Abstracts of Technical Papers

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Oral Presentation Abstracts

Canadian Triticologists: The Game Changers! R. M. DePauw[1]*, B. McCallum[2], H. Voldeng[3], R. E. Knox[1], N. Edwards[4], D. Hatcher[4], T. Fetch[2], O. Lukow[2], S. Fox[2], C. Pozniak[5], P. Hucl[5], A. Comeau[6], and A. K. Singh[1]. [1]Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, Swift Current, Canada S9H 3X2; [2]Cereal Research Centre, AAFC, Winnipeg, Canada R3T 2M9; [3]Eastern Cereal and Oilseed Research Centre, AAFC, Ottawa, Canada; [4]Grain Reseach Laboratory, Canadian Grain Commission, Winnipeg, Manitoba, Canada R3C 3G8; [5]Crop Development Centre, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8; and [6]Soils & Crops Research & Development Centre, Ste-Foy, Quebec, Canada G1V 2J3.

Wheat is not indigenous to North America. The first Europeans brought wheat with them to North America as a source of food and feed. Wheat was grown for local consumption for several hundred years in eastern and central regions of Canada. Opening of new western lands in the former Hudson Bay Company territories required new immigrants who could produce products that could be exported to Europe and be sold at a sufficiently high price to cover the cost of transportation. William Saunders was commissioned to establish agricultural research to support economic development in Canada. Wheat was only one among many crops. The production of wheat was fraught with ongoing challenges. The population of Canada exploded with new immigrants to the prairies that resulted in families establishing communities and concomitant economic activity fuelled primarily by wheat. By the late 1920s, the wheat industry rivalled mining and forestry in magnitude as a source of foreign exchange earnings. This achievement was underpinned by overcoming enormous biotic and abiotic challenges. Science disciplines evolved as the mysteries of the various pathogens, insects, soil nutrition, soil stresses, climatic stresses, and wheat genotype by environment interactions were unravelled. Breeders, geneticists, cytogenetists, pathologists, entomologists, cereal chemists, agronomists, biometricians, biotechnologists, and engineers have worked together to provide the research and development that underpinned the $5 billion wheat export and another $9 billion in value added processing of wheat today. Many people are behind the research and development that has led to the current wheat industry in Canada.

Canadian wheat pioneers. G. Martens*. Room 222 Agriculture building, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2.

Good farmers have always been persistent; always looking to the next year and the next variety of wheat. They will trail any leads on a new wheat like a hunting dog tracks game, oblivious of borders. Not only are good farmers persistent, they are observant and meticulous and they test their observations with experiments in order to learn from their observations. Farmers have made major contributions to wheat development in Canada by spending time in their fields and by being observant. They have contributed mostly by making selections of natural crosses. I will tell you a few stories about the persistence, the observations and the selections of Canadian wheat pioneering farmers.

The future of publicly funded wheat development in Canada. S. Fox*. Cereal Research Centre, AAFC, 195 Dafoe Rd, Winnipeg, Manitoba, Canada R3T 2M9.

Publicly funded wheat breeding in Canada has a history starting sometime after 1886 and became well established in western Canada in the 1920s and 1930s with the establishment of federal government and university programs. Currently about 92% of western wheat area can be attributed to publicly produced varieties. Large structural changes in the wheat industry are taking place: dismantling of single desk marketing is also removing the primary industry leader; several life science companies are establishing wheat breeding programs in western Canada; the producer check-off targeted to public breeding is expected to be broadened to encompass all wheat that is sold; the National Research Council is developing a ''wheat flagship'' research program to ''develop a strain of wheat resilient to environmental stress''. Breeding objectives have been broadened since the 1990s with the addition of resistance to wheat midge and Fusarium head blight; more recently, significant efforts to improve resistance to stem rust (Ug99) are being made and now there are increasing concerns about stripe rust. Together, these changes represent significant

challenges and likely redistribution of effort. In this changing environment, publicly funded wheat development programs will be asked to provide a balance to private investments, focus on public-good traits, develop long-term cooperative arrangements with private breeding programs, and develop intellectual property management capacity to allow for equitable exchange of germplasm, knowledge and technology.

Funding wheat research through partnerships: challenges and prospects. V. Galushko[1]* and R. Gray[2]. [1]3737 Wascana Parkway, University of Regina, Economics, Regina, Saskatchewan, Canada S4S 0A2; and [2]51 Campus Drive, University of Saskatchewan, BPBE, Saskatoon, Saskatchewan, Canada S7N 5A8.

In the past decade, the crop research industry has witnessed an increased role for corporate investment in crop breeding, with the involvement of the private sector varying across countries and across crops. With numerous research funding models emerging, there is a need to undertake a study of alternatives to publicly funded research to formulate a coherent crop research policy for Canada. The wheat breeding industry represents an excellent case study of different research funding models because, compared with other crops, its structure differs widely in Western Europe, in different regions of the United States, Canada, and Australia and, therefore, it offers a broad overview of possibilities to crop research industry structures.

As the private sector becomes a dominant player, intellectual property landscape is becoming more complex and new tools to increase breeding efficiency are sought. One such tool is the creation of alliances between public and private institutions, both nationally and internationally. While partnerships in research can increase efficiency through undertaking complementary rather than competing research, differences in incentives of private and public institutions can stand in the way. As public researchers partner more with industry a number of questions arise: What types of activities will these partnerships undertake? What kind of products will they produce? What will they not do? How will public-private partnerships change the role of public researchers?

The goal of our work within the Canadian Triticum Advancement through Genomics (CTAG) project is to map linkages among the wheat breeding industry participants to understand the structure of the industry and relationships among the players as well as ownership and availability of wheat genomic technologies. To this end a social network analysis is being employed. Once the linkages between organizations engaged in wheat genomics research are identified, case studies of partnerships will be undertaken to fully understand strengths and limitations of each partnership model.

Human health issues and wheat. C. Taylor*. Human Nutritional Sciences, University of Manitoba, Winnipeg, Manitoba, Canada.

Wheat is an important staple food, providing energy/carbohydrate, some protein and various vitamins and minerals. Consumption of wheat in its ''whole grain'' form is an important source of dietary fibre. Despite the good nutrition of wheat, there are increasing numbers of individuals ($\sim$1 in 133 Canadians) diagnosed with celiac disease who must avoid wheat in their diet for the rest of their life. Celiac disease is hereditary. The underlying cause is an immune reaction to gluten/gliadin present in wheat, barley and rye. This results in atrophy and flattening of the intestinal villi, which significantly decreases the surface area for brush border digestive enzymes, nutrient transporters, and the overall area for nutrient absorption. The types of symptoms and their severity vary among individuals and include gastrointestinal (abdominal pain, bloating, gas, chronic diarrhea, fatty stool), weight loss and fatigue. Long-term consequences include anemia, bone disease, muscle weakness, peripheral neuropathy, endocrine disorders and dermatitis herpetiformis. The gold standard for diagnosis is a biopsy of the intestinal tract before and after a gluten-free diet; blood tests for antibodies (tTG, EMA) are used for screening. A seminal paper published in Science in 2002 identified a 33 amino acid peptide in gliadin that is resistant to digestion and the authors proposed an enzyme approach (Glut-aid) to digest the peptide. Other research has focused on identification of the antigenic site(s) in gliadin; this may one day lead to breeding a wheat variety that does not illicit an immune response in individuals with celiac disease.

Characterization of wheat proteins responsible for allergies and food intolerances. S. B. Altenbach*. USDA-ARS Western Regional Research Center, 800 Buchanan Street, Albany, CA 94710 USA.

Wheat flour contains a complex mixture of proteins that are important for human nutrition and also confer the functional properties that make it possible to produce bread, noodles and various baked goods. Some of these proteins are responsible for celiac disease, a serious food intolerance that affects nearly 1% of the population in North America, while other proteins cause IgE-mediated food allergies or the occupational allergy referred to as baker's asthma. The identification of individual proteins that cause these health problems and their corresponding genes is critical for determining the roles of these proteins in grain development and flour quality and for developing strategies to reduce the allergenic potential of wheat flour. The presentation will summarize recent proteomic and molecular studies in developing grain and flour from the US bread wheat cultivar Butte 86. Transgenic approaches to decrease the

levels of immunogenic proteins in the flour will be described using the omega-5 gliadins that cause the food allergy wheat-dependent exercise-induced anaphylaxis as an example.

Goodness of wheat: Facts on health benefits of wheat. N. Ames*. Agriculture and Agri-Food Canada, 196 Innovation Drive, Winnipeg, Manitoba, Canada R3T 2N2.

In recent years, a trend towards eating a low carbohydrate diet, and increased awareness of the effects of wheat consumption for those suffering from celiac/allergies, together with the emergence of soluble fibre health claims for oats (USA and Canada) and barley (USA), may be contributing to a negative perception of wheat in the public eye. However, research on wheat and its bran components (arabinoxylans, beta-glucans, betaine, lutein, ferulic acid and other phenolic acids, and alkylresourcinols) has shown that there are many health benefits associated with the grain, which include reduction in adipose tissue, decreased insulin resistance, lower plasma glucose and insulin, reduction in total and LDL cholesterol, increased satiety, increased faecal bile acid excretion, and decreased inflammation. Research is ongoing in the area of improving the health benefits of wheat through breeding, enrichment with selected mill streams high in aleurone/bran, and chemical processing of the grain to release dietary fibre components (arabinoxylan, ferulic acid) from the cell wall matrix.

Precision farming with real-time optical sensors: Getting the wheat plant to tell us about its growth potential as a function of spatial and temporal conditions. G. P. Lafond[1], C. B. Holzapfel[2], and W. E. May[1]
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Producers are interested in knowing the level of crop inputs required to maximize returns in a given field. Nitrogen fertilizer represents one of the highest input costs, and accounts for the largest proportion of total energy consumption in wheat production. Nitrogen fertilizer also has the largest effect on grain yield, but is an environmentally active compound. Matching crop inputs to the production potential of a field requires an understanding of spatial and temporal variability. Spatial variability represents the differences in production potential as a function of its landscape characteristics due to glacial and human activity and the distribution of soil properties across a field. Temporal variability is the interaction of landscape and soil properties with weather. Current approaches to precision farming (PF) try to uncover the underlying spatial variability and manage it accordingly through the delineation of management zones and applying nitrogen fertilizer accordingly based on decisions made prior to seeding. A new approach involves real-time optical sensors, which indirectly measures above-ground biomass and applies nitrogen fertilizer according to a pre-determined algorithm. Plants are very good at integrating everything that has been experienced in the root zone accounting for not only spatial variability but temporal variability as well. A series of field and plot trials has been conducted since 2005 to assess optical sensors for PF. The positive results range from reduced N fertilizer use to higher grain yields with the same or more N fertilizer. This approach attempts to allocate N fertilizer across a field more efficiently based on measurements of plant biomass relative to biomass from a non-limiting nitrogen rich strip.

Sustainably growing wheat in western Canada-A producer's perspective. L. Moats*. Box 42, Riceton, Saskatchewan, Canada S0G 4E0.

