growing ideas

November 22 - 25

PROGRAM

3rd Canadian Wheat Symposium

3e Congrès canadien sur le blé

Ottawa
Ontario, Canada

3rd Canadian Wheat Symposium
3e Congrès canadien sur le blé

Delta Ottawa City Centre

Ottawa, Ontario, Canada

November 22-25, 2016

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3rd Canadian Wheat Symposium

Welcome

Welcome to the 3rd Canadian Wheat Symposium (CWS). We are excited to host this meeting of wheat experts and believe we have assembled a unique selection of Canadian and international speakers and panelists to present and discuss recent discoveries in wheat research, new trends in farming, health, marketing and communication issues, and much more. It is our hope that you will find the symposium inspiring and thought-provoking.

A symposium such as this invites networking. Take advantage of the informal setting to renew old acquaintances and to expand your network. Benefit from the many social opportunities to get to know a graduate student. The symposium is an ideal forum to decide how you can contribute to Canada's wheat industry and to meet the right partners with whom to make that contribution. With a farm cash receipt of nearly 6.4B last year, wheat is a major economic driver in this country, thanks to people like you.

Organizing a symposium requires financial support and the participation of enthusiastic, organized and dedicated people. I am indebted to the organizers at SeCan, to the program organizing committee and to the sponsors for their contributions, which are crucial to making this event a success.

On the eve of Canada's 150th anniversary, we hope you find some time to enjoy Ottawa, its culture and fabulous restaurants. But first and foremost, we wish you a fruitful, stimulating and rewarding symposium.

3e Congrès canadien sur le blé

Mot de bienvenue

Bienvenue au 3e Congrès canadien sur le blé. Nous sommes ravis d'organiser cette réunion d'experts du blé. Nous avons rassemblé une brochette unique de conférencier(ères) et panélistes nationaux et internationaux qui discuteront avec vous des découvertes en recherche dans le blé, des nouvelles tendances en exploitation agricole, des enjeux en santé, en commercialisation, en communication et plus encore. Nous espérons que le congrès soit inspirant et qu'il suscite la réflexion.

Un congrès tel que celui-ci stimule le réseautage. Profitez donc de ce cadre informel pour renouer d'anciens liens et en tisser de nouveaux. Tirez parti des multiples événements sociaux pour faire la connaissance d'un étudiant(e) de deuxième ou troisième cycle. Le congrès est un forum idéal pour décider comment vous pouvez contribuer à l'industrie canadienne du blé et pour y établir les partenariats pour y arriver. Avec des recettes monétaires agricoles de près de 6,4 milliards l'an dernier, le blé est un moteur économique d'envergure au Canada, et ça, c'est grâce à des gens comme vous.

L'organisation d'un événement comme celui-ci requiert un support financier et la participation de gens enthousiastes, organisés et dédiés. Je tiens à remercier les organisateurs chez SeCan, le comité organisateur du programme et les commanditaires pour leurs apports respectifs au succès de cet événement.

A la veille du 150ème anniversaire du Canada, nous espérons que vous trouverez le temps de jouir d'Ottawa, de sa culture et de ses superbes restaurants. Mais d'abord et avant tout, nous vous souhaitons un congrès fructueux, stimulant et enrichissant.

Sincerely yours | Très sincèrement,

Sylvie Cloutier
Program Chair | Présidente de programme
3rd Canadian Wheat Symposium | 3e Congrès canadien sur le blé

Welcome from SeCan

Welcome to Ottawa, and for some of you - welcome to Canada! Our country is huge and diverse, with a tremendous dependence on agriculture. And our biggest agricultural crop – in all its forms – is wheat.

