanthocyanidin mutation from *Arabidopsis thaliana*"

1:45 p.m. **Grant Woronuk**
University of Saskatchewan
"Characterization of genes relating to chilling stress in bean"

2:00 p.m. **Kiran Oberoi**
North Dakota State University
"Saturation mapping of species cytoplasm specific gene in durum wheat"

2:15 p.m. **Mukhlesur Rahman**
University of Manitoba
"Inheritance of seed coat colour genes of *Brassica napus* (L) and tagging the genes using SRAP molecular markers."

2:30 p.m. **Rajender Singh**
University of Saskatchewan
"Genetic mapping of pre-harvest sprouting resistance loci in bread wheat (*Triticum aestivum* L.)"

AFTERNOON COFFEE
2:45 p.m. – 3:00 p.m.

LOCATION: Agriculture Atrium

Sponsored by:

MIA

Special Thanks

Germinating Great Ideas!

Organizing Committee

Richard Cuthbert
Organizing Committee Chair

Mark Belmonte
Treasurer
Hospitality

Derek Law
Facilities
Transportation

Kevin Baron
Judging
Awards

Paul Gervais
A/V Systems

Jeremy Klassen
Tours

Special Thanks

Judging Panel

Agronomy & Pathology:	Dr. Jane Froese
	Dr. Lakhdar Lamari
	Dr. Mario Tenuta
Classical Plant Breeding:	Dr. Anita Brûlé-Babel
	Dr. Carla Zelmer
	Janice Cuthbert
Molecular Plant Breeding & Physiology:	Dr. G. Murray Ballance
	Dr. Fouad Daayf
	Patricia Cuthbert

A very special thank you to all the volunteers who made the Plant Science Graduate Student Symposium 2006 a great success.

Abstracts

Agronomy & Pathology

Is there genetic variation in *Fusarium oxysporum* f. sp *conglutinans* strains infecting canola?

Jeremy Klassen and Dilantha Fernando

University of Manitoba, Department of Plant Science, 222 Agriculture Building, Winnipeg, MB R3T 2N2. Email: Klassen_Jeremy@yahoo.ca

Fusarium wilt of canola (*Brassica napus* L.), caused by *Fusarium oxysporum* f. sp *conglutinans* (Wollenweber) Snyder & Hansen(FOC), is a disease that has recently been discovered in Western Canada. It has already been observed that canola cultivars differ in their susceptibility to this disease, with resistance likely coming predominantly from a monogenic source. Breeders and pathologists have been interested in investigating the variation in the pathogen population to assist breeding efforts. Sequence related amplified polymorphism (SRAP) molecular analysis is being used on approximately 100 isolates of the pathogen acquired from infected canola plants grown throughout Manitoba, Saskatchewan and Alberta. Determination of the degree of variation within the pathogen population is important not only in understanding the basic biology and epidemiology of this disease, but may also have implications in how resistance is screened for in the host and how durable that resistance could be in the long term. Preliminary data suggests that there are significant polymorphisms between FOC strains implicating diversity among isolates from Western Canada. .

Relatives of Wheat: A Novel Source of Resistance to Fusarium Head Blight

Rebekah E. Oliver[1*], Steven Xu[2], Robert Stack[3], and Xiwen Cai[1]

[1] Dep. Plant Sciences [2] USDA-ARS, Northern Crop Science Laboratory [3] Dep. Plant Pathology, North Dakota State University 166 Loftsgard Hall, North Dakota State University, Fargo, 58105. Email: Rebekah.Oliver@ndsu.edu

Fusarium head blight (FHB), caused by *Fusarium graminearum* Schwabe, is a destructive disease of wheat (*Triticum aestivum* L.) and has caused severe economic losses worldwide, both in yield loss and quality reduction. Genetic resistance is the most effective, cost-efficient, and environmentally friendly measure to control this disease; however, a lack of effective resistance sources has limited the progress in development of FHB-resistant cultivars. The objectives of this research are to: 1) identify novel sources of FHB resistance from relatives of wheat, 2) bring the alien resistance genes into wheat; and 3) develop breeder-friendly germplasm resistant to FHB. We evaluated FHB resistance of 293 lines derived from the crosses of wheat with its relatives, including *T. tauschii* (Coss.) Schmal., *Roegneria kamoji* C. Koch, *R. ciliaris* (Trin.) Nevski, *Leymus racemosus* Lam., *Thinopyrum ponticum* (Podp.) Barkworth & D.R. Dewey, *Th. elongatum* (Host) D.R. Dewey, *Th. junceum* (L.) Love, *Th. intermedium* (Host) Barkworth & D.R. Dewey, *Dasypyrum villosa* L., *Secale cereale* L., and *Avena sativa* L. Materials included wheat-alien species amphiploids, synthetic hexaploid wheat lines, and wheat-alien species addition, substitution and translocation lines. Seventy-four derivatives exhibited a level of resistance comparable to 'Sumai 3', the most widely used source of resistance to FHB, 153 appeared moderately resistant, and 66 were susceptible. Chromosome characterization and manipulation were conducted to understand the genetic constitutions, to minimize linkage drag, and to improve adaptation and agronomic characteristics. These resistant lines represent a novel source of FHB resistance for wheat breeding.

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…uilding, Winnipeg, MB R3T 2N2. Email:

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…nd agronomic characteristics. These resistant

Quantifying Re-growth Characteristics of Brome Grass Species Response to Defoliatio

Siligetu

Department of Plant Sciences University of Saskatchewan 51 Campus Drive Saskatoon, Saskatchewan Canada S7N 5A8 Email: xxb894@mail.usask.ca

When characterizing forage potential of grass species used for hay or especially for grazing pasture, it is important to evaluate the mechanisms and traits related to re-growth ability. The experiment was designed to study morphological changes of three type of brome grass (*Bromus*) species —leaf and tiller regrowth, tillering, leaf area index, aboveground and root biomass response to defoliation. Physiological studies regarding to photosynthetic rate, contribution of organic reserve and photosynthesis to the regrowth, N reserve remobilization during the regrowth will be carried out. (Research Proposal)

Hemp Agronomy 101

Anndrea Hermann and Kevin Friesen

University of Manitoba, Department of Plant Science, 222 Agriculture Building, Winnipeg, MB, Canada - R3T 2N2. Email: umhermaa@cc.umanitoba.ca

Industrial Hemp (*Cannabis sativa L*) is a dynamic plant that can be grown for grain and/or fiber. Hemp is recognized for its balanced blend of polyunsaturated oils, high protein and carbohydrate levels in addition to its high percentage of vitamins and minerals. Hemp fiber is prized for its long natural fiber strength that can be used for a multitude of industrial and commercial applications ranging from bio-composites textiles to fine fabrics. Industrial Hemp was legalized in 1998 for agriculture production under Health Canada's (HC) Industrial Hemp Regulations Program within the Office of Controlled Substances (OCS). Upon requiring the proper licensing for cultivation producers are allowed to cultivate a minimum of at least 10 acres. Under the OCS regulations each producer, field, distributor, laboratory and processor must acquire the proper licenses. The growing markets in both the grain and fiber industries have lead to the need for agronomic research. Extension programs and on farm experiments has lead to a firm understanding of hemp production requirements for the western prairies. This presentation will address details pertaining to hemp production, such as the current agronomic information on variety and field selection, seeding and fertility, THC analysis and harvest.