To sustain economic viability in the long term, producers need to generate profits without degrading the lands capability to produce and generate future profits. Cropping choices are a function of risk, profitability and agronomic considerations. The risk factors are numerous and include environmental conditions, market, political and others. LLAMM Acres has used no-till production practices for the past 20 yr as part of its strategy to address soil degradation issues. No-till has been the primary tool to rebuild soils that had been farmed under an intensive tillage regime for the past 80 yr. Rotating crops between cereals, oilseeds and pulses has addressed agronomic risks such as diseases, insects and to some extent market risks. Including wheat in the rotation is a function of wheat's competitive position in the international market place which, together with yield potential, drives per acre returns. Wheat's place in the rotation has been challenged by the significant improvement that other cropping choices have seen in yield, weed control and overall agronomic performance such as canola. Western Canadian producers need improved agronomic performance from wheat to improve its competitive position as a cropping choice which is essential to economic viability at the farm gate.

Assessing the ecological basis of a multi-pest approach to management of wheat-fallow systems. F. Menalled[1]*, E. Keren[1], D. Weaver[1], A. Dyer[2], and J. Robison-Cox[3].
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The concentration of wheat production in the Northern Great Plains has resulted in the development of

specialized multitrophic pest complexes whose members interact in both positive and negative ways. In this context, management recommendations based on the traditional single-species pest control paradigm may lead to undesirable outcomes. Our goal was to evaluate a modeling framework to make multi-pest management decisions that take into account the existence of direct and indirect interactions among pests belonging to different trophic levels. We adopted a Bayesian decision theory approach in combination with path analysis to evaluate interactions between *Bromus tectorum* (cheatgrass), Fusarium crown rot, and *Cephus cinctus* (wheat stem sawfly). We assessed the joint response of these pests to seeding rates, cultivar competitiveness, and cultivar wheat stem sawfly tolerance. Results indicate that yield differences can be more readily explained as a result of the effects of management on pests and multi-pest interactions, rather than just by the direct effect of any particular management scheme on yield. For example, wheat stem sawfly tolerant varieties should be planted at a low seeding rate under high insect pressure. However, this variety should be replaced by a competitive and drought tolerant cultivar at high seeding rates as *B. tectorum* levels increase, despite the persisting wheat stem sawfly infestation. Also, the incidence of Fusarium can be explained by the abundance of *B. tectorum*, an alternative host for this disease. Our research suggests a framework for establishing a balance between model simplicity and the complexity of the process being modeled.

High-throughput approaches to genome-wide analysis of genetic variation in polyploid wheat. E. Akhunov[1]*, S. Chao[2], C. Saintenac[2], S. Kiani[2], D. See[3], G. Brown-Guedira[4], M. Sorrells[5], A. Akhunova[6], J. Dubcovsky[7], C. Cavanagh[8], and M. Hayden[9]. [1]Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA; [2]USDA-ARS Biosciences Research Laboratory, Fargo, ND, USA; [3]USDA Western Regional Small Grains Genotyping Lab, Johnson Hall, WSU, Pullman, WA, USA; [4]USDA-ARS Eastern Regional Small Grains Genotyping Lab., 4114 Williams Hall, NCSU, Raleigh, NC, USA; [5]Plant Breeding & Genetics, Cornell University, NY, USA; [6]Integrated Genomics Facility, Kansas State University, Manhattan, KS, USA; [7]Department of Plant Sciences, University of California, Davis, CA, USA; [8]CSIRO, Food Futures National Research Flagship, Canberra, ACT 2601, Australia; and [9]Department of Primary Industries Victoria, Victorian AgriBiosciences Center, 1 Park Drive, Bundoora, VIC 3083, Australia.

Genome-wide analysis of genetic variation is a powerful tool for detecting marker-trait associations in diversity panels and mapping populations. Genome scale genotyping data can be generated using high-throughput assays capable of detecting allelic variation in a predefined set of SNP loci or by direct sequencing. The combined effort of several research groups in collaboration with the International Wheat SNP Working Group developed high-throughput SNP genotyping assays based on the Illumina iSelect platform. The assay was used to genotype 12 000 wheat lines including cultivars, landraces, wild relatives and the progeny of several mapping populations. Out $\sim$9000 SNP assays 95% produced high-quality genotype calls with up to 70% being polymorphic in a diverse sample of wheat cultivars with a minor allele frequency >0.05. Two high-density genetic maps based on SynOp and 4-way MAGIC populations were developed. An alternative approach to SNP detection relies on next-generation sequencing technologies for direct sequencing of complexity reduced genomic libraries prepared either by restriction digestion or by selective capture of genomic regions of interest. These sequence-based genotyping approaches demonstrated high efficiency for detecting allelic variation in the wheat genome. The applicability of iSelect assay and genotyping-by-sequencing approaches for the analysis of genetic variation and genotype-phenotype relationships in wheat will be presented.

Overview and progress of the CTAG project. C. McCartney[1], C. Pozniak[2], A. Sharpe[3], R. MacLachlan[3], P. Hucl[3], M. Jordan[3], R. Knox[4], H. Randhawa[5], D. Spaner[6], F. Bekkaoui[6], V. Galushko[7], and R. Gray[8]. [1]AAFC-Cereal Research Centre, 195 Dafoe Road, Winnipeg, Manitoba, Canada; [2]Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK; [3]Plant Biotechnology Institute, National Research Council of Canada, Saskatoon, Saskatchewan, Canada; [4]AAFC-Semiarid Prairie Agricultural Research Centre, Box 1030, Swift Current, Saskatchewan, Canada; [5]AAFC-Lethbridge Research Centre, 5403 1st Ave South, Lethbridge, Alberta, Canada; [6]Department of Agricultural, Food and Nutritional Science, University of Alberta, 4-16D Agriculture/Forestry Ctr, Edmonton, Alberta, Canada; [7]Department of Economics, University of Regina, 3737 Wascana Parkway, Regina, Saskatchewan, Canada; and [8]Department of Bioresource Policy, Business & Economics, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, Canada.

The Canadian Triticum Advancement through Genomics (CTAG) project aims to provide genetic information and tools for the improvement of molecular breeding in wheat. The project has four major activities: (1) generating the first complete sequence of chromosome 6D, (2) capturing and sequencing genomic coding sequences from Canadian wheat varieties, (3) identifying, validating, and mapping SNP markers in Canadian wheat germplasm, and (4) examination of the role of public-private partnerships in wheat genomics and breeding (GE3LS research). Sequencing of chromosome 6D will be done on a BAC by BAC basis, as agreed

upon by the International Wheat Genome Sequencing Consortium. Prior to the CTAG project, shotgun survey sequencing of the 6D chromosome arms generated 70x coverage. The survey sequence was mined for resistance gene analogs for marker development. Evaluation of these markers is underway. The development of new SNPs in Canadian germplasm will begin once a liquid-based gene capture technology is available for wheat. In the meantime, a panel of 66 Canadian spring and durum wheat varieties and breeding lines are being tested against available SNPs from the USA (9k Infinium assay) and UK (KASP assay). Data collection is complete on 1046 UK SNPs. Nineteen percent of the KASP markers were monomorphic on 61 Canadian spring wheat lines. PIC values ranged from 0 to 0.59 with a mean of 0.20. Twenty-six and sixteen percent of the KASP markers were polymorphic on the bread wheat population RL4452/AC Domain and the durum wheat population W9262/Kofa, respectively.

Plant organelle transfection using cell penetrating peptide. F. Eudes*. Agriculture and Agri-Food Canada, Lethbridge Research Centre, P.O. Box 3000, Lethbridge, Alberta, Canada T1J 4B1.

Cell-penetrating peptides (CPPs) are nanocarriers with the property to translocate across cell membranes and target specifically subcellular localisation. CPPs also have the capacity to non-covalently bind to cargo molecules, such as nucleic acid and protein, and transport them to its final subcellular destination. The nuclear targeting CPP-cargo uptake pattern between the mammalian system and the plant system is very similar. The dimer Tat 49-57 RKKRRQRRR basic domain has been extensively used for wheat and triticale nuclear targeting and delivery of dsDNA, ssDNA and proteins. Synthetic or in vivo produced nucleic acid, proteins and CPPs are blocks that conjugate to form nanocomplexes in a relatively predictable manner. ssDNA binding proteins such as RecA, Rad51 and VirD2 were used to form with ssDNA various cargo complexes, and increased the integrity of ssDNA in the haploid plant genome of microspore. Two novel classes of CPPs were recently discovered with property to carry dsDNA specifically into the chloroplast or ethioplast, and mitochondria of protoplasts and microspore. The distinct ability of CPPs to deliver functional macromolecules cargoes specifically in one of the three organelles that are otherwise restricted to cross the membrane has led to the development of novel nanocarrier-mediated gene and protein delivery methods in somatic cells and microspores. CPPs offer an alternative to Agrobacterium and biolistic mediated transformation for the production of transgenic plants. CPP mediated transfection in plant microspore opened new possibilities for precision genetic engineering of the three organelles of this unique cell type and crops of commercial importance.

An alternative approach for identifying the chromosome location of new genes. C. Hiebert[1]*, J. Thomas[1], and H. Ghazvini[1]. [1]AAFC-Cereal Research Centre, 195 Dafoe Road, Winnipeg, Mantiba, Canada R3T 2M9.

Identifying an approximate chromosome location is the primary difficulty when genetically mapping new wheat genes. There are several methods for this purpose that are based either in cytogenetics or molecular genetics, such as bulked segregant analysis (BSA) and genome mapping. Cytogenetic techniques are laborious, time consuming and require accurate maintenance of cytogenetic stocks. BSA is rapid but particularly sensitive to the degree of linkage between the gene of interest and adjacent DNA markers. This may result in linked markers, and thus the chromosome location, going undetected. Genome mapping is reliable for locating new genes but is labour intensive and expensive. Here we propose an alternative approach for locating new genes. Our method, multiple bulked segregant analysis (MBSA), is based on 14 "mini-bulks" that combines the reliability of genome mapping with the efficiency of BSA. A set of 423 simple sequence repeat (SSR) markers was chosen based on profile simplicity and degree of polymorphism. Primers were preloaded and dried in 384-well PCR plates with multiple sets of these plates produced concurrently. Each primer was dispensed in 16 wells, 14 for the mini-bulks and two for the parents of the population. Each mini-bulk contains the equivalent of four gametes with known genotypes at the locus/loci of interest from a segregated population. Following PCR and product analysis, a putative gene location is determined by the SSR allele pattern across the mini-bulks. The criteria for a "hit" were determined by simulation experiments. Examples of the successful implementation of this protocol are reported.

Epidemiology and management of stripe rust in North America. E. A. Milus*. Department of Plant Pathology, University of Arkansas, Fayetteville, AR 72701, USA.

Since 2000, stripe rust has been a constraint to wheat production on all continents where wheat is grown, even in regions where stripe rust had never occurred before 2000. The major reason for this change has been the development and rapid global spread of a new pathogen strain (based on AFLP fingerprint pattern) that is more aggressive (causes more disease more quickly) and causes disease at warmer temperatures than the old strain. Pathogen survival between wheat crops is a key factor in determining the severity of epidemics, and production of winter and spring wheat in the same region favors a high level of survival. In 2010, winter and spring wheat crops in the western United States and Canada were delayed in maturity due to cool, wet weather such that spring wheat maturity overlapped with winter wheat emergence, resulting in an

unprecedented level of fall infection across the region. A mild winter with snow cover facilitated widespread overwintering of races capable of attacking multiple winter and spring wheat cultivars. Cool, wet weather during the 2011 season completed the conditions for a "perfect storm" of a stripe rust epidemic and set the stage for more fall infection of winter wheat. An integrated strategy that includes avoiding very susceptible cultivars, late-planted spring wheat and early-planted winter wheat, applying foliar fungicides, diversifying resistance genes, and perhaps applying seed treatments to winter wheat will be needed to manage stripe rust.