It is a privilege for all of us at SeCan to have played a part in organizing this 3rd Canadian Wheat Symposium in collaboration with Agriculture and Agri-Food Canada. SeCan is a national consortium of private independent Canadian seed companies – who combined – are the major supplier of wheat seed to Canadian farmers. Those farmers run increasingly sophisticated and heavily capitalized enterprises that depend on cutting edge genetics and production practices in order to be competitive in today's global market for agricultural commodities. This need for the latest production tools creates a unique challenge in a country like Canada, where we are engaged in the production of such a broad array of wheat classes and types – spring, winter, hard, soft, red, white, and durum – all with distinctive desirable end-use traits, and all with their own unique challenges, regional adaptation and production requirements.

Despite the challenges with such a complex crop and national geography, we hope wheat continues to be Canada's largest and most important crop well into the future. In order for that to happen, we believe both national and international collaboration amongst researchers is necessary to overcome the challenges we face.

We hope you will seize every opportunity at this symposium to expand your individual circles of collaboration and will take away new inspiration for the valuable work you do – which is critical to our collective health and prosperity the world over. Thank you.

Bienvenue de SeCan

Bienvenue à Ottawa et, pour certains d'entre vous, bienvenue au Canada! Notre pays est vaste, diversifié et fortement dépendant de l'agriculture. Et notre plus grande culture agricole, sous toutes ses formes, est le blé.

C'est un privilège pour nous tous chez SeCan d'avoir joué un rôle dans l'organisation de ce 3e Congrès canadien sur le blé en collaboration avec Agriculture et Agroalimentaire Canada. SeCan est un consortium national d'entreprises semencières canadiennes, indépendantes et privées, qui combinées, constituent le principal fournisseur de semences de blé aux agriculteurs canadiens. Ces agriculteurs exploitent des entreprises toujours plus sophistiquées et fortement capitalisées qui dépendent d'une génétique et de pratiques de production de fine pointe afin de soutenir la concurrence dans le marché mondial actuel des produits agricoles. Ce besoin de disposer des outils de production les plus modernes crée un défi unique dans un pays comme le Canada, où nous sommes engagés dans la production d'un si large éventail de blés (blé de printemps, blé d'hiver, blé vitreux, blé tendre, blé roux, blé blanc et blé dur), chaque type ayant ses caractéristiques propres en matière d'utilisation finale, ainsi que ses défis particuliers à relever sur le plan de l'adaptation régionale et des exigences de production.

Malgré les défis liés à une culture et à une géographie nationale aussi complexes, nous espérons que le blé va continuer d'être la plus grande et la plus importante culture du Canada, et ce, pour de nombreuses années encore. Pour ce faire, nous croyons qu'une collaboration nationale et internationale est nécessaire entre les chercheurs pour surmonter les défis auxquels nous faisons face.

Nous espérons que vous saisirez chaque occasion que vous offre ce congrès afin d'élargir votre réseau de collaboration et que vous repartirez nouvellement inspirés par l'important travail que nous effectuons, travail qui est essentiel pour la santé et la prospérité collectives du monde entier. Merci.

Jeff Reid
General Manager | Directeur général

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La Coop fédérée

RICHARDSON

3rd Canadian Wheat Symposium

Tuesday 22 November 2016

17:30 – 18:00	**Bus Transfer to Banquet** ***Sponsor: FP Genetics***	Ballroom Lobby
18:00 – 19:00	**Cocktail Reception** ***Sponsor: Bayer***	Museum of Nature
19:00 – 21:30	**Banquet** ***Dinner Sponsor: SeCan*** ***Wine Sponsor: Bayer*** ***Entertainment Sponsor: Crop Development Centre***	