The effect of different temperature regimes during autumn dormancy induction on subsequent spring deacclimation of hybrid poplar (*Populus x* spp.) clones

Lee Kalcsits

University of Saskachewan

Over the next 75 years, temperatures during autumn when trees are entering dormancy, are predicted to increase between 3-5°C. Dormancy and cold acclimation are closely interrelated and changes in one factor often affect the other. Dormancy is a cycle where factors affecting dormancy induction and acclimation will affect bud break and deacclimation. Four different poplar clones ('Walker', 'WP-69', 'Katepwa' and 'Prairie Sky') will be placed in controlled environment growth chambers under short days with six different temperature regimes (16°C day/ 6°C night, 18.5°C/ 3.5°C, 21°C/ 11°C, 23.5°C/ 8.5°C, 26°C/ 16°C and 28.5°C/ 13.5°C). Dormancy acquisition will be determined by sampling trees every 14 days to determine the number of days to bud break under forcing conditions (warm temperature/ long days). Once dormancy has been acquired in all treatments and clones, the trees will be placed under chilling conditions at 2°C. Chilling requirement fulfillment will also be determined by sampling every 14 days and assessing the number of days to bud-break under forcing conditions. Once chilling has been fulfilled in all clones and treatments, the trees will be placed in conditions that induce deacclimation in hybrid poplar clones (10°C day/ 0°C night). Trees will be sampled every five days and LT_{50} tests performed to develop deacclimation profiles for the four clones under different temperature regimes. NMR imaging will also be performed to identify differences in water status, water mobility and metabolic activity during deacclimation. From this experiment, it is hoped that a better understanding of the crossover effect of temperature change during dormancy induction on deacclimation of hybrid poplar will be gained.

The Effect of Cover Crops on Arbuscular Mycorrhizal Fungi Mediated Nutrient Uptake

Marie-Soleil Turmel

University of Manitoba, Department of Plant Science, 222 Agriculture Building, Winnipeg, MB R3T 2N2.

Sustainable agricultural ecosystems must emphasize biological processes in order to achieve a sufficient level of productivity and food quality with minimal detrimental impact on the ecosystem. Cover crops enhance agricultural sustainability in many ways such as reducing nitrogen leaching, erosion and nitrogen volatilization, adding organic matter to the soil, nitrogen fixation and enhancing beneficial soil biota. Soil quality is a fundamental indicator of sustainable agricultural ecosystems. Beneficial soil microorganisms are an essential element of good soil quality. Arbuscular mycorrhizal fungi (AMF) are one of the most beneficial soil microorganisms. AMF symbiosis increases the phosphorus and micronutrient uptake and growth of their plant host by contributing an extraradical mycellial network (EMN) which increases the volume of soil explored by the roots. The phosphorus uptake in roots colonized by AMF can be three to five times greater than in non-mycorrhizal roots. The benefits of AMF symbiosis are most substantial in sustainable low input systems where plant available soil phosphorus concentrations are low. Cover crops extend the time for EMN growth into the autumn, winter and spring. A well established EMN provides rapid spring colonization and early season symbiosis and adequate phosphorus nutrition during early growth which greatly improves the crop yield. Arbuscular mycorrhizal fungi are invaluable beneficial plant symbionts and it is imperative that our agricultural practices enable mycorrhizal symbiosis to flourish. My research will establish how Black Medic (*Medicago lupilina*, cv George) and Kura Clover (*Trifolium ambiguum*) cover crops enhance soil arbuscular mycorrhizal fungi and subsequent uptake of phosphorus and micronutrients by the main crop.

Relationships among Previous Cropping Practices, *Fusarium* Inoculum of Spring Wheat and Rainfall.

X.W. Guo[1], W.G.D. Fernando[1], H. Sapirstein[2], and P. Bullock[3].

1: Department of Plant Science; 2: Department of Food Science; 3: Department of Soil Science, University of Manitoba, Winnipeg, Manitoba, Canada

The relationships among cropping practices, *Fusarium* inouculum levels on wheat stubble and heads, number of spores on single head, FHB index, and DON levels in the grains, and the effect of rainfall on these relationships are investigated in 14 fields in 2003 and 17 fields in 2004 for two spring wheat cultivars "AC-Superb" (moderate susceptible to FHB disease) and "AC-Barrie" (moderate resistant to FHB disease) in Manitoba. Cropping practice index had a strong relationship with *Fusarium* inoculum levels on wheat stubble for cultivars "AC-Superb" and "AC-Barrie". Rainfall showed a strong relationship with FHB index for cultivar "AC-Superb" in 2003 and cultivars "AC-Superb" and "AC-Barrie" in 2004. *Fusarium* inoculum levels on wheat stubble were correlated to the inoculum levels on wheat heads, FHB index and spores per head in 2004. Rainfall at the flowering stage was correlated to the inoculum levels on stubble and spores per head for both cultivars in 2004. The number of spores on a single wheat head was correlated to DON levels in the grains in 2004. Rainfall showed a weak effect on DON levels in 2003 and 2004. A new DON prediction model is being developed based on these relationships.

New pathogenicity groupls (pgs) of *Leptosphaeria maculans* in Western Canada and North Dakota

Y. Chen and Dilantha Fernando.

Dept. of Plant Science, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2

A total of 512 isolates of *Leptosphaeria maculans* collected from 50 locations between 1994 and 2004 from North America, Brazil, Australia and Europe were characterized into pathogenicity groups (PGs) based on their host-pathogen interaction using *Brassica* host differentials. Seven day old cotyledons of the *Brassica napus* cultivars Westar, Glacier and Quinta were wound inoculated with each isolate and interaction phenotypes (IP) characterized on a 0-9 scale 12-d after inoculation. Five PGs; PG-1, PG-2, PG-3, PGT or PG-4 were assigned to each isolate according to the resistant or susceptible reaction on the differential set. Isolates obtained before 2001 in Western Canada and U.S.A belonged to weakly virulent PG-1 or virulent PG-2, whereas isolates from Brazil, Australia and UK were mainly in PG-3 or occasionally in PG-4 or PG-1. This suggested that virulent structure of isolates between these regions are different. In Western Canada and U.S.A, similarity of pathogenicity of isolates collected from the 1980s up to the early 21st century, reveals that

L. maculans populations have remained relatively unchanged (PG-2 or PG-1) over the past two decades. In 2002 and 2003, the presence of PG-3, PGT and PG-4 were detected across Western Canada and North Dakota U.S.A, indicating that new virulent types have surfaced for first time in these regions. Analysis of these isolates have shown that they are different from PG-3 or PG-4 isolates from Ontario, Canada or Georgia, U.S.A. Co-existence of five PG types in one population from a single field in Manitoba, Canada points to the occurrence of sexual recombination of *L. maculans* which could possibly be one reason of appearance of new virulent isolates.