Integrating the building blocks of agronomy and biocontrol into an IPM strategy for wheat stem sawfly. B. L. Beres[1]*, H. A. Cárcamo[2], D. K. Weaver[3], L. M. Dosdall[4], M. L. Evenden[5], B. D. Hill[5], R. H. McKenzie[6], R.-C. Yang[6], and D. M. Spaner[6]. [1]Agriculture and Agri-Food Canada, Lethbridge Research Centre, 5403 1st Avenue South, Lethbridge, Alberta, Canada T1J 4B1; [2]Agriculture and Agri-Food Canada, Lethbridge Research Centre, 5403 1st Avenue South, Lethbridge, Alberta, Canada T1J 4B1; [3]Montana State University Department of Land Resources and Environmental Sciences, P.O. Box 173120, Bozeman, Montana 59717-3120, USA; [4]University of Alberta Department of Agricultural, Food, and Nutritional Science, 410 Ag/Forestry Building, Edmonton, Alberta, Canada T6G 2P5; [5]University of Alberta Department of Biological Sciences, CW405, Biological Sciences Building, Edmonton, Alberta, Canada T6G 2E9; and [6]Alberta Agriculture and Rural Development, Lethbridge Research Centre, 100, 5401 1st Avenue South, Lethbridge, Alberta, Canada T1J 4V6.

The wheat stem sawfly (*Cephus cinctus* Norton [Hymenoptera: Cephidae]) is a serious threat to wheat (*Triticum aestivum* L.) in the northern Great Plains. Insecticides have proven ineffective and can be detrimental to beneficial insects. The management of wheat stem sawfly, therefore, requires the integration of host plant resistance, agronomic and biological control strategies. Studies in Alberta, Canada, assessed the response of wheat stem sawfly and its natural enemies to cultivar selection, residue management, seeding rates, fertility regimes, and harvest management. Solid-stemmed cultivars are usually agronomically superior to susceptible cultivars when sawflies are present. The stubble disturbance associated with residue management and direct-seeding in a continuous cropping system can reduce sawfly populations compared with a wheat-fallow system. Increased seeding rates can optimize yield, but an inverse relationship between pith expression (stem solidness) and higher seeding rates may occur. Positive yield responses are typically observed with N rates >30 kg N ha^{-1}, but increased stem cutting by sawfly can occur with higher N rates. Increasing cutter bar heights during combine harvest can conserve natural enemies, and chopping straw for improved residue management in the spring will not likely affect wheat stem sawfly parasitoids that overwinter in the straw. In summary, an integrated strategy to manage wheat stem sawfly consists of diligent pest surveillance, planting solid-stemmed cultivars, continuous cropping with appropriate pre-seed residue management, seeding rates no greater than 300 seeds m^{-2}, 30 to 60 kg N ha^{-1}, and harvest cutting heights of at least 15 cm to conserve parasitoids.

Managing damage by the wheat midge to spring wheat with genetically tolerant cultivars. I. Wise[1]*, M. Smith[1], and S. Fox[1]. [1]Cereal Research Centre, Agriculture and AgriFood Canada, 195 Dafoe Road, Winnipeg, Manitoba, Canada R3T 2M9.

The wheat midge, *Sitodiplosis mosellana* Géhin, is the most serious insect pest of spring wheat in western Canada. Larvae feed on newly developing seed, either causing the complete loss of the seed or its partial damage, which can result in the down-grading of the grain. The discovery of the *Sm1* R-gene at the Cereal Research Centre and its addition to commercial spring wheat cultivars has enabled growers to mitigate damage by the midge. Varietal blends of 90:10 resistant:susceptible seed are being used to minimize the potential for the selection of virulent midge biotypes. *Sm1* works by deterring feeding by the larva, resulting in its subsequent death. The initial feeding by larvae on resistant seed can cause some seed damage. The degree of damage has been found to vary between cultivars. Our future research focus is to better understand the causes for the differences in the expression of *Sm1* in wheats with different pedigrees. A second potential genetic source of resistance is with antixenotic genes, which deter oviposition on the wheat spikes. Antixenosis by Waskada spring wheat can reduce seed damage by the midge by up to 70%. It is not known how many genes are involved in oviposition deterrence by Waskada, or how environmental factors may affect their expression.

Chromosomal locations for leaf rust resistance genes in Toropi. S. B. Rosa[1]*, B. McCallum[2], A. Brule-Babel[3], C. Hiebert[2], and S. Shorter[4]. [1]Cereal Research Center, Agriculture and Agri-Food Canada, Winnipeg, Manitoba, Canada R3T 2M9; Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2; [2]Cereal Research Center, Agriculture and Agri-Food Canada, Winnipeg, Manitoba, Canada R3T 2M9; [3]Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2; and [4]Plant and Food Research, Christchurch, New Zealand.

Breeding for leaf rust resistance of wheat is a challenge as the *Puccinia triticina* (leaf rust pathogen) population

presents high virulence shifts. To date, 59 Lr genes have been described; however, just three genes, *Lr34*, *Lr46* and *Lr67*, show partial durable resistance. Toropi (Frontana 1971.37/Quaderna A//Petiblanco 8) has retained its leaf rust resistance for more 40 yr. Previously, two complementary adult plant resistance (APR) genes were reported to be present in Toropi. To characterize the source of resistance present in Toropi and to map the genes, double haploid and backcross populations were developed by crossing Toropi with Thatcher. Toropi and the double haploid population were tested in the field in Canada, Brazil and New Zealand. The leaf rust reaction of Toropi was always below 15 MR. Evaluation in greenhouse and field indicated that resistance in Toropi is conferred by one dominant race specific seedling gene, two recessive complementary race non-specific APR genes and one race specific adult plant gene, which was mapped on 4BL chromosome. The seedling genes were not effective in the field in Canada, but they conferred immunity in New Zealand and improved the resistance of lines with the APR genes. The race specific adult plant gene showed little to no effect in Canada, but was moderately effective in New Zealand. The two recessive complementary race non-specific APR genes were effective in Canada, New Zealand and Brazil. The DH population is being used to map the APR genes using SSR and SNPs markers.

The systemic approach: Faster genetic progress for complex goals. A. Comeau[1], F. Langevin[1], H. Voldeng[2], S. Haber[3], J. Gilbert[3], H. Randhawa[4], Y. Dion[5], S. Rioux[6], B. McCallum[6], T. Fetch[6], F. Eudes[6], B. Blackwell[6], R. A. Martin[7], P. Scheeren[8], Caetano. V. R.[9], J. A. Frégeau[9], and G. Fedak[9]. [1]CRDSGC, Agriculture and Agri-Food Canada, Québec City, Québec, Canada G1V 2J3; [2]ECORC, Agriculture and Agri-Food Canada, Ottawa, Ontario, Canada K1A 0C6; [3]CRC, Agriculture and Agri-Food Canada, Winnipeg, Manitoba, Canada R3T 2M9; [4]Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada T1J 4B1; [5]CÉROM, Saint-Mathieu-de-Beloeil, Québec, Canada J3G 2E0; [6]CÉROM, Québec City, Québec, Canada G1P 3W8; [7]Agriculture and Agri-Food Canada, Charlottetown, Prince Edward Island, Canada C1A 4N6; [8]EMBRAPA Trigo, CP 451, 99001-970, Passo Fundo, RS. Brazil; and [9]EMBRAPA Clima Temperado, CP 403, Pelotas, RS, 96001-970, Brazil.

The ideal way to deal with quantitative traits is to improve all of them simultaneously. We co-developed new and multi-disciplinary approaches and many micro-methods that lead to faster progress through more efficient use of genetic diversity coupled with severe selection combining biotic and abiotic stresses. This helps rapidly develop germplasm that embodies nearly all of the desired resistance and agronomic traits, long before any yield testing steps. Hundreds of lines combining high FHB resistance with most of the other desired traits were created. For example, it recombined resistance to leaf and stem rust, leaf spots, mildew, barley yellow dwarf, root rot, and other diseases. Our new targets include other quantitative genetics goals, such as yield increase. New strategies get annual validation through multivariate approaches. The fine-tuned responses of living beings to their inner and external environments are highly interactive and include epigenetic events. Genomics, proteomics, studies of epigenome, metabolome and interactome can help systemic strategies whenever proven cost-effective. Crosses between moderately susceptible parents can give fully resistant progenies with the best agronomics. Methods to assess end-user quality in F_3–F_4 are now part of the approach. The initial goal was to deliver germplasm to breeders. Some new germplasm has an unusual package of good traits. Results surpassed expectations, and a non-negligible number of systemic lines can be described as quasi-cultivars. Collaborations remain essential to the success and validation of evolving approaches. We hope more wheat workers see the value of participating in a systemic approach network.

Weathering and pre-harvest sprouting resistance. D. G. Humphreys[1]*, R. M. DePauw[2], R. E. Knox[2], A. K. Singh[2], R. Cuthbert[2], S. L. Fox[2], and H. S. Randhawa[3]. [1]Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Rd., Winnipeg, Manitoba, Canada R3T 2M9; [2]Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1030, Swift Current, Saskatchewan, Canada S9H 3X2; and [3]Lethbridge Research Centre, 5403-1 Avenue South, P.O. Box 3000, Lethbridge, Alberta, Canada T1J 4B1.

Precocious germination of wheat grain is a serious problem in wheat production. Preharvest sprouting (PHS) in spring wheat (*Triticum aestivum* L.) and durum wheat (*T. turgidum* L. var. *durum*) causes significant economic losses due to a reduction in grain yield, end-use quality and viability of seed for planting. The annual cost of PHS to the Canadian wheat industry is estimated at $100 million. Western Canadian wheat breeding programs annually screen both segregating and later generation materials for sprouting response. For early generation screening mostly visual scoring is used, while in later generations Hagberg falling number is also determined. The high levels of PHS resistance found in the Canada Western Red Spring marketing class are due in part to the use by breeders of RL4137, a highly, sprouting resistant breeding line. A white-seeded derivative of RL4137 is the primary source of PHS in the hard white spring wheat market classes. Genetic resistance to PHS is complicated by the influence of factors such as spike morphology, seed dormancy, environmental influences and kernel diseases. Quantitative trait loci (QTLs) that involved in PHS response have been identified on chromosomes 3A, 3B, 3D, 4A, 4B, 5A,

5D and 7D in Canadian hexaploid wheat. In durum wheat, PHS response QTLs were identified on chromosomes 1A, 2A and 7B. Multiple measures of PHS response appear necessary to maximize QTL and transgressive segregant identification. An overview of recent wheat PHS research efforts in western Canada will be presented.