Wednesday 23 November 2016

7:30 – 8:30	**Breakfast**	Ballroom A&B
8:30 – 8:45	Welcome	Ballroom A&B
	New Trends in Farming Co-chairs: Gina Feist and Lorena Pahl	Ballroom A&B
8:45 – 9:20	*The Agriculture Manifesto - 10 Key Drivers that will Shape Agriculture in the Next Decade* **Rob Saik**	
9:20 – 9:40	*John Deere Small Grain Production Solutions* **Steve Reynolds**	
9:40 – 10:00	*Using Satellites to Monitor the Canadian Agricultural Landscape* **Leander Campbell**	
10:00 – 10:30	**Morning Break** ***Sponsor: Western Grains Research Foundation***	Ballroom C
	The Changing Landscape of Wheat Co-chairs: Gavin Humphreys and Jason Reinheimer	Ballroom A&B
10:30 – 10:45	*Will Public Wheat Breeding Remain Pertinent in Canada?* **Robert Graf**	
10:45 – 11:00	*Public and Private Sector Plant Breeding - How to Get the Best of Both Worlds?* **Marcus Weidler**	
11:00 – 12:00	*Discussion Panel* **James Anderson** **Robert Graf** **Garth Patterson** **Henry Van Ankum** **Marcus Weidler**	
12:00 – 13:00	**Lunch** ***Sponsor: Canadian Grain Commission***	Ballroom A&B
	What's New in Breeding? Part I: Genetics Co-chairs: Sylvie Cloutier and Christopher Barker	Ballroom A&B
13:00 – 13:30	*Plant Science into Practice: the Pre-Breeding Revolution* **Alison Bentley**	
13:30 – 14:00	*Welcome to the Future: a Pan Genome of Wheat* **Curtis Pozniak**	
14:00 – 14:15	*Functional Characterization of GLK1 and GLK2 in Wheat by CRISPR-CAS9 Editing* **Gopal Subramaniam**	
14:15 – 14:30	*Characterizing and Modulating Homoeologous Recombination in Wheat* **Sateesh Kagale**	

14:30 – 15:00	**Afternoon Break** ***Water Station Sponsor: La Coop fédérée***	Ballroom C
	Combatting Disease and Insect Pest Problems Co-chairs: Brent McCallum and Albert Tenuta	Ballroom A&B
15:00 – 15:30	*Wheat Midge Resistance: Breeding and Genetics* **Curt McCartney**	
15:30 – 15:45	*Prevalence and Virulence of Stripe Rust in Western Canada* **Reem Aboukhaddour**	
15:45 – 16:00	*Advances in Agronomic Management of FHB in 20 Years* **David Hooker**	
16:00 – 16:15	*Pyramiding Genes with Resistance to UG99* **George Fedak**	
16:15 – 16:30	*Harnessing Genetic Resources to Improve Resistance of Wheat to Viral and Fungal Diseases* **Frank Ordon**	
16:30 – 18:00	**Poster Session** ***Sponsor: CANTERRA SEEDS&Limagrain Cereals Research Canada***	Ballroom C

Thursday 24 November 2016

7:30 – 8:30	**Breakfast** ***Sponsor: BASF***	Ballroom A&B
	Wheat, Health and Misinformation Co-chairs: Christine Lowry and Nancy Ames	Ballroom A&B
8:30 – 9:10	*Is Wheat Bad for Health?* **Fred Brouns**	
9:10 – 9:30	*Nutritional Value of Canadian Heritage and Modern Wheat Varieties is Similar Based on Grain Composition Analysis* **Ravindra Chibbar**	
9:30 – 9:45	*Consumer Trends and Solutions in Wheat Bakery Products* **Bob Beard**	
9:45 – 10:00	*Addressing Consumer Needs: Potential for Developing Wheat Products with Lower Glycemic Response* **Nancy Ames**	
10:00 – 10:30	**Morning Break** ***Sponsor: Warburtons***	Ballroom C
	The Farm Gate and the Export Gate Co-chairs: Todd Hyra and Adam Dyck	Ballroom A&B
10:30 – 11:10	*Farm Decision Making: Why We Do What We Do* **Kevin Auch**	
11:10 – 11:45	*A Veteran Wheat Merchant's Perspective on the Changing Market for Canadian Wheat Over the Past 25 Years* **Rhyl Doyle**	
11:45 – 12:00	*Wheat Market Support: Overview of Cereals Canada* **Karen Churchill**	
12:00 – 13:00	**Lunch** ***Sponsor: Alberta Wheat Commission***	Ballroom A&B
	What's New in Breeding? Part II: Phenotyping Co-chairs: Faouzi Bekkaoui and Maurice Moloney	Ballroom A&B
13:00 – 13:30	*Above and Below-Ground Phenotyping Technologies for Wheat Breeding* **Michelle Watt**	
13:30 – 14:00	*Developments in Wheat Phenotyping at Rothamsted* **Malcolm Hawkesford**	
14:00 – 14:15	*Insights from Above: Overview of High Throughput Phenotyping in the Cornell Small Grains Program* **Mark Sorrells**	