Pyramiding Different Sources of Fusarium Head Blight Resistance into Spring Wheat

Emma Gamotin[1*], William Berzonsky[1], Tika Adhikari[2], Shaukat Ali[2], Gene Leach[1]

[1]NDSU, Plant Sciences Dept., Fargo, ND 58105 [2]NDSU, Plant Pathology Dept., Fargo, ND 58105*Corresponding Author: PH: (701) 231-5998, Email: Emma.Gamotin@ndsu.edu

Fusarium head blight (FHB) is a serious disease of cereal crops worldwide. The causal fungus, *Fusarium graminearum* Schwabe [telemorph *Gibberella zeae* (Schwein.)] infects heads at flowering causing significant yield losses and poor seed quality. Alsen is an adapted hard red spring wheat cultivar with resistance to FHB. The source of resistance in Alsen was derived from Sumai 3, a Chinese wheat cultivar. Another source of resistance has been identified in the tetraploid wheat, *Triticum turgidum* L. var. *dicoccoides*. Both sources of resistance prevent the spread of infection within the spike. In other crops, pyramiding different genes for disease resistance has resulted in the expression of a higher level of resistance. The objectives of this study were to pyramid resistance from Sumai 3 and *T. dicoccoides* into two Alsen backcross-derived lines and to compare the expression of FHB resistance to lines containing only the Sumai 3 source. Lines were produced from hybridizations between a synthetic hexaploid carrying the *T. dicoccoides* gene and Alsen. Hybrids were backcrossed twice to Alsen and pollinated with maize (*Zea mays* L,) to produce doubled-haploid lines. The SSR markers, *Xgwm2* and *Xgwm533*, were employed to independently identify doubled-haploid lines containing either the Sumai 3 source or both the Sumai 3 and *T. dicoccoides* sources. Pots were arranged in a RCB with four replications in a greenhouse experiment, and 10 µl inoculum with a spore concentration of 50,000 spores ml^{-1} was injected into a single floret in the middle of each spike. Visual evaluations of spread within each inoculated spike were made at 7, 14, and 21 days post-inoculation. Measurements of visually diseased kernels and DON content will be made after harvest. Statistical comparisons of the resistance of genotypes will be made, and the results of these comparisons will be presented.

Map-based cloning of avirulence gene of *Leptosphaeria maculans*, fungal pathogen of *Brassica napus*.

Kaveh Ghanbarnia, Dilantha Fernando

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Previous studies showed that two lines ddm-12-6-1 and ddm-12-6-2 possess a novel resistance gene (*LepR1*) to the most of the PG2 (such as WA-74) and a few PGT (99-43 & 99-56) isolates except isolate 87-41(PG2). It is supposed that the avirulence of isolates WA-74, 99-43 and 99-56 on lines ddm-12-6-1 and ddm-12-6-2 are governed by the *Avr1/LepR1* and the virulence of isolate 87-41 is governed by *avr1/LepR1*. Among them, two isolates 87-41 and 99-56 have been selected as virulence and avirulence isolates .They crossed and the progenies have been segregated based on phenotypic reaction on the line ddm-12-6-1. The 87-41 X 99-56 *L.maculans* map will be constructed with PCR-based markers including SSR and SRAP. Polymorphic bands will be recorded as present or absent in the parents and whole progeny. Once the physical distance of *Avr* gene with its markers are identified, the genomic BAC library from *L. maculans* isolate 99-56 will be constructed. Then, the library will be screened using the closely linked markers and combination of markers could then be used to narrow down the positive clones.

Classical Plant Breeding

Precocious Seed Color Development in Common Bean (*Phaseolus vulgaris*)

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Seed coat color is an important attribute that determines the price of dry bean. Inheritance of bean seed coat color has been extensively investigated, however the timing and rate of color initiation and finish, and the genetics of these traits as well as the relationship between color deposition and seed coat cell structure have not been reported. This proposal seeks to investigate these characteristics through various approaches that will be outlined.

Inheritance of stem rust resistance in an Amagalon-derived oat line

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Few effective genes are available that confer resistance to prevalent North American races of oat stem rust incited by *Puccinia graminis avenae*. Lines derived from Amagalon, a synthetic hexaploid line developed from a cross between *Avena longiglumis* (2n=14) and *A. magna* express resistance to stem rust race NA67. NA67 has been increasing in prevalence in North America, and nearly all cultivars grown in the northern plains of North America are susceptible. To determine the inheritance of this source of stem rust resistance, we evaluated the F_2 segregation of NA67 resistance in nine populations derived from crosses of ND990232 and one other Amagalon-derived line, to NA67 susceptible genotypes. Seedling resistance to NA67 of F_2 progeny from ND990232 crossed with a line possessing *pg-a* stem rust resistance was evaluated to determine the allelic relationship of Amagalon-derived stem rust resistance with resistance conferred by *pg-a*.

Nine segregating F2 populations of 100 plants each, produced from crosses involving Amagalon-derived NA67 resistant lines with diverse NA67 susceptible lines, were evaluated in the seedling stage after inoculation with NA67. Eight of the populations fit a 3 resistant (R):13 susceptible (S) ratio, but did not fit 1 R:3 S or 1 R:15 S ratios. Homogeneity of error allowed combining the populations and the combined population fit a 3:13 ratio but did not fit other tested ratios. The data suggest the Amagalon resistance is conferred by one dominant and one recessive gene through dominant suppression epistasis. $F_{2:3}$ lines derived from the seedlings evaluated in the greenhouse were evaluated in the field and verified the results obtained in seedling tests. While resistance of *pg-a* is conferred by the presence of at least two homozygous recessive genes (Erpelding, 1987), resistance of Amagalon-derived lines appears to involve a dominant gene.