Differential redox proteomic analysis of pre-harvest sprouting tolerance. N. V. Bykova*. Department of Biology, Memorial University of Newfoundland, St. John's, Newfoundland and Labrador, Canada.

Physiological seed dormancy is thought to be under the control of two distinct processes, the accumulation of damaging reactive oxygen (ROS) and nitrogen species, a critical level of which leads to dormancy alleviation and a hormonal balance, which regulates dormancy directly and also likely interacts with ROS and/or antioxidative pathways. The role of redox active proteins that undergo reversible cysteine oxidation in dormant, non-dormant, ABA and GA treated seed protein extracts from RL4137, a wheat cultivar with extreme dormancy, was addressed by a thiol-redox proteomic approach. The total and redox-sensitive proteomes were quantitatively monitored by 2D-gel mapping after solubility fractionation, fluorescent thiol-specific labelling, and mass spectrometry analysis in conjunction with wheat EST sequence libraries. We have shown dynamic changes in redox-sensitive proteome upon after-ripening of wheat seeds. Differential proteomic analysis of six hybrid lines of spring wheat (*Triticum aestivum* L.) doubled haploid population, derived from the cross between 8021-V2 and AC Karma segregating transgressively for pre-harvest sprouting tolerance was used to gain further insight into biochemical mechanisms of dormancy control. Our findings suggest that in dormant seeds, there is a shift in the accumulation of proteins from those active in biosynthesis and metabolism to those with roles in storage and protection against biotic and abiotic stresses. The results give an insight into the dormancy-related alteration of thiol-redox profiles in seed proteins that function in a number of major processes in seed physiology, and provide evidence for an increased capacity of potent antioxidant machinery in wheat seeds of high dormancy genotypes.

Analysis of traits associated with winter-survival in winter wheat (*Triticum aestivum*). M. Båga[1]*, P. Jain[1], D. B. Fowler[1], and R. N. Chibbar[1]. Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, Canada S7N5A8.

The over-wintering capacity in winter wheat (*Triticum aestivum* L.) is largely dependent on the amount of low temperature (LT) tolerance accumulated during cold acclimation/vernalization in the fall. To exclude vernalization effects and facilitate identification of quantitative trait loci (QTLs) affecting freezing tolerance, we have studied cold hardiness traits in a winter wheat doubled haploid population derived from a Norstar ($LT_{50} = -20.7°C$) × winter Manitou ($LT_{50} = -14.3°C$) cross. A major quantitative trait locus (QTL) for LT tolerance obtained upon cold acclimation was mapped to frost resistance region *Fr-A2* on chromosome 5A. Norstar alleles at the locus were also associated with high winter survival and high threshold induction temperature. Partial sequence analysis of *Fr-A2* revealed a cluster of ≥ 23 C-repeat binding factors (CBFs) along with CBF gene duplications. Allelic CBF variation is likely to underlie the *Fr-A2* QTL. The level of LT tolerance is intricately associated with the developmental program of the plant. The final leaf number (FLN) is a measurement floral transition time and QTLs for the trait were mapped to *Fr-A2* and five other regions on the wheat genome. Norstar alleles at five of the loci delayed floral transition, which allowed more LT tolerance to be accumulated during cold acclimation. A higher FLN was associated with higher winter survival and prostrate growth habit, which is commonly seen in winter-hardy cultivars. Several of the QTLs for winter survival, FLN and prostrate growth habit were localized to the same regions on the Norstar genome.

Screening of cytogenetic stocks for resistance to Ug99. G. Fedak[1]*, W. Cao[1], D. Chi[1], L. Zhang[1], A. Xue[1], and T. Fetch[2]. [1]Eastern Cereal and Oilseed Research Centre, AAFC, Ottawa Ontario, Canada K1A 0C6; and [2]Cereal Research Centre, AAFC, Winnipeg, Manitoba, Canada R3T 2M9.

The best method to protect crops of wheat from threatening new races of stem rust (such as Ug99) is to incorporate genes for resistance. For stem rust, the majority of available resistance genes come from alien sources. Previous work by Drs. Peter Dyck and Eric Kerber at the Cereal Research Centre in Winnipeg had isolated a number of resistance genes from *Triticum monococcum*, *Aegilops speltoide*, *Ae. tauschii*. These new genes are currently being deployed, so there is a need to find new genes for stem rust resistance. Our initial attempt at finding new genes involved the screening of accessions of wild species in our holdings and cytogenetic stocks obtained from interspecific/intergenetic hybridization with the TTKSK variant of the stem rust isolate. Genotypes with scores of; to 1 to were considered to be resistant. Resistance was detected in a wide range of materials. Screening of wild species revealed resistance in 8 of 21 accessions tested of *T. monococcum* (A genome) and one accession of *T. miguschovae* (AGD). Two Brazilian rye Landraces, Boller and Vacaria were resistant as were the primary triticales derived from them. Amphiploids or partial amphiiploids originating from hybrids of wheat with *Thinopyrum elongatum* (E genome), *Th. intermedium*

(EESt), *Lyphopyrum ponticum* (EsEsEEE) and *Haynaldia villosa* (V) also had resistant lines. Fifteen of twenty-one translocation lines derived from wheat *Th. ponticum* hybrids were resistant. A number of combinations of synthetic hexaploids derived from crosses of durum wheat with an array of accessions of *Ae. tauschii* were also tested for resistance.

Markets and end use characteristics for Canadian wheat – understanding the customer. M. Reimer*. Canadian International Grain Institute, 1000-303 Main Street Winnipeg, Manitoba, Canada.

The Canadian wheat brand has become synonymous with high quality and consistency and has allowed Canada to be highly competitive in the global market despite its geographic challenges. The quality and consistency of Canadian wheat has been rooted in a deep understanding of the market requirements and desired end-use characteristics for Canadian wheat. In a new marketing environment in western Canada, what steps need to be taken to ensure this high quality standard is maintained and market information is gathered and distributed? The dual wheat marketing system in Ontario provides an example of some of the differences encountered in managing wheat quality without a single marketing desk as well as the new responsibilities the industry must consider. The Ontario wheat experience provides insight into not only what challenges can occur, but also the necessity to have an industry body that gathers market intelligence and wheat quality information to provide the guidance necessary to monitor and maintain quality. This presentation will review activities that have been initiated in Ontario to achieve a better understanding of the challenges and requirements of producers, breeders and end-users in order to develop and maintain a high quality wheat supply.

Research investment and diversity in western Canadian wheat classes. J. Thomas*. Agriculture and AgriFood Canada, 195 Dafoe Road, Winnipeg, Manitoba, Canada R3T 2M9.

Currently, grain handlers have emphasised the need to simplify the class structure of wheat while other opinions envisage a market subdivided into speciality end uses or ''niche wheats''. These desiderata would seem to be mutually exclusive. In particular, casual arguments in favour of niche-type wheats usually lack specific details of marketing or quality. A review of past and ongoing wheat breeding research investment was conducted in terms of the adoption and performance of Canada Prairie Spring, extra-strong types (CWES), winter wheat (CWRW) and hard white spring wheat (CWHWS) relative to hard red spring wheat. This extensive quality-driven research agenda for spring wheat breeding has failed to establish the targeted classes of spring wheat in extensive amounts. Optimistic market projections coupled with disappointing rates of agronomic gain have created a complex class structure for spring wheat where useful advantage is lacking in both marketability and the combination of yield and price. For winter wheat, the combination of yield and price offers some advantage over CWRS as well as agronomic and ecological diversification. Development of new classes of wheat consumes scarce research resources and diverts breeding efforts away from the improvement of existing classes. A simplified class structure that is coupled with intensified trait-driven research agenda (agronomics and pest resistance) is probably in the best interests of western wheat producers.

The economics of moving western Canadian wheat and barley. E. Froystad*. Canadian Wheat Board, 423 Main Street, Winnipeg, Manitoba, Canada R3C 2P5.

The Canadian Wheat Board (CWB) sells western Canadian wheat and barley to customers in over 70 countries. With annual sales of $4 billion to $8 billion, the CWB is the largest marketer of wheat and barley in the world. This presentation examines the costs associated with moving western Canadian grain to international markets.

Poster Presentation Abstracts

A high-speed/ high-throughput, biallelic, "perfect", SNP-DNA marker for Lr34 leaf rust resistance used in seed fingerprinting. S. Prashar[1], S. L. Fox[1], and J. D. Procunier[1]*. [1]AAFC-CRC, 195 Dafoe Road, Winnipeg, Manitoba, Canada R3T 2M9.

The wheat Lr34 gene enhances the resistance to both leaf rust (*Puccinia triticina*) and stem (*P. graminis*) rust and is the most important rust resistance wheat gene cloned to-date. The Lr34 gene has remained durable for more than 50 yr since no effective pathogen virulence has emerged. It has been proposed that all Canadian cultivars have the Lr34 gene plus other Sr/Lr gene combinations for both stem (Sr-Ug99) and leaf (Lr) rust resistance. Such gene combinations can only be identified by co-dominant DNA markers.

Making DNA diagnostics affordable for breeders: single seed analysis and SNP markers are used in the Rapid ID Technology (RIDT) scoring platform. The single seed SNP-assay is preferred since this eliminates growing of seedlings/plants which saves greenhouse space, staff resources, time and money. In addition, using single seed assays is the most accurate for determining the percent contamination of a single commercial variety by other undesirable varieties. Single nucleotide polymorphisms (SNPs) are becoming the next generation of molecular markers due to their relative abundance and their suitability for genotyping by high-throughput, automated, scoring platforms.

The RIDT platform uses simple microplate technology and an inexpensive fluorescent plate reader. Single seeds are dispensed into 96-well microplates (one seed/well) by a hand-held, 96-well plate dispenser. The most limiting factor in analyzing large seed/plant populations on the molecular level is the extraction and purification of DNA from the thousands of individual samples. For the RIDT Seed DNA Extraction System Coupled with Fast Thermocycling TM, there is no maceration, cutting or crushing of seed. This seed extraction releases minute amounts (nanograms) of genomic DNA per single seed. There is no purification of seed DNA and no time consuming ethanol precipitation of DNA, centrifugation and washing of the DNA precipitate. Subsequent exponential amplification (PCR) of the target DNA sequence plus the linear signal amplification (Invader) provides sufficient target oligos for detecting the SNP allele for >50 Invader reactions per single seed. This combination of the dual amplification steps allows for the ultrasensensitive detection of SNP alleles. The RIDT scoring platform is high throughput, fingerprinting by the Invader assay in microwells. Up to 1000 single seeds can be fingerprinted individually and simultaneously in under 2 h "from seed to base call". This "perfect", co-dominant/biallelic SNP marker was derived from the Lr34 gene sequence. The SNP-marker was used to show the Lr34 presence/absence in any line tested (60 correct calls out of 60 lines tested).

Seed quality of durum wheat grown in a controlled sealed environment suitable for artificial life support. M. Stasiak[1], D. Gidzinski[1], M. Jordan[2]*, and M. Dixon[2]. [1]Controlled Environment Systems Research Facility, University of Guelph, 50 Stone Road East, Guelph, Ontario, Canada N1G 2W1; and [2]Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Rd, Winnipeg, Manitoba, Canada R3T 2M9.