14:15 – 14:30	*Utilizing Aerial Imaging from Drones for Wheat Phenotyping* **Andrew Sharpe**	
14:30 – 15:00	**Afternoon Break** ***Water Station Sponsor: FP Genetics***	Ballroom C
	Coping with Abiotic Stresses Co-chairs: Alireza Navabi and Harvey Voldeng	Ballroom A&B
15:00 – 15:30	*Utilization of Genetic Diversity to Enhance Tolerance to Abiotic Stresses in Winter and Spring Wheat* **Alexey Morgunov**	
15:30 – 15:50	*In Search of Molecular Breeding Tools to Improve Freezing Tolerance in Wheat* **Jitao Zou**	
15:50 – 16:10	*Identification of the Wax and Inhibitor of Wax Loci in Wheat – Key Genes for the Glaucous Trait* **Allan Feurtado**	
16:10 – 16:30	*Heat Stress Responsive miRNA are Transiently Expressed to Impart Stress Tolerance in Wheat Plants* **Sridhar Ravichandran**	

Friday 25 November 2016

7:30 – 8:30	**Breakfast**	Ballroom A&B
	The Yield Challenge Co-chairs: Sheri Strydhorst and Ellen Sparry	Ballroom A&B
8:30 – 9:00	*Achieving Sustainable Wheat Production* **Brian Beres**	
9:00 – 9:20	*Keeping Wheat in the Rotation – If it doesn't Yield, It doesn't Stay!* **Paul Sullivan**	
9:20 – 9:40	*Improving Agronomic Input Efficiency and Maximizing Yield by Managing Wheat on a Cultivar Basis* **Sheri Strydhorst**	
9:40 – 10:00	*The Research of Yield* **Ellen Sparry**	
10:00 – 10:30	**Morning Break** ***Sponsor: University of Guelph Wheat Breeding*** ***Water Station Sponsor: C&M Seeds***	Ballroom C
	Building Public Trust in Food and Farming Co-chairs: Brenda Trask and Erin O'Hara	Ballroom A&B
10:30 – 11:00	*Social Media for Scientists: Good Management Practices for Using Online Networks* **Lindsay Chichester**	
11:00 – 12:00	*Building Public Trust in Food and Farming* **Kim McConnell**	

3rd Canadian Wheat Symposium

Wednesday 23 November 2016

New Trends in Farming

S01 **THE AGRICULTURE MANIFESTO – 10 KEY DRIVERS THAT WILL SHAPE AGRICULTURE IN THE NEXT DECADE**

Robert Saik

AGRI-TREND a Trimble organization, #102, 8026 Edgar Industrial Cr, Red Deer, AB, Canada, T4P 3R3

Agriculture is no longer Murray McGlaughlan's "dusty old farmer bent over the tractor wheel" but a full-fledged modern business integrating all the tools available to it. We will look at how Science and Technology are being integrated with modern agricultural practices to provide society with a safe, reliable food supply in an environmentally sustainable manner AND we will look at some of the threats that could potentially erode our ability to feed the people on the planet. There are major technology currents pulling on all of humanity. We can choose to fight the current or be aware of their strength and swim in the same direction...and be ahead of the competition. Rob will take you on a quick journey showing how farmers are integrating technology to feed a growing world population. He will touch on exponentially, robotics, artificial intelligence, sensor integration, bio synthesis (GE and GMO), data systems and environment sustainability. Finally, we will look at HOW we could integrate all these technologies to best serve our farmer customers through new business opportunities offered by our dealerships. And lastly, you will walk away with a sense that, in spite of what the media reports, things are actually pretty good and getting better all the time.