Baking Quality of Durum Wheat Cultivars: Studying the Rheological Properties and Gluten Protein Components Associated with Enhanced Baking

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Durum wheat (*Triticum turgidum ssp. durum*), is an economically important cereal crop used to make pasta, semolina and baked goods. Although durum wheat is predominantly used for pasta products, there is increasing use in bread making, particularly in Mediterranean regions. Attempts to improve the baking quality by incorporating the D genome of hexaploid wheat cultivar 'Len' to durum wheat cultivars Renville and Langdon have not been successful. However, we have obtained an Emmer wheat accession (*Triticum turgidum ssp. dicoccoides)* designated as 97Emmer19 which has been reported to have improved baking quality over current durum wheat varieties. The objectives of this study are to assess the agronomical potential and compare the baking potential of Emmer-derived durum wheat lines with Canada Western Red Spring and durum lines. A total of 25 genotypes will be used in this study, which include six currently registered durum wheat varieties, one unregistered durum wheat cultivar, three Canadian Western Red Spring wheat varieties (as positive controls), 97 Emmer19, six lines developed by crossing 97Emmer19 with AC Navigator and

WB881, and remaining eight are translocation lines. Durum wheat cultivars containing the 1A.1D translocation have been obtained from CIMMYT and USDA-ARS will also be included in the study. Plant height, days to heading, days to maturity, lodging resistance, and yield data will be used to compare the agronomical potential of the Emmer-derived durum lines. Test weight, 1000-kernel weight, kernel texture (degree of hardness or softness) will be studied to evaluate the physical quality whereas grain protein concentration (GPC), alpha-amylase assay, flour color, Gluten Index (GI), Alveograph, Farinograph, and Canadian Short Process (CSP) bake test data will be used to compare the baking potential of all 25 lines.

Genetic Diversity in Plains Rough Fescue as Revealed from Seed and Tiller Samplings Using AFLP Markers

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Plains rough fescue [*Festuca hallii* (Vasey) Piper] (PRF) is the characteristic species in the Fescue Prairie of Western Canada. Little is known about the genetic diversity of this species in natural populations and in seed collections. Three sample types, which were reproductive tillers, vegetative tillers and seeds, were collected from six natural populations of PRF in Manitoba and Saskatchewan. Three amplified fragment length polymorphism (AFLP) primer pairs were employed to screen 529 samples representing about 30 samples for each sample type collected in each location, and 330 polymorphic AFLP markers were scored for each sample. Analysis of these scored bands revealed that > 90% of the total AFLP variation was presented within natural populations (reproductive and vegetative tillers) and within seed samples. The among-population variation was relatively small (7-10%) but statistically significant. Comparisons of AFLP profiles among sample types indicted that the reproductive and vegetative tillers revealed more loss of polymorphic bands and greater inter-population distances (*Phi* statistic) than seed samples. Larger genetic variation and population isolation were found in reproductive and vegetative tillers among the six PRF populations, but not in the seed samples. These findings indicate tiller samples are more effective than seed samples in assessing genetic diversity of PRF population and are useful for determining the appropriate strategies for conservation and management of PRF in Fescue Prairie.

Meiosis in the absence of chromosome pairing and recombination

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Meiosis includes two successive cell divisions and leads to formation of four haploid daughter cells. The fidelity of meiosis is ensured by control mechanisms called checkpoints. Chromosomes also play an important role in the control of meiotic cell division. Extensive research has been done on meiosis using meiotic mutants. The attempt of this study was to crack this complex process using haploids that lack chromosome pairing and recombination during meiosis. We produced haploids of a tetraploid wheat line Langdon (LDN) (*Triticum turgidium* L. var. *durum*, 2n=4x=28, genomes AABB) and an F_1 hybrid of another tetraploid Israel-A (ISA) (*T. turgidium* L. var. *dicoccoides*, 2n=4x=28, genomes AABB) with *T. tauschii* (2n=2x=14, genome DD) in which all the genomes appeared as a haploid. Meiotic process of the pollen mother cells (PMCs) in the tetraploids, haploid, and F_1 hybrid were characterized using indirect immunofluorescence techniques. Both tetraploids went through a normal meiosis with a monopolar kinetochore-microtubule attachment on each of the paired homologous chromosomes (bivalent) at metaphase I (MI) and a bipolar kinetochore-microtubule attachment on each of the individual chromosomes at metaphase II (MII). No chromosome pairing was observed and all the chromosomes appeared as univalents in the haploid and F_1 hybrid. Either a bipolar or a monpolar kinetochore-microtubule attachment formed to a univalent at MI. Some univalents lay outside the spindle and their kinetochores were not captured by the microtubules at all. Sister chromatids of the unpaired chromosomes did not separate until anaphase II. Then LDN haploid produced restituted nuclei at the end of meiosis. Our results suggested that microtubules initially formed around chromosomes and chromosome pairing had a significant impact on the spindle assembly and cytokinesis in wheat PMCs.

Elucidating the genetic basis of flax (*Linum usitatissimum* L.) fibre production.

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Linum usitatissimum is better known as linseed or flax. Recently, the uses of flax fibres have been undergoing a considerable change. New applications of flax fibre such as composites and paper and pulp making do not require very long or fine fibres which are needed by textile industry (Kessler and Tubach, 1995) and this increases the possibility of using the same plant for producing both fibre and seed, thus making *Linum usitatissimum* a potential dual purpose crop. To increase the fibre yield and identify superior varieties for fibre production it is very important to know in detail the ultrastucture of the fibre bearing stem tissues as well as the genetic makeup of the plant with regard to fibre formation. Molecular markers coupled with gene expression studies are powerful tools for gaining insight into the inheritance of complex quantitative characters. Henceforth, in the proposed project, using florescence microscopy the stem ultrastructure of two diverse flax types viz., Viking (fibre type) and E1747 (oil type) will be studied to find the differences in anatomical structure specially the fibre cells. The same parents along with 96 RILs derived from their crossing will be then used to construct a linkage map utilizing AFLP and SSR markers. Further, gene expression studies using microarray techniques will be undertaken to identify potential genes involved in fibre production. The data collected thereby will be used to standardize selection criteria for identifying dual purpose flax varieties.

Leaf Rust Studies in Barley Using Bowman Backcross-Derived Lines

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Barley leaf rust caused by *Puccinia hordei* Otth is an important disease worldwide. Although it causes minor losses in North Dakota, it can be severe in some fields because the current cultivars do not have any resistance to this pathogen. Several sources of genetic resistance to barley leaf rust have been identified in barley cultivars as well as in related wild species. These accessions differ in flowering time, photoperiod response, and plant height, and some hybridize poorly with cultivated barley. To minimize this problem, a set of Bowman backcross-derived lines was previously developed and used in this study.

The lines were tested to confirm that each source of resistance was transferred, and their reactions to 11 isolates were compared to the reactions of the donor parents. Fifteen Bowman backcross-derived lines were selected as a Bowman differential set for leaf rust studies. Experiments were conducted to test allelism among *Rph15* genes transferred to Bowman backcross-derived lines from accessions of *Hordeum vulgare* subsp. *spontaneum.* Based on their reaction types to isolates 90-3, 89-3, and Neth 28, thirty-one Bowman backcross-derived lines were identified as possibly having the *Rph15* gene.