Four durum wheat cultivars were grown hydroponically in a controlled sealed environment to assess suitability in artificial life support systems for manned spaceflight as part of the MELiSSA program of the European Space Agency. The MELiSSA project aims to construct a closed loop ecosystem based on microorganisms and higher plants that can recycle waste products and produce food, water and oxygen in a closed regenerative system, and this study is part of a broad examination of initial cultivar tests utilizing the Canadian durum varieties Avonlea, Commander, Eurostar and Strongfield. Due to optimal growth conditions for nutrient and water availability, high intensity lighting, high CO_2 concentration and a lack of pests and diseases the genetic yield potential of these cultivars can be assessed. Additionally, end-use quality was assessed to determine if high yield under optimal conditions and very high CO_2 concentration would negatively affect important quality characteristics. There were few fundamental differences in durum quality parameters between hydroponically and field-grown wheat; however, yields of Avonlea and Strongfield exceeded average field trial yields by 41 and 87%, respectively. Falling number was lower than field-grown checks for all cultivars except Commander, likely due to chamber humidity. Future work is aimed at improving productivity and volumetric efficiency of the MELiSSA closed environment ecosystem.

Virulence of Ug99 (race TTKSK) and race TRTTF on Canadian wheat cultivars. T. Fetch[1]*, T. Zegeye[1], D. Singh[2], R. Wanyera[3], M. Penner[4], and K. Rashid[4]. [1]Cereal Research Centre, Agriculture and Agri-Food Canada, Winnipeg, Manitoba, Canada R3T 2M9; [2]Plant Breeding Institute, Cobbitty, NSW, Australia 2570; [3]Kenya Agricultural Research Institute, Njoro, Kenya; and [4]Morden Research Centre, Agriculture and Agri-Food Canada, Morden, Manitoba R6M 1Y5.

Stem rust, caused by *Puccinia graminis* f. sp. *tritici*, is a major disease worldwide on wheat (*Triticum aestivum*). Many epidemics occurred in Canada up to 1955, but stem rust has been controlled since then using resistant cultivars. Recently, Ug99 (race TTKSK and variants) arose in east Africa and has virulence to most Sr genes. Furthermore, race RRTTF (present in Ethiopia, Yemen, and Pakistan) has virulence to most Sr genes and is highly virulent to durum wheat because it attacks gene *Sr13*. Virulence of Ug99 was evaluated on Canadian wheat cultivars and breeding lines at Njoro, Kenya from 2005 to 2010, and virulence of TTKSK and RRTTF was evaluated in seedling tests. In the Njoro nurseries, only two bread wheat cultivars (Peace and AC Cadillac) were highly resistant to Ug99 and three lines had moderate resistance. These five lines were positive for the FSD_RSA marker linked to *Sr42*. About 78% of Canadian bread wheat lines were susceptible to Ug99, but only 55% were susceptible to race RRTTF. Of durum cultivars tested, eight of nine had intermediate to high levels of resistance to TTKSK. All durum lines tested were resistant to RRTTF, probably due to gene *Sr9e*. All soft white spring wheat cultivars were highly susceptible to TTKSK, and only Sadash had seedling resistance to RRTTF. Variants of Ug99 and race RRTTF would threaten production of bread and soft white wheat in Canada, but durum wheat appears to contain an effective level of resistance.

Linkage maps of two new stem rust resistance genes on chromosomes 2B and 6A of wheat line Tr129. H. Ghazvini*[1], C. W. Hiebert[1], J. Thomas[1], T. Zegeye[1], and T. Fetch[1]. [1]Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, Manitoba, Canada R3T 2M9.

Stem rust, caused by *Puccinia graminis* f. sp. *tritici* (Pgt), is a devastating disease of wheat worldwide. During the last decades of 20th century, deployment of stem rust resistance (Sr) genes in wheat cultivars effectively controlled the disease. Since 1999, new Pgt races commonly known as Ug99 arose in Africa. These races are virulent to most Sr genes and are a threat to world wheat production. Wild relatives of wheat are an important source of disease resistance. A preliminary study indicated that line Tr129, which contains one or more *Aegilops triuncialis* translocations, is resistant to Ug99. To characterize the inheritance of seedling resistance to stem rust and map the Sr gene(s) a population was generated by crossing RL6071 × Tr129. F_2 and F_3 progeny were inoculated with Pgt race MCCF at the first leaf stage. Segregation of F_2 and F_3 progeny fit a 15:1 ratio indicating two dominant genes in Tr129 (*SrTr1* and *SrTr2*) conditioned resistance to race MCCF. To estimate the location of each gene, haplotype data generated by SSR markers were used to select $F_{2:3}$ families from the population that putatively segregated for either *SrTr1* or *SrTr2*. Two $F_{2:3}$ families, each segregating for one of these genes, were inoculated with race MCCF. Segregation fit a 3:1 ratio indicating one dominant Sr gene in both families. Molecular mapping confirmed the estimated location of each gene; *SrTr1* mapped on chromosome 2BL in the first $F_{2:3}$ family and *SrTr2* mapped on chromosome 6AS in the second $F_{2:3}$ family.

Efficacy of *Sphaerodes mycoparasitica* in controlling FHB and mycotoxin accumulation in cereal grains. V. Vujanovic*. Food and Bioproduct Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, Canada.

Sphaerodes mycoparasitica Vujanovic is a groundbreaking discovery in the efficient biocontrol of *Fusarium* Head Blight (FHB). *S. mycoparasitica* SMCD 2220 biotrophism, or specificity to *Fusarium* pathogens, ensures the eco-friendly nature of the biocontrol product. Its impact is twofold: it helps the bioeconomy by preventing multi-billion dollar losses from FHB damage to the cereal industry and it helps the agroecosystems by minimising the accumulation of mycotoxins. In this study, we described the morpho-structural and behavioural features related to *S. mycoparasitica's* efficiency, including its specificity – an evolutionary adaptation or ability to control *Fusarium* species. The discovery required optimization of several modern approaches, including PCR, pyrosequencing, qRT-PCR, DGGE, fluorescence and confocal microscopy, and proteomic tools. The phylogeny, interaction, coevolution, and attack mechanisms of *S. mycoparasitica* on *F. graminearum* including mycotoxigenic 3- and 15-acetyldeoxynivalenol chemotypes, *F. culmorum*, *F. avenaceum*, *F. oxysporum*, and *F. equiseti* have been elucidated. With Pest Management Regulatory Agency (PMRA) permission, the efficacy of *S. mycoparasitica* against FHB and mycotoxins was tested and proved on wheat and barley in phytotron, greenhouse, and field (AAFC-Melfort and U of S-Saskatoon) trials. Best efficacy was achieved using a SMCD 2220 liquid formulation of 10^5 CFU mL^{-1}. The biofungicide's application reduced FHB by an average >60% and DON >80%; and increased yield by >35% in the cereal field tests compared to untreated control.

Downy brome (*Bromus tectorum*) increases disease induced over-winter mortality in wheat (*Triticum aestivum*). Z. Miller[1], F. Menalled[2]*, and M. Burrows[2]. [1]Department of Plant Sciences and Plant Pathology. Montana State University. Bozeman, MT 59717, USA; and [2]Department of Land Resources and Environmental Sciences. Montana State University. Bozeman, MT 59717, USA.

Over-winter mortality, i.e., winterkill, reduces cereal crop competitive ability and yield. Winter annual weeds may increase wheat winterkill through interspecific resource competition and by facilitating the survival and spread of plant pathogens. However, the extent and magnitude of these factors are largely unknown. We evaluated the impact of summer- (wild oat, *Avena fatua*) and winter-annual (downy brome, *Bromus tectorum*) weeds in the over-winter mortality of winter wheat over 3 yr. Wild oat infestation had no impact on crop survival rates. In contrast, during the second and third years of this study, winter wheat survival in downy brome infested plots was 50% percent less than in the weed-free control plots with wheat over-winter survival negatively correlated with downy brome density. Pink snow mold, *Microdochium nivale*, a winterkill pathogen known to infect downy brome and wheat, was isolated from dead and dying wheat plants. Overall, these observations suggest that winter annual grassy weeds could increase winterkill of winter wheat by enhancing plant pathogen survivorship and spread.

Biotic vs. abiotic factors causing dark discolouration on durum wheat kernels. M. R. Fernandez[1]*, M. Sissons[2], R. L. Conner[3], H. Wang[3], and J. M. Clarke[3]. [1]Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1030, Swift Current, Saskatchewan, Canada S9H 3X2; [2]Tamworth Agricultural Institute, NSW Department of Industry and Investment, 4 Marsden Park Rd., Calala, NSW 2340, Australia and Value Added Wheat, CRC Locked Bag 1345, North Ryde, NSW 1670, Australia; and [3]Morden Research Station, Unit 100-101 Route 100, Morden, Manitoba, Canada R6M 1Y5.

Blackpoint (BP, discolouration restricted to the germ end) and dark smudge (DS, discolouration mostly along the crease) are believed to be caused by fungal infection

in grain exposed to high humidity, although it has also been reported that BP might result from abiotic stresses causing physiological and biochemical changes in the grain. The objective of this study was to determine the effects of abiotic (temperature and high humidity) and biotic (infection by *Cochliobolus sativus*, CS or *Alternaria alternata*, ALT) factors on BP and DS development in durum wheat. Plants were exposed to five treatments under two temperature regimes (Low T, 17°C day/12°C night or High T, 26°C day/18°C night): inoculation with ALT or CS at mid-milk with 30 h incubation at 100% humidity; one exposure to 100% humidity at mid-milk (HUMo); multiple exposures to 100% humidity from heading to maturity (HUMm); and no exposure to high humidity or inoculum (DRY). The highest incidences of kernel discolouration occurred in the CS, followed by the ALT treatment, with HUMm producing low incidences, and HUMo and DRY only occasional discolouration. In general, High T favoured BP and Low T favoured DS. Fungal infection by *C. sativus* or *A. alternata* was thus the main factor associated with discolouration of durum wheat kernels. Whether fungal infection was promoted, or unhindered, by a primary effect of high humidity on the physiology of the kernel and its defenses could not be determined given that exposure to high humidity is a requirement for fungal infection.

***Fusarium* populations in roots/crowns of spring wheat in organic vs. non-organic management systems in west-central Saskatchewan.** M. R. Fernandez[1]*, D. Ulrich[2], S. A. Brandt[2], R. P. Zentner[2], H. Wang[2], A. G. Thomas[3], and O. Olfert[3]. [1]Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, P.O. Box 1030, Swift Current, Saskatchewan, Canada S9H 3X2; [2]Scott Research Farm, Agriculture and Agri-Food Canada, P.O. Box 10, Scott, Saskatchewan, Canada S0K 4A0; and [3]Saskatoon Research Centre, AAFC, 107 Science Place, Saskatoon, Saskatchewan, Canada S7N 0X2.