S02 **JOHN DEERE SMALL GRAIN PRODUCTION SOLUTIONS**

Steven Reynolds

John Deere Canada ULC, 295 Hunter Rd, Grimsby, ON, Canada, L3M 4H5

John Deere offers a wide range of solutions for producing small grains in Canada. The new 76 foot 1870 air-hoe drill coupled with the 9RX Series 4-Track tractor allows producers to get more crop seeded in less time. Integrated Precision Ag technologies such as SectionCommand™, TruSet™, and Wireless Data Transfer (WDT) enable another level of efficiency. This discussion explores how John Deere technologies address current and future agronomic needs for growing small grains.

S03 **USING SATELLITES TO MONITOR THE CANADIAN AGRICULTURAL LANDSCAPE**

Leander Campbell, Thierry Fisette, Andrew Davidson, Patrick Rollin, Bahram Daneshfar, Ziad Aly and Benjamin Deschamps

AgroClimate, Geomatics, and Earth Observation Division, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6

Understanding the state and trends in agriculture production is essential to combat both short-term and long-term threats to stable and reliable access to food for all, and to ensure a profitable agricultural sector. However, because Canada's agricultural landscape is extensive and diverse, our ability to manage it is only as good as the information available to make informed decisions. Space-based Earth

Observation (EO) can deliver cost-effective, timely and accurate information to better support policies, programs, performance measurement and market access. Agriculture and Agri-Food Canada (AAFC) is in a unique position to capitalize on the integration of EO technology, ground observation data and other monitoring systems to provide information relating to agricultural production. AAFC is a leader in the development and use of EO technologies for this type of agricultural assessment, and has already demonstrated that these technologies can deliver cost-effective, timely and accurate information.

The Changing Landscape of Wheat

S04 **WILL PUBLIC WHEAT BREEDING REMAIN PERTINENT IN CANADA?**

Robert Graf

Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South, Lethbridge, AB, Canada, T1J 4B1

In Canada, there are several examples in which major private industry investment in plant breeding of specific crops resulted in reductions in public sector plant breeding. Over the past five years, several global life sciences companies have made substantial investments in wheat breeding around the world, including Canada. Canada has a long and successful history of public sector wheat breeding that, in recent years, has been supplemented through producer check-offs. Several key questions may need to be addressed in the future and will centre on the answer to whether public wheat breeding will remain pertinent in Canada.

- Is it important to maintain public sector wheat breeding programs?
- Will public sector breeding programs remain competitive?
- How can public and private breeding programs optimize resources to ensure the industry moves forward as quickly as possible?
- How do we ensure that producers remain the primary focus of breeding efforts?

S05 **PUBLIC AND PRIVATE SECTOR PLANT BREEDING – HOW TO GET THE BEST OF BOTH WORLDS?**

Marcus Weidler

Bayer CropScience Inc., #200-160 Quarry Park Boulevard SE, Calgary, AB, Canada, T2C 3G3

All over the world various ways of interaction and collaboration between public and private plant breeding efforts have evolved in many key crops. In most cases this development started from an exclusively public breeding effort (e.g. Wheat in Australia, almost all crops in Eastern Europe) and developed over a decade or two into a shared breeding effort between public and private sector. In my introductory presentation I will discuss selected country-crop cases and identify key learnings with the focus to answer the following key questions:

- How to attract and secure necessary resources for innovation in plant breeding and R&D?
- How to optimize the use of the available resources for breeding and R&D – avoiding redundancies and duplication of work?
- How to prioritize R&D and breeding targets? How to establish the right balance between long-term, high-risk/high-gain research projects and short-term, incremental breeding efforts in order to establish a sustainable flow of innovation?
- How to communicate the benefits of agriculture and innovation in agriculture to the general public?