Tepary bean as a potential source of frost tolerance for common bean

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Phaseolus acutifolius, or tepary bean, belongs to the secondary gene pool of common bean (*Phaseolus vulgaris*) and has shown some levels of frost tolerance. An intensive screening of a few accessions from *P. acutifolius var. acutifolius* and *P. acutifolius var. tenufolius* is underway to determine the level of frost tolerance in this species. Preliminary observations indicate that at least one accession of *P. acutifolius var. acutifolius* is more tolerant to frost compared to the previously identified frost-tolerant wild bean *P. angustissimus.* An intensive crossing program will be carried out between common bean, and the accessions of tepary bean that demonstrate the greatest levels of frost tolerance. It is anticipated that successful introgression of genes into common bean through interspecific hybridization with *P. acutifolius* will be more feasible than introgression using more distantly related wild relatives such as *P. angustissimus.*

Flowering Phenology and Reproductive Capability of Volunteer and Crop Canola in Western Canada and Potential Gene Flow

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Crop-to-crop gene flow or the movement of genes within the same species could be more detrimental to the environment compared to crop-to-wild or crop-to-weedy gene flow (Ellstrand 2003). However, there is less information on volunteer-crop gene flow because of prior research focus on gene movement from crops to wild or weedy relatives (Manasse and Kareiva 1991; Kwon et al. 2001). Crops with novel traits produced through recombinant DNA techniques allow the plant to possess characteristics not exhibited by their conventional counterparts. A decade after the first commercial release of novel trait crops, these now occupy 230 million acres of global arable land (James 2005). This massive production emphasizes the need to fill the research caveat on crop-to-crop gene flow because of their implications on weedy volunteers, gene flow and potential environmental risks (Warwick et al. 1999; Kwon and Kim 2001). The proposed project aims to elucidate information on the mechanisms of volunteer-crop gene flow in spring canola. Specifically, the proposed project will focus on the extent of flowering synchrony between herbicide-tolerant (HT) volunteer and crop canola (*Brassica napus* L.), and their combined reproductive capability in terms of viable seeds. In the short term, this project aims to achieve three goals: (1) conduct field experiments to determine the effect of crop planting density and planting dates on volunteer-crop flowering synchrony and seed production; (2) estimate the relative amount of gene flow that occurred in experimental plots using herbicide resistance as a marker for gene movement; and, (3) develop a volunteer-crop (V-C) gene flow model for canola grown in western Canadian conditions and production practices. Data generated from the field experiments and simulations produced from the V-C model can contribute to the long-term objective in developing a containment strategy for movement of the HT gene in canola. Furthermore, this project could provide baseline information for future research on similar initiatives for other crops with novel traits.

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Molecular mapping of hybrid necrosis genes *Ne1* and *Ne2* in hexaploid wheat using microsatellite markers

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Hybrid necrosis is the gradual pre-mature death of leaves or plants in certain F_1 hybrids of wheat (*Triticum aestivum L.*), and it is caused by the interaction of two dominant complementary genes *Ne1* and *Ne2* located on chromosome arms 5BL and 2BS, respectively. To date, molecular markers linked to these genes have not been identified and linkage relationships of the two genes with other important genes in wheat have not been established. We observed that the F_1 hybrids from the crosses between the bread wheat variety 'Alsen' and four synthetic hexaploid wheat (SHW) lines (TA4152-19, TA4152-37, TA4152-44, and TA4152-60) developed at the International Maize and Wheat Improvement Center (CIMMYT) exhibited hybrid necrosis. This study was conducted to determine the genotypes of TA4152-60 and Alsen at the *Ne1* and *Ne2* loci, and to map the genes using microsatellite markers in backcross populations. Genetic analysis indicated that Alsen has the genotype *ne1ne1Ne2Ne2* whereas the SHW lines have *Ne1Ne1ne2ne2*. The microsatellite marker *Xbarc74* was linked to *Ne1* at a genetic distance of 2.0 cM on chromosome arm 5BL, and *Xbarc55* was 3.2 cM from *Ne2* on 2BS. Comparison of the genetic maps with the chromosome deletion-based physical maps indicated that *Ne1* lies in the proximal half of 5BL, whereas *Ne2* is in the distal half of 2BS. Genetic linkage analysis showed that *Ne1* was about 35 cM proximal to *Tsn1*, a locus conferring sensitivity to the host selective toxin Ptr ToxA produced by the tan spot fungus. The closely linked microsatellite markers identified in this study can be used to genotype parental lines for *Ne1* and *Ne2* or to eliminate the two hybrid necrosis genes using marker-assisted selection.

Molecular characterization of *PgAGO*, a novel conifer gene of the ARGONAUTE family expressed in the apical cells and required for somatic embryo development in *Picea glauca*

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A new member of the ARGONAUTE (AGO) family of proteins was isolated from conifer and designated as *Pg*AGO (Gene Bank Accession No. DQ068741; protein ID. AAY67884). The complete coding sequence of *PgAGO* was obtained through screening of cDNA libraries generated from white spruce (*Picea glauca*) somatic embryos. The *PgAGO* gene has an open reading frame of 2880 bp and encoded a protein of 960 amino acids. The predicted protein has an isolectric point of 9.17, a molecular weight of 107 kD and lacks prominent hydrophobic domains, which makes its cellular location inconclusive. The novel protein contains the two conserved regions (the PAZ and the PIWI domains) which are typically found in all members of the AGO family. The PAZ domain of *PgAGO* is composed of 117 amino acid residues and it shares a low degree of homology with similar domains in other species. The C-terminal PIWI domain is composed of 86 amino acids and is more conserved. Localization and transformation studies suggest that PgAGO is required for embryo development, specifically for proper shoot and root apical meristem differentiation. RNA in-situ hybridization shows that PgAGO transcripts are preferentially localized in cells of the shoot and root apical meristems from the early phases of embryo development. RNA-mediated suppression of PgAGO also results in pronounced structural abnormalities of the apical meristems. In embryos with suppressed PgAGO expression the root meristems lack the group of mitotically inactive central cells, whereas the shoot apical meristems are poorly organized and lack a defined layer of apical initials. These abnormalities result in poor post-embryonic performance culminating in meristem abortion and growth cessation.