The impact of cropping system management on root and crown rot of spring wheat was examined on a Dark Brown Chernozem soil in the Canadian prairies. This systems approach tried to reflect the most common practices of organic and conventional producers in this region. The study consisted of a factorial combination of three input levels [high, with tillage, fertilizer and pesticides); reduced (RED), with conservation tillage, targeted fertilizer and weed control; and organic (ORG) with tillage and N-fixing legumes]; and three levels of cropping diversity (low diversity with wheat and summerfallow or legume green manure fallow; diversified using annual grain crops; and diversified using annual grain crops and perennial forages). All rotations were 6 yr long. Subcrown internodes and crowns/lower culms of wheat plants were scored for discolouration, and fungi in discoloured tissue were identified and quantified. Overall, input level had a greater impact on disease levels and fungal frequency than cropping diversity. Discolouration severity was lowest in the RED systems, which was attributed to lower percentage isolation of *Cochliobolus sativus*, the most common pathogen. *Fusarium* species varied with input level. The pathogens *F. avenaceum* and *F. culmorum* were most associated with RED and/or least associated with ORG systems, whereas the weak pathogen/saprophyte *F. equiseti* was most associated with ORG systems. Thus, ORG management helped to reduce populations of F. *avenaceum* and *F. culmorum*, two of the most important *Fusarium* pathogens in the Canadian prairies.

Mycotoxin production and genetic variability of Czech *Fusarium graminearum* isolates on wheat. T. Sumikova[1]*, M. Zabka[1], L. Kucera[1], and J. Chrpova[1]. Crop Research Institute, Drnovska 507, Prague, 16106 Czech Republic.

The most important pathogen causing Fusarium head blight of wheat in the Czech Republic is *Fusarium graminearum*. The species is known for its ability to produce trichothecenes, mainly deoxynivalenol and its derivates. 105 *F. graminearum* isolates were isolated from naturally infected wheat ears from 20 localities of the Czech Republic. DON content was determined in ground ears by ELISA. Trichothecene production ability was detected using PCR assays for *Tri3*, *Tri7* and *Tri13* genes. Maximum value limit for DON in EU was exceeded in 55% of the samples. All the isolates belonged to DON producing chemotype, no NIV producer was detected. Genetic variability of the isolates was evaluated by AFLP. The population was highly heterogeneous, both within and between the localities. No clear evidence for association between AFLP profile and geographic origin was found out.

Gene pyramiding for resistance to Ug99 stem rust in Canadian spring wheat. W. Cao[1], G. Fedak[2]*, T. Fetch[3], A. G. Xue[3], and S. Briere[4]. [1]Eastern Cereals and Oilseeds Research Centre, AAFC, Central Experimental Farm 960 Carling Ave. Ottawa, Ontario, Canada K1A 0C6; [2]Eastern Cereals and Oilseeds Research Centre, AAFC, Central Experimental Farm 960 Carling Ave. Ottawa, Ontario, Canada K1A 0C6; [3]Cereal Research Centre, 195 Dafoe Road, Winnipeg, Manitoba, Canada R3T 2M9; and [4]Plant Pathology Laboratory, Canadian Food Inspection Agency.

Stem rust race TTKSK (Ug99) and its variants are migrating from East Africa and threaten wheat production worldwide. An efficient way to control stem rust is by using resistant wheat cultivars containing a pyramid of genes. The Canadian wheat cultivars AC Cadillac and Peace are highly resistant to Ug99, but have only one major gene (*SrCad*). The Australian wheat cultivar Lang

has *Sr36* and is resistant to races TTKSK and TTKST. The objective of this study was to pyramid *Sr36* with SrCad in a Canadian wheat background. The crosses Cadillac/Lang and Hoffman/Lang were made, and 98 F_2 progeny were evaluated for segregation of resistance to race TTKST. For the Cadillac/Lang cross, the progeny segregated 15 Resistant:1 Susceptible, indicating two independent genes. Homozygous resistant progeny will be selected, and the two genes will be pyramided using molecular markers linked to *Sr36* and *SrCad*. For the Hoffman/Lang cross, the progeny segregated 3 Resistant: 1 Susceptible, indicating only *Sr36* from Lang provided resistance to Ug99. The backcross Hoffman*[2]/Lang was made to develop an improved Hoffman with resistance to Ug99.

The detection of virulence to *Lr21* in Canada during 2011. B. McCallum[1]*, P. Seto-Goh[1], and A. Xue[2]. [1]Cereal Research Centre, AAFC, 195 Dafoe Rd. Winnipeg Manitoba, Canada R3T 2M9; and [2]2ECORC, Agriculture and Agri-Food Canada, Ottawa, Ontario, Canada K1A 0C6.

The leaf rust resistance gene *Lr21* was discovered by Gordon Rowland and Eric Kerber at the Cereal Research Centre, Winnipeg, in 1974, and it conditioned resistance to all virulence phenotypes of *Puccinia triticina* Eriks. present in North America. It was first deployed in the Canadian cultivar AC Cora, registered in 1994, and has subsequently been incorporated into many other Canadian cultivars including McKenzie, CDC Alsask, and Lovitt, and North Dakota and Kansas wheat cultivars. *Lr21* remained completely effective until 2010 when virulence was reported in a small proportion of isolates sampled in the United States. Virulence to *Lr21* was not detected in a sample of 399 isolates from across Canada collected in 2010. However, from 2011 collections six isolates were virulent to *Lr21* from 54 isolates tested to date. These were found throughout southern Manitoba. There were some variations in the virulence phenotypes for these isolates but they were commonly TDBG or TDBJ, which were the most common phenotypes identified in 2010. Although wheat lines with *Lr21* were not severely infected in 2011 the effectiveness of this gene could decrease if these virulent isolates were to increase in frequency in the population. Future wheat cultivars should have race non-specific resistance genes such as *Lr34* or *Lr67* to ensure adequate levels of leaf rust resistance.

SNP genotyping based on the oligo-nucleotide pooled Assay (OPA) to understand patterns of genetic diversity and population structure in pigeonpea (*Cajanus cajan* (L.) Millsp.) and wild relatives. M. T. Kassa[1]*, R. V. Penmetsa[2], N. Carrasquilla-Garcia[2], E. J. B. v. Wettberg[3], and D. R. Cook[3]. [1]Agriculture and Agri-Food Canada, Cereal Research Centre, 195 Dafoe Road,Winnipeg, Manitoba, Canada R3T 2M9; [2]University of California, Department of Plant Pathology, One Shields Ave, Davis, California, 95616, USA; and [3]Florida International University, Department of Biological Sciences, 11200 SW 8th Street, Miami, FL 33199, USA.

Pigeonpea (*Cajanus cajan*) is a widely adapted and drought-tolerant pulse crop of acute regional importance, providing significant protein to the human diet in regions of Asia and Africa. Despite considerable diversity for phenotypic characters, pigeonpea lacks most of the genetic diversity present in wild relatives. Thus, pigeonpea improvement is increasingly reliant on introgression of genes and traits from wild relatives, a process that would be aided by increased understanding of the genetic structure and relationships among cultivated and wild forms. Here, we use single nucleotide polymorphisms (SNP) markers derived from 670 low copy orthologous genes to understand the genetic diversity and population structure of pigeonpea (79 accessions) and its wild relatives (31 accessions). The average polymorphic information content (PIC) of the SNP markers was 0.266 and 79% of the SNPs were informative (PIC >0.1). The patterns of population structure identified three well-supported lineages that are geographically clustered. We estimated genetic diversity and differentiation at various levels of organization and *Cajanus cajanifolius* was resolved as the most probable progenitor of cultivated pigeonpea. Genetic admixture was evident between wild and cultivated genomes, suggesting the involvement of recent and successive rounds of gene flow during domestication. We find abundant allelic variation and genetic diversity among the wild relatives and we reported the loss of $\sim$ 75% of the ancestral allelic diversity, which indicates a severe genetic bottleneck during pigeonpea domestication. A second and more recent nested population bottleneck focused in tropical regions was evident, that is the likely consequence of pigeonpea breeding.

Genetics and mapping of loose smut resistance in the cross BW278/AC Foremost. M. Kassa[1]*, J. Menzies[1], and C. McCartney[1]. Agriculture and Agri-Food Canada, Cereal Research Centre, 195 Dafoe Road, Winnipeg, Manitoba, Canada R3T 2M9.

Loose smut, caused by *Ustilago tritici* (Pers.) Rostr., is a seed-borne disease of wheat (*Triticum aestivum* L.), which can cause considerable yield losses in the absence of appropriate management techniques. Loose smut resistance in wheat lines is an effective control measure. Evaluating loose smut resistance is highly labour and time-intensive, which has slowed genetic progress on this trait. The development of DNA markers linked to loose smut resistance would assist in the development of loose smut resistant varieties. The genetics of loose smut

resistance was studied in an F_5-derived recombinant inbred line population of the cross BW278/AC Foremost. BW278 is resistant to *U. tritici* race T9 and susceptible to race T10, whereas the reverse is true for AC Foremost. Wheat spikes were inoculated with teliospore suspensions of each race at anthesis. Seed from inoculated spikes were harvested and sown to determine the percent infected plants. A single gene segregated for resistance to race T9 and an independent second gene segregated for resistance to race T10. A preliminary SSR linkage map was developed for resistance to race T10 from AC Foremost, which located the resistance gene to chromosome 5B. Additional markers are being added to the linkage map. Efforts are ongoing to locate linked SSR markers for the loose smut resistance gene from BW278.

Effects of plant density on durum crop production. B. Perry[1], J. Isidro[1]*, A. K. Singh[1], H. Wang[1], R. M. DePauw[1], C. J. Pozniak[2], R. D. Cuthbert[2], B. L. Beres[3], and E. N. Johnson[4]. [1]Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada (AAFC), Swift Current, Saskatchewan, Canada; [2]Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, Canada; [3]Lethbridge Research Centre, AAFC, Lethbridge, Alberta, Canada; and [4]Saskatoon Research Centre, AAFC, Saskatoon, Saskatchewan, Canada.

Plant density in crop production systems is an important factor that determines the ability of the crop to capture resources. The choice of a seeding rate may vary between regions according to climate conditions, soil type, sowing time and other agronomic practices. Insufficient information is available for optimum seeding rate on durum wheat (*Triticum turgidum* L. var. *durum*) for some production zones, and response to plant density is unknown for recently registered durum cultivars. The objective of this study is to determine the effects of plant density on Canada western amber durum wheat (CWAD) cultivars in a prairie ecosystem. Eight durum wheat cultivars were sown at densities of 163, 217, 272, 326 and 380 plants m^{-2} to study the effect of plant density on grain yield, grain volume weight and leaf area index. Each experiment was planted as a factorial RCBD with three replications near Swift Current in 2009 and 2010 and near Regina in 2010. The results show an increase in grain yield as the seed rate augmented. No significant differences were observed for volume weight, which suggests that inter-plant competition did not alter grain filling. A high genetic and environmental response to seed rate was observed between cultivars. Grain yield showed a positive relationship with leaf area index (LAI), and LAI showed a linear increase with seed rate. Information generated from this study could be beneficial to producers as planting density can be adapted to their needs and can lead to crop grain profitability.

Molecular mapping of leaf rust and stripe rust resistance QTL in durum wheat. A. Singh[1]*, M. P. Pandey[1], A. K. Singh[1], J. M. Clarke[2], R. E. Knox[2], K. Ammar[3], R. P. Singh[3], C. J. Pozniak[3], R. M. DePauw[3], F. R. Clarke[3], B. D. McCallum[4], R. D. Cuthbert[4], and H. S. Randhawa[5]. [1]Semiarid Prairie Agricultural Research Centre, AAFC, Swift Current, Saskatchewan, Canada; [2]Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, Canada; [3]CIMMYT, Mexico; [4]Cereal Research Centre, AAFC, Winnipeg, Manitoba Canada; and [5]Lethbridge Research Centre, AAFC, Lethbridge, Alberta, Canada.