Ultimately, these findings will help us to answer the ultimate question: How to further increase the competiveness of the Canadian growers and the long-term sustainability of Canadian agriculture in a constantly changing environment?

What's New in Breeding? Part 1: Genetics

S06 **PLANT SCIENCE INTO PRACTICE: THE PRE-BREEDING REVOLUTION**

Alison Bentley, Ian Mackay, Richard Horsnell, Phil Howell and Emma Wallington

The John Bingham Laboratory, National Institute of Agricultural Botany (NIAB), Huntingdon Road, Cambridge, CB3 0LE, United Kingdom

In 2007, NIAB embarked on a pioneering programme of wheat pre-breeding to deliver systematically developed and validated resources for UK and European wheat improvement. Beginning as a small-scale introgression program the NIAB vision for pre-breeding has now expanded to encompass the development and exploitation of complex populations, the application of quantitative genetic methods and the use of functional genomics tools (including gene-editing) for crop improvement. At the same time, the research and breeding community in the UK has also embraced pre-breeding as a crucial step towards accelerating genetic gain in wheat and other crop species. This presentation will describe the evolution of the NIAB pre-breeding programme and the integration of germplasm and genomics to deliver better resources to UK wheat breeding. It will describe the resources developed at NIAB, including re-synthesized hexaploid wheats and next-generation Multi-founder Advanced Generation Inter-Cross (MAGIC) populations, and the strategies in place for their exploitation. New opportunities and challenges in pre-breeding, including the use of functional genomics tools such as gene-editing, will also be considered for their potential impact to wheat breeding.

S07 **WELCOME TO THE FUTURE: A PAN GENOME OF WHEAT**

Curtis J. Pozniak[1], Pierre J. Hucl[1], Nils Stein[2], Jesse Poland[3], Andrew Sharpe[4], Kevin Koh[4], Beat Keller[5], Gil Ronen[6], Luigi Cativelli[7], Assaf Distelfeld[8], Klaus Mayer[9], Hikmet Budak[10], Kellye Eversole[11], Jane Rogers[11] and the International Wheat Genome Sequencing Consortium[11]

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[9]Plant Genome and Systems Biolgy, Helmholtz Center München, German Research Center for Environmental Health (GmbH), 1 Ingolstädter Landstraße, 85764 Neuherberg/Munich, Germany
[10]Department of Plant Sciences and Pathology, Montana State University, PO Box 173150, Bozeman, Montana, 59717-3150, USA
[11]International Wheat Genome Sequencing Consortium, 5207 Wyoming Road, Bethesda, Maryland, 20816, USA

Wheat (*Triticum spp*.) remains one of the last major crop species for which a fully assembled and annotated genome is available. This has slowed identification of genes underlying phenotypic expression of agriculturally important traits. Recently, the International Wheat Genome Sequencing Consortium (IWGSC) announced the most comprehensive and contiguous assembly of the "Chinese Spring"

hexaploid (2n=6x=42; AABBDD) wheat genome. This sequence will represent the gold standard reference of hexaploid wheat and is already paving the way for innovations in wheat biology and breeding. In the case of tetraploid wheat (2n=4x=28; AABB), two assemblies have been produced: one for wild emmer wheat (WEWSeq Consortium) and a second of the commercial cultivar "Svevo (International Durum Wheat Genome Sequencing Consortium). In addition, 10 additional cultivars are currently being sequenced as part of a "Ten Genomes Project" being conducted under the auspices of the Wheat Initiative. The goal of this activity is to define the core and pan-genomes of hexaploid wheat. As part of this project, we have already completed sequencing of "CDC Stanley" and CDC Landmark", two commercial wheat cultivars developed at the Crop Development Centre. CDC Stanley carriers the "VPM" introgression and CDC Landmark carry genes that confer resistance to the orange wheat blossom midge and the wheat stem sawfly. Here we will report on the current status of these reference sequences, and provide a high level comparison of presence/absence variation based on these assemblies. We will also discuss the expected impact on wheat biology research and breeding.