Isolation and Mapping of Novel Proanthocyanidin Mutation from *Arabidopsis thaliana*

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Flavonoids comprise a diverse group of phenolic compounds, which serve a variety of ecological and physiological functions in plants and have important nutraceutical, agricultural, and environmental applications. Flavonoids are involved in auxin transport, attraction of pollinators, defense against predators and pathogens, and protection against UV damage. Flavonoid polymers, called proanthocyanidins or condensed tannins, are especially advantageous for controlling ruminant digestion and insect foraging. They have wide-ranging benefits in human health, but are considered undesirable in non-ruminant diets. Seventeen flavonoid genes have been characterized by other researchers in *Arabidopsis*, including six types of regulatory genes, a vacuole transporter, and a stereo-specific flavanol reductase, but genes defining the last steps in polymer formation are still unknown. A T-DNA/activation-tagged *Arabidopsis* population (approximately 70, 000 lines) developed at SRC has been screened to find novel proanthocyanidin-free or enhanced seed colour mutations. Candidate mutants were stained histochemically through to the T_6 generation using DMACA, butanol-HCL, and Vanillin-HCL to confirm proanthocyanidin deficiency or over-expression. Then candidate lines were crossed with published proanthocyanidin-free *transparent testa (tt)* mutants and two wild types (Columbia and Landsberg). So far, four lines with novel allelic variation and four new mutants have been recovered from this population. One novel structural gene has bas also been identified. Phenotypes for several of these lines(from seed to the adult plant) will be discussed. Progeny lines from diallelic cross between one line and all *tt* mutation were also established and will be reported.

Characterization of Genes Relating to Chilling Stress in Bean

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Episodic late spring and early fall frosts are a major limitation to dry bean (*Phaseolus vulgaris* L.) production in the northern prairies. Under controlled conditions, *P. vulgaris* dies at the moment of ice formation (-1.5°C). Previous research by our group has identified a relative of *P. vulgaris*, *Phaselous angustissimus* L., which is capable of withstanding temperatures of –2.5°C under controlled conditions. We used two approaches to identify genes related to chilling tolerance in these species. One approach was to hybridize transcripts from non-chilled and chilled beans to a macroarray featuring ~2000 *Medicago sativa* cDNA clones, while another approach was to produce a subtraction suppression cDNA library using transcripts isolated from non-chilled and chilled beans. Results show that both approaches identify genes of similar gene categories being up- and down-regulated in *P. angustissimus* during chilling stress. The hybridization approach shows that *P. vulgaris* has a relatively more elaborate transcriptional response to chilling than *P. angustissimus*. Current efforts are underway to further characterize key genes and analyze their roles to chilling stress. Identifying and characterizing genes using these methods will give researchers a greater understanding of how beans respond to chilling stress, as well as giving breeders tools for selecting chilling tolerant beans.

Saturation Mapping of *species cytoplasm specific* Gene in Durum Wheat

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A *Triticum turgidum* L. var durum nucleus is not compatible with a *T. longissimum* cytoplasm. The two genes, scs^{ti} (species cytoplasm specific gene derived from *T. Timopheevi*) and *Vi* (vitality), together restore this interaction. The main objective of this research is to develop a saturated map spanning a 3cM segment surrounding scs^{ti}. The initial mapping population was 129 F_2 individuals derived from crossing a Langdon- *T. dicoccoides* chromosome 1A substitution line [LAN (Dic 1A)] with a euplasmic line homozygous for the scs^{ti} gene. The saturation mapping is followed by expanding this

population to approximately 2800 meiotic products and development of a BAC contig spanning the region surrounding *scs*^{H}. This would provide the necessary tools for cloning the gene and ultimately understanding its function and role in the evolution of polyploid species. Molecular markers such as RFLP, microsatelites and EST derived primers were used to create a high resolution linkage map. The flanking markers found for the *scs*^{H} gene were *Xbcd1449b* and *WMC120* with distances of 0.5 and 0.4 cM, respectively.

Inheritance of seed coat color genes of *Brassica napus* (L) and tagging the genes using SRAP molecular markers

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Inheritance of seed coat color in *Brassica napus* was studied using five black seeded varieties/ lines to three pure breeding yellow seeded lines, in the F_1, F_2, F_3, and backcross progenies. Seed coat color in *B. napus* was thought to be of maternal inheritance, but a pollen effect was found when yellow seeded lines were used as the female parent. Seed coat color varied from black to dark brown, brown, partially brown, yellowish brown and yellow. Seed coat color was found to be under multi-genic control, with black color dominant over yellow color. Partially brown/yellowish brown seed color lines have been identified in the F_3 generation. These F_3 lines are presumed to be single locus heterozygous plants. Two hundreds F_3 lines were selfed to F_4 lines segregating 3:1 for partially brown/yellowish brown : yellow seed. We used Bulk segregant analysis (BSA) on DNA from pure yellow-seeded and pure black-seeded parental and F_3 populations and identified several SRAP (sequence-related amplified polymorphism) molecular markers linked to the seed coat color gene(s). These molecular markers will be applied to the segregating F_4 lines to tag single genes for seed color in this multi-gene family. This is a new approach to molecular marker development for the individual genes of a multi-gene family.

Genetic mapping of pre-harvest sprouting resistance loci in bread wheat (*Triticum aestivum* L.)

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Hard white wheat is a new market class of spring wheat being developed for production in western Canada. There is a world wide demand for white wheat because consumers prefer the taste and appearance of food prepared from white wheat. With fewer phenolic compounds and tannins in bran, white wheat also imparts a less bitter taste and a more favorable appearance to the final product. When milling wheat to flour color standard, hard white wheat has flour yield advantage over hard red wheat. Introduction of hard white wheat cultivars would allow Canada to compete more directly with Australia which grows white wheat and is the world's leading hard white wheat exporter. For all its advantages, white wheat does have one drawback, i.e., pre-harvest sprouting. Pre-harvest sprouting (PHS) is the germination of mature grain while still in spike. Pre-harvest sprouting in bread wheat (*Triticum aestivum* L.) crop causes downgrading of grain quality which severely limits its end-use utilization. In western Canada, cool and wet weather during harvest makes the crops susceptible to PHS. Breeding for PHS tolerance in wheat is challenging on phenotypic basis because PHS is inherited quantitatively and strongly affected by environmental conditions. A mapping population of one hundred and fifty one doubled haploid (DH) lines from a cross between two spring wheat cultivars ND690 (non-dormant) and W98616 (dormant) was developed for molecular mapping of PHS resistance loci. Initially, 20 dormant and 20 non dormant lines were used for molecular mapping with SSR (Simple sequence repeat) and AFLP (Amplified Fragment Length Polymorphism) markers. A total of 550 markers (300 SSR markers and 250 AFLP) markers have been mapped on different chromosomes. A putative QTL was detected on the long arm of chromosome 4A in this mapping population.