Leaf rust (*Puccinia triticina* Eriks.) and stripe rust (*P. striiformis* f.sp. *tritici* Eriks.) cause major production losses in durum wheat (*Triticum turgidum* L. var. durum). The Mexican leaf rust race BBG/BN and its variants are virulent on predominant Canadian durum cultivars. Stripe rust is becoming a bigger threat and ability of new races to survive at higher temperatures is putting the western Canadian wheat crop at risk. The objective of this research was to identify and map leaf and stripe rust resistance gene(s) from the French cultivar Sachem. A doubled haploid (DH) population was developed from Sachem/Strongfield. The DH population was genotyped with DArT and select SSR markers. Statistical analyses were done using SAS v 9.2 and linkage mapping was conducted using softwares JOINMAP and MapQTL. The parents and DH lines were phenotyped for BBG/BN and BBG/BP reactions (seedling resistance) and adult plant response was determined in three field rust nurseries near El Batan, Obregon and Toluca in Mexico. Sachem was resistant and Strongfield was susceptible to leaf and stripe rust. A major leaf rust QTL was identified in the interval *Xgwm146-Xgwm344.2*, and possibly another linked small effect QTL on chromosome 7B. The results indicate that Sachem likely carries *Lr14a* and a tightly linked minor rust gene on 7B. In Toluca, DArT marker wPt3451 on chromosome 1BS was found to be significantly associated with leaf ($R^2 = 15.9\%$) and stripe rust ($R^2 = 28.6\%$) resistance. Previously, markers linked to wPt3451 have been mapped in a Yr gene rich region.

Arbuscular mycorrhiza interaction with historical and modern wheat genotypes. W. Ellouze[1]*, H. Yong[1], C. Hamel[1], H. Wang[1], K. Hanson[1], and A. K. Singh[1]. [1]Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada (AAFC), Swift Current, Saskatchewan, Canada.

The beneficial effects of arbuscular mycorrhizal (AM) fungi include improved plant nutrient uptake and tolerance to biotic and abiotic stresses, and improved soil structural quality. We conducted two

field experiments to assess the presence of genetic variation in the compatibility of wheat cultivars with AM fungi naturally occurring in cultivated soils. In the first experiment, 32 durum wheat genotypes (heritage varieties and modern cultivars) were grown in high fertility soil near Swift Current and Regina, SK. In the second experiment, two durum genotypes (Strongfield and Pelissier) and two hexaploid wheat genotypes (Stettler and Red Fife) were seeded in low fertility soil. Root samples were taken at heading to determine their AM colonization level. Results showed that genotypes were a significant source of variation and displayed a wide range of AM colonization levels (8–44% in Regina and 11–28% in Swift Current for the high fertility soil experiment; and 46–58% for the low fertility soil experiment). The extent of AM root colonization in recent wheat cultivars was greater than in heritage varieties in low fertility soils. No trend between AM colonization and year of release was observed in the high fertility experiment. Modern cultivars showed a better ability to adapt to their environment than heritage varieties. For example, Strongfield, a modern cultivar, developed higher levels of mycorrhizal colonization under conditions of low fertility. However, in highly fertile soil where Strongfield does not depend on AM fungi for nutrient uptake, it seemingly reduces carbon allocation to AM fungi.

Mapping field reaction to leaf and stripe rust in the spring wheat cross 'RL4452' × 'AC Domain'. K. Nilsen[1]*, G. Humphreys[2], H. S. Randhawa[3], R. A. Martin[4], C. McCartney[4], B. McCallum[4], and C. Pozniak[5]. [1]Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, Canada S7N 5A8; [2]Cereal Research Centre, AAFC, 195 Dafoe Rd, Winnipeg, Manitoba, Canada R3T 2M9; [3]5403-1 Avenue South, PO Box 3000, Lethbridge, Alberta, Canada T1J 4B1; [4]Crops and Livestock Centre, 440 University Avenue, Charlottetown, Prince Edward Island, Canada C1A 4N6; and [5]Crop Development Centre, University of Saskatchwan, 51 Campus Drive, Saskatoon, Saskatchewan, Canada S7N 5A8.

Leaf and stripe rust of wheat are caused by the fungal pathogens *Puccinia triticina* Eriks. and *Puccinia striiformis* f.sp. *tritici*, respectively. Previously, 'AC Domain' was reported to carry an adult plant resistance gene which was believed to be *Lr34*, but recent molecular evidence has shown that 'AC Domain' is not a carrier. To localize additional rust resistance genes, a mapping population of 182 doubled haploid (DH) lines from the cross 'AC Domain' and 'RL4452' was used. 'RL4452' is a carrier of *Lr34*. The DH population was evaluated for leaf rust severity in field trials at Saskatoon (SK), and Portage (MB), and for stripe rust at Lethbridge (AB). Phenotypic expression of leaf rust was variable, ranging from highly resistant to completely susceptible. Early results indicate that DH lines with *Lr34* showed increased resistance to both diseases, but 40% of the DH lines lacking *Lr34* showed an intermediate reaction to leaf rust. These results suggest other rust resistance gene(s) are segregating in this population. The DH population is known to segregate for *Lr16*, but contrast analysis suggested only a small main effect. At Lethbridge, 'RL4452' was immune to stripe rust, but 'AC Domain' was susceptible. The presence of *Lr34* resulted in reduced stripe rust severity, but some *Lr34*-carrying lines showed elevated disease. Also, resistant lines lacking *Lr34* were noted, suggesting segregation of additional stripe rust resistance gene(s). Work is currently underway to test single nucleotide polymorphism markers to localize the additional leaf and stripe rust resistance genes segregating in this population.

Rethinking wheat research basics. M. Entz*. University of Manitoba, Department of Plant Science, Winnipeg, Manitoba, Canada.

Canada's wheat research accomplishments are one of this countries great success stories. However, the research focus must change dramatically to meet future needs. Research now focuses very much on economic efficiency and markets. This has resulted in near monoculture production systems that are increasingly reliant on external inputs of pesticides, fertilizers and fossil fuels as well as government support payments. In order to make Canadian and indeed global wheat production more sustainable and resilient, wheat research must focus on the production system – built first on ecological principles. To use a popular metaphor, we must once again shift our focus to the goose, and not the eggs – a healthy goose will produce eggs that everyone will want. Key principles of this new paradigm are diversity, integration and natural nutrient cycling. For example, by developing wheat genotypes better able to interact and draw nutrients from a biological soil system, many of the problems associated with modern agriculture (pollution, the need for biocides, poor nutritional status) will be reduced. Another critical feature of this new research paradigm is integration with other crops. Silos of scientists focussed only on one crop will not work. This poster will focus on organic production as the first step in shaping this new research paradigm. This new initiative will reinvigorate all scientific disciplines and add ecologists onto our research teams. Canadians want to ''green'' all industries including agriculture. We have the capacity to respond to these goals and inspire the world.

Investigating emerging wheat pathogens, new wheat leaf rust virulence in Ontario. K. Marsh[1]*, B. McCallum[2], X. Wang[2], A. Tenuta[3], S. Hambleton[4], and B. Saville[1]. [1]Forensic Science Program, Trent University, 1600 West Bank Drive, Peterborough, Ontario, Canada K9J 7B8; [2]Cereal Research Centre,

Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, Manitoba, Canada R3T 2M9; [3]Ontario Ministry of Agriculture and Rural Affairs, Ridgetown Resource Centre-Agronomy Bldg, Main St E PO Box 400, Ridgetown, Ontario, Canada N0P 2C0; and [4]Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, K.W. Neatby Bldg., 960 Carling Ave, Ottawa, Ontario, Canada K1A 0C6.

In this presentation we will provide an overview of a project that was recently funded by Grain Farmers of Ontario. This collaborative project focuses on the recently emerged virulence type of wheat leaf rust that was found on the previously resistant wheat variety Vienna. This collaborative project seeks to build on surveys that have identified changes in the wheat leaf rust population in Ontario; it will involve continued monitoring of this population and its virulence on wheat. The monitoring will be carried out in the field and via analysis of airborne spores using methods originally established for monitoring soybean rust. It will continue to inform wheat breeders regarding emerging threats. Parallel research will utilize new advances in DNA sequencing technology to determine the basis of disease development by these rusts. To do this we will investigate transcriptome changes in a series of race by variety interactions that will allow us to identify the gene expression differences in races with the more recently emerged virulence type relative to possible ancestor virulence types. Identifying these changes will uncover the molecular weapons that rusts use against wheat and how these can change leading to new virulence types. Identifying these rust genes provides a means to identify the corresponding wheat genes. The information gained will also be used in the development of new diagnostic tests targeting the identification of new races of rust. The presentation will outline the project and possible outcomes.

Leaf extracts from Thatcher inoculated with the avirulent race of *Puccinia triticina* confer race-specific resistance in Thatcher-*Lr2a* through infiltration. X. Wang[1]*, B. D. McCallum[1], T. Fetch[1], G. Bakkeren[2], and B. Saville[3]. [1]Agriculture and Agri-Food Canada, Cereal Research Center, Winnipeg, Manitoba, Canada R3T 2M9; [2]Agriculture and Agri-Food Canada, Pacific Agri-Food Research Center, Summerland, British Columbia, Canada V0H 1Z0; and [3]Trent University, Peterborough, Ontario, Canada K9J 7B8.

Thatcher and Thatcher near isogenic line (NIL) carrying *Lr2a* (Thatcher-*Lr2a*) were infiltrated with leaf extracts from Thatcher inoculated with *Puccinia triticina* races BBBD (avirulent on *Lr2a*) and SBDG (virulent on *Lr2a*), followed by inoculation with *P. triticina* race SBDG (virulent on *Lr2a*). A significant reduction of pustule formation was observed on leaves of Thatcher-*Lr2a* infiltrated with the leaf extract from Thatcher inoculated with *P. triticina* race BBBD whereas such reduction of pustule formation was not observed on Thatcher-*Lr2a* infiltrated with leaf extracts from un-inoculated Thatcher and Thatcher-*Lr2a* inoculated with *P. triticina* race SBDG. No reduction in pustule formation was observed on Thatcher infiltrated with leaf extracts from un-inoculated Thatcher or Thatcher inoculated with P. *triticina* race BBBD and SBDG. Additionally, the occurrence of a defence responses including autofluorescence from necrotic cells, hypersensitive cell death and accumulation of reactive oxygen species (AOS) were investigated in infiltrated leaves at 3 and 5 d after infiltration (DAI). An extensive induction of autofluorescence from necrotic cells, hypersensitive cell death and the accumulation of AOS were only observed in Thatcher-*Lr2a* infiltrated with the leaf extract from Thatcher inoculated with *P. triticina* race BBBD at 3 and 5 DAI suggesting the presence of (a) specific elicitor(s) associated with the resistance mediated by *Lr2a* in the leaf extract from Thatcher inoculated *P. triticina* race BBBD and such elicitor(s) was not produced in Thatcher inoculated with *P. triticina* race SBDG or un-inoculated Thatcher plants.