S08 **FUNCTIONAL CHARACTERIZATION OF *GLK1* AND *GLK2* IN WHEAT BY CRISPR-CAS9 EDITING**

Gopal Subramaniam[1], Jhadeswar Murmu[1], Jas Singh[1], Li Wang[1], Johann Schernthaner[1] and Raju Datla[2]

[1]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
[2]Aquatic and Crop Resources Development, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK, Canada, S7N 0W9

Golden2-Like transcription factors, GLK1 and GLK2 regulate chloroplast development in a redundant manner. Studies in *Arabidopsis*, tomato, and other crops show that these genes are also involved in diverse plant responses that include defense, fruit ripening, and senescence. Our studies show that overexpression of the *Arabidopsis GLK1* in wheat improved photosynthetic capacity in flag leaves and reduced photochemical quenching. This indicated that GLKs could be used to increase crop yield and tolerate abiotic stresses in wheat. The completion of the bread wheat genome sequence and the advent of CRISPR-Cas9 genome editing technology provide an opportunity to use functional genomics to rapidly associate genes with phenotypes in plants with complex genomes. We are using this technique to generate mutants of *TaGLKs* in wheat to delineate their roles in photosynthesis and other traits. We have generated *sgRNA* constructs to target both *GLK1* and *GLK2* in wheat. We assessed the efficacy of *sgRNA* constructs in wheat protoplasts and transgenic wheat by amplicon sequencing. Results of these experiments will be presented.

S09 **CHARACTERIZING AND MODULATING HOMOEOLOGOUS RECOMBINATION IN WHEAT**

Venkatesh Bollina[1], Arun S. K. Shunmugam[1], Pankaj Bhowmik[1], Kevin Rozwadowski[2], Curtis J. Pozniak[3], Andrew G. Sharpe[1,4] and Sateesh Kagale[1]

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Transfer of high value target loci from diverse wild relatives to adapted elite cultivars is seen as a key to the future of wheat breeding. Pairing and recombination between chromosomes of the alien donor and

those of cultivated crops is the key to such gene introgressions. In wheat, the *Ph1* (pairing homoeologous 1) locus on Chr5B controls orderly pairing of homologous chromosomes. A *Ph1*-deficient mutant (*Ph1b*) of Chinese Spring (CS) has been used for inducing homoeologous recombination between wheat chromosomes and homoeologues from wild species; however, the CS background is not suitable for use in Canadian breeding programs and would require extensive time and resources to eliminate the CS-*Ph1b* background via backcrossing. Thus a *Ph1*-deficient Canadian elite wheat cultivar would have tremendous potential for application in introducing new genetic variation in wheat breeding programs. To this end we have initiated a project to assess the phenotype of a candidate *Ph1* gene (*C-Ph1*) by developing an RNAi line to assess the impact of its suppression in North American germplasm. Meiocytes from the RNAi plants showed expected *Ph1* mutant phenotypes, such as multivalent formation, aberrant pairing and misalignment of chromosomes along metaphase I plate, thus confirming the functional role of C-*Ph1* in meiosis and chromosome pairing behavior. These results along with our efforts towards (1) characterizing gene regulatory networks specifically involved in chromosome pairing and subsequent recombination initiation during meiosis in wheat, and (2) developing pollen-based single cell genomic sequencing approach for monitoring recombination frequency in F_1 wheat plants will be discussed.