Mapping of qtl for high grain protein content in Canadian durum wheat genotypes

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Durum wheat (*Triticum turgidum* L. var. *durum*) cultivars with high grain protein content (GPC) produce pasta products with greater cooking firmness and increased tolerance to overcooking. Negative correlation between GPC and grain yield, as well as the large effect of genotype x environment interaction on GPC have slowed breeding progress for high GPC. Identification of molecular markers associated with high GPC would aid durum wheat breeders to select for this important trait earlier in the plant breeding program. The objective of this research was to determine if QTL with elevated effect on GPC is conserved in Canadian durum wheat genotypes. A preliminary genetic map was constructed by screening polymorphic microsatellite markers on a set of 95 double haploid lines derived from the cross Strongfield (high GPC) X DT695 (low GPC). QTL analysis using simple interval mapping was performed on GPC data collected from the 95 DH lines grown at Swift Current and Regina in 2002 and Swift Current, Regina and Saskatoon in 2003. To date, we have identified two QTL for GPC flanked by *Xgwm339* and *Xgwm448* on chromosome 2AS, and by *barc158* and wmc332 on chromosome 2BL. No QTL for high GPC could be detected on chromosome 6BS, the location of a high GPC gene isolated previously from durum wheat suggesting that Strongfield contains novel QTL for high GPC not previously reported in the literature. The molecular markers flanking the QTL identified in this study can be used by durum wheat breeders to enhance selection of high GPC in durum wheat.

Sequence diversity analysis of the chalcone isomerase gene in common bean

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Common bean (*Phaseolus vulgaris* L.) represents about 50% of consumed grain legumes worldwide. Sequence based diversity studies reveal population structure and breeding history of different genotypes. The main objective of our project is to sequence various genes and build phylogenetic trees that uncover the evolutionary patterns within the species. A diversity analysis of dihydroflavonal-4-reductase (DFR) intron 1 was published by McClean et. al. (2004). We will add chalcone isomerase (CHI) sequencing to that phylogenetic analysis. CHI is a gene in the same flavonoid biosynthetic pathway as DFR. We analyzed the complete gene, including the promoter, coding sequence, and three introns to uncover evolutionary patterns among each of these. The results and statistics along with phylogenetic trees will be presented. This research also allows the development new SNPs and indel markers to benefit breeders.

ABAP1 is an abscisic acid receptor modulating barley seed dormancy and germination

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Seed dormancy and germination are adaptive traits that help plants to propagate and survive. Unbalanced dormancy and germination leads to major losses to agriculturally important crops. For example, germination of seeds on the mother plant (preharvest sprouting) severely damages the quality of grains. Plant hormones like abscisic acid (ABA) and gibberellic acid (GA) play a crucial role in governing dormancy and germination. GA promotes germination and ABA counteracts this action. ABA has also been implicated in the prevention of precocious germination during seed maturation and in the maintenance of dormancy state in mature seeds.

Genetic screens and biochemical and pharmalogical studies have not only revealed several components involved in ABA signaling but also provided compelling evidence for the existence of multiple perception mechanisms for ABA. To date, however, no ABA receptor has been identified in seeds. A gene encoding a protein, designated ABAP1, was cloned from barley aleurones in our laboratory and shown to bind ABA in a mole to mole ratio. Here we show evidence that ABAP1 is an ABA receptor that meets ABA-binding kinetics and modulates ABA-mediated inhibition of seed germination. The rate at which germination is inhibited is correlated with the abundance of *ABAP1* transcript levels as determined by quantitative real time PCR. Using a transient gene expression system to overexpress ABAP1, the germination response

of dormant and non-dormant embryos significantly altered after *ABAP1* overexpression. Embryos overexpressing *ABAP1* were more sensitive to ABA, an indication that ABAP1 action was tied to ABA. Furthermore, ABAP1 downregulated GA-activated genes and thus inhibited germination. In conclusion, our data present evidence that ABAP1 is an ABA receptor capable of inhibiting germination and promoting dormancy in barley. It therefore highlights the first characterization of an ABA receptor in cereals.

Genetic characterization and molecular mapping of Hessian fly resistance genes derived from *Triticum tauschii* in synthetic wheat

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Two synthetic hexaploid wheat lines (×*Aegilotriticum* spp., 2n=6x=42, genomes AABBDD), SW8 and SW34, developed from the crosses of the durum wheat cultivar Langdon (*Triticum turgidum* L. var. *durum*, 2n=4x=28, genomes AABB) with two *T. tauschii* (Coss.) Schmal accessions (2n=2x=14, genome DD), were determined to carry Hessian fly [*Mayetiola destructor* (Say)] resistance genes derived from the *T. tauschii* parents. SW8 was resistant to the Hessian fly biotypes Great Plains (GP) and *vH13* (virulent to *H13*). SW34 was resistant to the biotype GP, but susceptible to *vH13*. Allelism tests indicated resistance genes in SW8 and SW34 were allelic to or the same as *H26* and *H13*, respectively. *H26* and *H13* were localized to chromosome 4D and 6D in previous studies, respectively. Molecular mapping in the present study, however, assigned the *H26* locus to chromosome 3D rather than 4D. On the other hand, mapping of the resistance gene in SW34 verified the previous assignment of the *H13* locus to chromosome 6D. Linkage analysis and physical mapping positioned the *H26* locus to the chromosomal deletion bin 3DL3-0.81-1.00. A linkage map for each of these two resistance genes was constructed using SSR (simple sequence repeat) and TRAP (Target region amplification polymorphism) markers.

Manipulation of Biosynthesis of Aliphatic Glucosinolates in *Brassica Crops* through Gene Replacement and RNAi Gene Silencing in *Arabidopsis thaliana*

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Brassica species, such as canola, rapeseed, cabbage, cauliflower and broccoli, are important crops worldwide. Aliphatic glucosinolates are a large group of plant secondary metabolites with anti-nutrient, goitrogenic or antithyroid activity. So, Canola or double zero (low Glucosinolates and zero Erucic acid) *Brassica napus* are required for food purposes. But isothiocyanate, a metabolite of some specific aliphatic glucosinolates such as glucoraphinin, has anti-tumorogenic effects, the ratio of glucoraphinin in total aliphatic glucosinolates need to be improved to develop isothiocyanate-enriched vegetables. It has been inferred that ALK gene involved in the glucosinolates biosynthesis pathway, changing glucoraphinin to gluconapin or changing glucoiberin to sinigin. Two homologs of ALK gene, BoGSL-ALK$^+$ (functional alleles) are in Chinese cabbage and BoGSL-ALK$^-$ (null alleles) are in Brocolli. We will use interspecific crosses between Chinese cabbage and broccoli, followed by marker assistant selection to replace the functional alleles by null alleles and to create new germplasm with high specific glucosinolate. Some candidates genes' functions, such as MAMs-like genes (methylthioalkylmalate synthase) which are relate to aliphatic glucosinolates in *Arabidopsis* have not been confirmed yet. RNAi (RNA interference) mediated gene silencing is one of the most effective methods in analyzing the target gene's function. In my research, I will make two RNAi constructs and silence four MAM-like genes in *Arabidopsis,* to confirm if MAM-like genes regulate the content of alphatic glucosinolates.