Agronomic evaluation of a wheat breeding population in weed competitive organic and weed free conventional management systems. M. Asif[1]*, H. S. Randhawa[2], R.-C. Yang[3], A. Navabi[4], and D. Spaner[4]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada T6G 2P5; [2]Lethbridge Research Centre, Agriculture and Agri-Food Canada, 5403-Ist Ave South, P.O. Box 3000, Lethbridge, Alberta, Canada T1J 4B1; [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada T6G 2P5 and Research and Innovation Division, Alberta Agriculture and Rural Development, #307, 7000-113 Street, Edmonton, Alberta, Canada T6H 5T6; and [4]Agriculture and Agri-Food Canada, Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1.

We used a randomly derived recombinant inbred line (RIL) population ($n = 171$) from a cross between the Canadian spring wheat cultivar CDC Go and the CIMMYT spring wheat cultivar Attila to elucidate selection differentials of various traits in very weedy organic and non-weedy conventional management systems. The RILs, along with parents and checks, were planted in replicated designs in paired organic and conventional management system trials from 2008 to 2010. Heritability and correlation estimates for various traits were different in both management systems and varied significantly over years. Overall, gain yield, plant height, 1000-kernel weight, test weight, tillers m^{-2} and canopy coverage was lower and lines mature earlier in the organic system, but protein contents were higher

during 2008 and 2010. However, the presence of dry/drought conditions in 2009 resulted in lower grain protein in the organic as compared with the conventional management system. Selection differentials were also noted between two management systems, which suggested that wheat breeding for organic farming should be conducted on organically managed lands. These data will be further subjected to genome wide QTL analyses to uncover putative QTL conferring competitive ability.

Genetic analysis of flowering gene complex in historical and elite Canadian wheat germplasm. A. Kamran[1], M. Asif[1]*, H. S. Randhawa[2], and D. Spaner[2]. [1]Department of Agricultural Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada. T6G 2P5; and [2]Agriculture Agri-food Canada, Lethbridge Research station, Lethbridge, Alberta, Canada T1J 4B1.

Wheat has inherent genetic potential to synchronize its flowering and maturity to a broad growing period and is thus one of the most widely adapted and grown food crops in world. Vernalization and photoperiod response genes are of primary import to this adaptability. We screened 102 historical and elite Canadian cultivars/lines released from 1875 to 2008, in the Canada Western Red Spring (CWRS), Canada Prairie Spring Red (CPSR) and Canada Western Soft White Spring (CWSWS) classes; and studied their phenotypic response both in field and greenhouse. We found *Vrn-A1a* gene alone was the most potent gene conferring early maturity overall. *Vrn-A1a* was also epistatic to *Vrn-B1* and *Vrn-D1*. *Vrn-B1* gene ranked second in potency to eliminate the vernalization requirement and to induce early flowering. *Vrn-A1b* in combination with *Vrn-B1* gene delayed flowering and maturity in comparison with *Vrn-B1* alone, which suggests that either *Vrn-A1b* has an antagonistic effect in terms of inducing flowering or maturity, or *Vrn-B1* has an epistatic effect. The *Ppd-D1* gene did not alter flowering, anthesis and maturity in the CWRS cultivars tested in the field, but did in the greenhouse. In the CWSWS class, this effect was significant in reducing the days to flowering and anthesis but was non-significant on maturity. There was a positive correlation between days to flowering and yield, and a negative correlation in yield and protein content. The findings of this study may aid Canadian wheat breeders selecting parents with appropriate vernalization and photoperiod gene complexes.

Effect of antioxidant on the regeneration of green plantlets in isolated microspore culture (IMC) derived doubled haploid in wheat and triticale. A. Goyal, L. Bihari, E. Amundsen, F. Eudes, and H. S. Randhawa*. Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada.

Doubled haploid techniques enable plant breeders to speed up the production of homozygous lines for cultivar development. However, the production of doubled haploids using isolated microspore culture (IMC) has been a challenge in cereals because of the higher frequency of albino plants. The effect of various antioxidants on embryo formation, embryo development, and frequency of green plant regeneration through IMC for wheat and triticale was studied. Four spring wheat lines (Fielder, Sadash, SWS 366 and SWS 411) and one spring triticale (AC Ultima) were used. Two sets of antioxidants were added in the induction media. In the first set, 10 mM DMAP, 10 mM MB, 10 mM Proline, 10 mM NtBHA were used and in the second set, salicylic acid (SA), glutathione (GSH), and ascorbate (ASC) were used. The results indicate that the highest frequency of green plant regeneration was obtained with the application of 10 mM NtBHA and 10X GSH in wheat, and 10 mM MB and 10X GSH in triticale. The effect of antioxidants on embryo formation and green plant regeneration was significant and dependent upon the genotype. There was no observed synergistic effect on wheat and triticale when all of the antioxidants were used together.

Genetics of resistance to common bunt, leaf and stripe rust in N9195 spring wheat. A. Goyal[1], B. Puchalski[1], D. Gaudet[1], R. Graf[1], B. McCallum[2], and H. S. Randhawa[2]*. [1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada; and [2]Cereal Research Centre, Agriculture and Agri-Food Canada, Winnipeg, Manitoba, Canada.

Among the major diseases that can cause significant economic losses to wheat production, stripe rust (caused by *Puccinia striiformis* Westend f. sp. *tritici*), leaf rust (caused by *P. triticina* Eriks) and common bunt (caused by *Tilletia tritici* Bjerk) are the most important diseases in southern Alberta, Canada. Growing resistant wheat cultivars is the most economical and environmentally safe approach to reduce the use of fungicides and to reduce crop losses due to these diseases. However, with the occurrence of new virulent races, deployed resistance genes can be rapidly rendered ineffective. Continuous identification and characterization of new resistance genes is essential in order to minimize economic losses. We have identified resistance to stripe rust, leaf rust and common bunt in the spring wheat line'N9195'. Soft white spring wheat line'AC Reed', which is susceptible to all three diseases, was crossed with N9195 to generate 110 doubled haploid lines. These lines were screened in the greenhouse for both common bunt and leaf rust resistance and in the field in 2011 for stripe rust resistance. Data analysis indicated the segregation of three independent single genes controlling resistance for each disease. Genetic mapping using bulk segregant analysis indicated that the gene for common

bunt resistance is on chromosome 3BL. Genetic mapping for the stripe and leaf rust resistance genes is underway.

The occurrence of stripe rust epidemic in western Canada. H. S. Randhawa[1*], B. Puchalski[1], S. Wogsberg[1], R. Graf[1], R. Kutcher[2], and D. Gaudet[2]. [1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada; and [2]Crop Development Centre, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, Saskatchewan, Canada.

High infection levels of wheat stripe rust were observed throughout southern Alberta and in western and central Saskatchewan in 2011. Winter wheat seedlings became heavily infected in fall 2010. Over-wintering of the pathogen in the counties of Warner, Lethbridge, Taber and Bow Island was observed in a number of commercial fields, attributed to the presence of a more persistent, protective winter snow cover. In the spring, severely infected winter wheat fields were observed 40 d earlier than in previous years. A cool, wet spring favoured high infection levels in winter wheat leading to its subsequent spread to juvenile spring wheat. By mid-July, most susceptible varieties of spring and winter wheat were highly infected. Progression of the disease was slower north of Highway 1 and west of Alberta Highway 36, where severe stripe rust levels were not observed until mid-August. Juvenile infections were common in most spring and winter wheat varieties; this is consistent with the fact that the majority of resistance to stripe rust in spring wheat varieties is imparted by Yr18, an adult plant resistance gene. Fungicide application to control of stripe rust was common and occurred far earlier than previous years. There was also a moderate increase in the number of hectares sown to susceptible wheat varieties in 2011 compared with 2010.

New virulence races of stripe rust in Western Canada. H. S. Randhawa*, D. Gaudet, B. Puchalski, and R. Graf. Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada.

A prolonged warm autumn in 2010 allowed rapid development of the stripe rust pathogen on the establishing winter wheat crop. High inoculum loads from the 2010 spring wheat crops quickly re-established such that incidence of stripe rust in fields of Radiant winter wheat approached 100%. The winter was uncharacteristically cold, allowing accumulated snow to persist in the fields for extended periods of time, broken only by a few short snow-free periods. Snow drifts persisted throughout the entire winter. These conditions permitted stripe rust to overwinter in a number of locations in southern Alberta and Saskatchewan, resulting in severely diseased fields by mid-May. During the 2011 growing season, nighttime low temperatures did not exceed 15°C, permitting the pathogen to cycle quickly and move from winter wheat to the spring wheat. Juvenile infections were common in many varieties. As the cool conditions persisted, inoculum loads increased and the expression of high temperature adult plant resistance (HTAP) genes such as *Lr34/Yr18*, which occurs in many varieties, was incomplete. The disease progressed through southern and eastern Alberta, and through most of Saskatchewan, with higher stripe rust severity observed over a wide area. Stripe rust reactions in the set of differential lines possessing Yr genes in southern Alberta indicated that an expanded virulence occurred in prairie races compared with the virulence pattern observed in Creston, BC. This suggested that stripe rust populations in the Pacific Northwest were different and less virulent than those observed on the western Canadian prairies in 2011.

Mapping quantitative trait loci for leaf angle in durum wheat. J. Isidro[1], R. Knox[1], A.K. Singh[1], F. Clarke[1], R. DePauw[1], J. Clarke[2], and D. Somers[3]. [1]Agriculture and Agri-Food Canada, Semiarid Prairie Agriculture Research Centre, Swift Current, Saskatchewan, Canada; [2]University of Saskatchewan. Saskatoon, Saskatchewan, Canada; [3] Vineland Research and Innovation Centre, Vineland, Ontario, Canada.

Leaf angle and the spatial arrangement of leaves affect interception of solar radiation and its penetration through the crop canopy. The aim of this research was to show the genetic variation in flag and penultimate leaf angle and to identify and map quantitative trait loci (QTL) influencing leaf angle. A doubled haploid population of 90 durum wheat (*T. turgidum* L. subsp. *durum*) lines from the cross 'Strongfield' × 'Blackbird' was evaluated in greenhouse experiments in 2009 and 2010. Main stem leaf angle was measured at three developmental stages (heading, anthesis and late milk) on flag and penultimate leaves. Leaf angle frequency istributions suggest this trait to be under quantitative control at heading and anthesis, but controlled by a major gene at the late milk stage. The analysis revealed a QTL in the interval *Xcfd219* to *Xgwm133* on chromosome 5B and in the intervals *Xgwm389* to *Xbarc75* and *Xcfa2134a* to *Xwmc418* on chromosome 3B. Erectness has been associated with brassinosteroid activity in rice and barley, but not in wheat. Chromosome 5B has synteny with chromosome 9 of rice and 3B with 3H of barley, where the leaf angle trait was previously reported. In a previous report of related research on the same population to assess the responsiveness of wheat to different concentrations of brassinosteroid, we found QTL on chromosomes 3A and 3B. This information will aid further research on the role of leaf angle in wheat biomass production and its relationship with brassinosteroids.