Cloning and expression of *shootmeristemless* from adventitious buds of the perennial weed leafy spurge

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Leafy spurge (*Euphorbia esula* L.) was introduced into North America from Eurasia and has spread across the mid-west and northern plains. Leafy spurge has an extensive root system and large number of dormant underground adventitious buds on its lateral roots, making it an ideal plant for studying growth and development of adventitious buds. There are numerous genes responsible for the initiation and maintenance of shoot apical meristems. *SHOOTMERISTEMLESS* (*STM*) a key member of the *KNOTTED* gene family is one such gene. *STM* encodes a homeodomain protein and is responsible for maintaining a pool of undifferentiated cells in the central zone of the shoot meristem. The expression or function of *STM* in dormant buds is not well understood. Our objective was to clone and characterize the expression pattern of *STM* after induction of adventitious root buds in leafy spurge and throughout different seasons. We designed primers for conserved region of *STM* and PCR amplified the *STM* sequence from cDNA derived from growing meristems. The amplified fragment was then used to identify near full length cDNA and genomic clones of *STM* from respective leafy spurge DNA libraries. We have obtained 1,939 bp of the *STM* promoter sequence from the genomic clone and is currently being mapped for conserved regions and *cis*-elements. It was found that *STM* was up-regulated in as little as 8 hours after induction and continues to increase in expression through 72 hrs. *STM* was also found to be minimally down-regulated in eco-dormant crown buds, but rapidly reaches control levels in mid- to late winter.

Studies on the physiological and molecular analyses of Zinc (Zn) transporting gene (s) in *Arabidopsis thaliana*

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Zn is a mineral nutrient, which is essential for normal growth and development of the plants. While Zn deficiency results in reduced plant growth and yield, higher Zn levels in soil behave as a heavy-metal and cause environmental contamination. Hence, it is imperative to find solutions for increased Zn uptake and use efficiency. Several genes and gene families are reported to be involved in nutrient transportation and accumulation in plant system. Hence preliminary experiments were conducted to study the role of nutrient transporting gene (s) in Zn uptake and transport, in the model plant *Arabidopsis thaliana*. The study was approached with forward and reverse genetic screening experiments. Forward screening experiments were carried out with T-DNA inserted *Arabidopsis* mutants obtained from Nottingham Arabidopsis Stock Centre (NASC). Reverse screening experiments were conducted with SALK lines, with known disruption in the gene, which were obtained from The SALK Institute, USA. In the forward genetic screen, two mutants from the line N75087 and in the reverse genetic screen, line At2g41560-N522936 that may have altered Zn uptake were rescued. Presence of T-DNA insert and homozygosity of the line At2g41560-N522936 was confirmed with PCR experiments. These preliminary results need further confirmation and detailed characterization of these lines is undergoing.

Radiation Mapping of the Species Cytoplasmic-Specific (scs^{ae}) Gene in Durum Wheat

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The improvement of *Triticum turgidum* L. *var. durum* (genome AABB) by introgression of agronomically important genes from wild species is limited by nuclear-cytoplasmic incompatibility between alien cytoplasms and the durum nucleus. This incompatibility can cause male sterility, decreased vigor, delayed maturity and other undesirable effects. Compatibility is restored by species cytoplasm-specific (*scs*) nuclear genes and vitality (*Vi*) genes. This study focuses on

scs^{ae}, localized on chromosome 1D of *T. aestivum* (genome AABBDD). The 1D *scs*^{ae} chromosome is transmitted without recombination, which precludes traditional mapping strategies for *scs*^{ae}. Radiation hybrid (RH) mapping presents an alternative means for the localization of *scs*^{ae} on chromosome 1D.

Radiation hybrid mapping is based on radiation-induced chromosome breakage and analysis of chromosome segment retention or loss using molecular markers. Radiation hybrid mapping is especially advantageous in species with large, complex genomes, and where classical recombination mapping is not feasible. Thus, RH mapping is ideally suited to addressing the difficulties presented with mapping *scs*^{ae}.

In this study, an RH mapping population was developed from an alloplasmic (and hemizygous for scs^{ae}) durum line [(lo) durum] with 1D from *T. aestivum* L. using 35 krad gamma rays. The objectives of this study are: 1.) the development of a saturated RH map for the region surrounding *scs*^{ae} on chromosome 1D, and 2.) to determine the relationship between level of radiation and its effect on the physical size of retained 1D segments. Radiation-induced breaks will be assayed on a population of 87 individuals utilizing expressed sequence tags (ESTs) specific for chromosome 1D. The analysis of molecular marker retention in the resulting RH map will allow localization of *scs*^{ae} on chromosome 1D.

Quantitative trait loci (QTL) mapping of pre-harvest sprouting in two barley populations

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Pre-harvest sprouting (PHS) in barley (*Hordeum vulgare* L.) is often associated with rainy or wet weather following physiological maturity. Kernels sprout in the field prior to harvest of the grain, leading to reduction in barley and malt quality. The objective of this research is to map quantitative trait loci (QTL) in two barley populations Harrington/Morex and Chevron/Stander. Each population and its parents were grown in the greenhouse in year 2004 and 2005 using an RCBD design. Spikes were harvested at harvest maturity, put into plastic bags, sealed, and stored at -20 °C to maintain seed dormancy. Germination energy (GE), defined as percent germination at 72 hr in 4 ml of water in a petri dish, was determined for each line using hand-threshed seeds. QTL analysis was performed using Mapmanager QTXb17. A major QTL was identified in similar regions at the end of the long arm of chromosome 5H for both populations. In the Harrington/Morex population, the marker MWG851B accounted for 61% and 79% of the phenotypic variation, respectively, in the two years. The QTL identified in the Chevron/Stander population was located in the region Xmwg584-Xcdo785a, and the marker Xabg463 explained 12% and 17% of the total phenotypic variation, respectively, in the two years.

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The Faculty had its beginnings in Winnipeg in 1906 with the formation of the Manitoba Agricultural College, located on the south bank of the Assiniboine River (today's Tuxedo area of Winnipeg). The first agricultural diplomas were conferred in 1908 and the first agricultural degrees in 1911.

Home Economics students began enrolling in the college in 1910, but several years elapsed before degrees were conferred. It wasn't until eight years later, in 1918, that the first graduates of the degree program were recognized.

In 1913, the Manitoba Agricultural College moved to the site of the Fort Garry campus which later became the University of Manitoba. In 1924, the administration of the Manitoba Agricultural College, now the Faculty of Agriculture and Home Economics, was transferred to the University of Manitoba.

Agriculture and Home Economics became separate faculties in 1970 and, in July 1991, the name was changed from Faculty of Agriculture to the Faculty of Agricultural and Food Sciences.