Combatting Disease and Insect Pest Problems

S10 **WHEAT MIDGE RESISTANCE: BREEDING AND GENETICS**

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Orange wheat blossom midge (OWBM, *Sitodiplosis mosellana* Géhin) is a damaging insect pest of wheat. Tools for integrated OWBM management include midge resistant varieties, early seeding of spring wheat, foliar insecticide application, and the parasitic wasp *Macroglenes penetrans* (Kirby). OWBM resistant varieties have been registered in Canadian spring and durum wheat classes. The genetic basis of this resistance is the gene *Sm1*, which is the only described OWBM resistance gene. *Sm1* is easily selected based on phenotype with trained personnel but DNA markers are desirable for breeding. A saturated genetic map of the *Sm1* region of chromosome arm 2BS has been developed. Progress on map-based cloning of *Sm1* will be reported. Oviposition deterrence is another mechanism of managing OWBM damage with host genetics. OWBM oviposit fewer eggs on spikes of deterrent wheat lines relative to non-deterrent wheats. Research to date indicates that deterrence is the result of a volatile compound(s). Reduced midge damaged kernels can also arise from aberrant egg laying behavior where eggs are

oviposited on the rachis rather than the florets. Oviposition deterrence has been identified in Canadian and American spring wheat varieties, a few American winter wheat varieties, and a few durum wheat lines. Present and future research in this area will be discussed. Testing of wheat accessions is also underway to search for additional resistance genes. The genetic research underway will assist in the development of varieties with improved OWBM resistance coupled with oviposition deterrence.

S11 **PREVALENCE AND VIRULENCE OF STRIPE RUST IN WESTERN CANADA**

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Stripe rust, caused by *Puccinia striiformis f. sp. tritici*, is a destructive wheat disease worldwide. In Canada, stripe rust has been detected every year since 2000 with serious epidemics reported in parts of western Canada in 2005, 2006, 2011 and 2014. This year disease incidence and severity was assessed in commercial wheat fields in southern Alberta and Saskatchewan from early June to late August. The pathogen likely overwintered in Alberta; it was observed in early March in Lethbridge. In total, 54 fields were surveyed in southern Alberta; 38% of these fields had stripe rust infection and 11% suffered severity of ≥ 20% measured using the modified Cobb scale. The disease was widespread this year, but extensive fungicide application may have limited severe yield losses by this pathogen. In Saskatchewan, infection with stripe rust was observed in relation to the different *Yr* genes carried by wheat varieties. Rust resistance genes *YrSP*, *Yr5*, and *Yr15* are still effective against existing races, but *Yr8*, *Yr10*, *Yr27*, *Yr28* have been defeated by most of the races. Differentials carrying *Yr1*, *Yr32*, *YrSu*, and *Yr4* were effective against most pathogen races until 2013, but were defeated at few locations in SK in 2016, indicating virulence change in pathogen populations. Stripe rust incidence, severity and changes in pathogen virulence in the last decade will be discussed.

S12 **ADVANCES IN AGRONOMIC MANAGEMENT OF FHB IN 20 YEARS**

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In 1996, an epidemic of Fusarium head blight (FHB) caused catastrophic losses to the wheat industry across Ontario. Since then, much research has been conducted to manage FHB for reducing deoxynivalenol (DON) in wheat grain. FHB has develops in at least some parts of Ontario in every year, mainly due to favorable weather for infection and disease development, and the reluctance for growers to plant tolerant wheat varieties. Research during the last 20 years has shown that managing FHB and DON requires an integrated approach. The data clearly shows that the combination of moderately-tolerant wheat varieties and a fungicide applied at heading with the best nozzles for optimal coverage are most important in reducing the risk for FHB and DON contamination of grain. Risk can be further reduced using prediction models, blowing out infected grain while combining, and with the application of phosphorus in-furrow or with the seed at planting for more uniform heading.

S13 **PYRAMIDING GENES WITH RESISTANCE TO UG99**

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Pyramids with Sr33, Sr35, Sr36, Sr42, Sr43

Most of the current stem rust resistance genes (Sr) in Canadian wheat varieties are ineffective against the *Pgt* race Ug99 lineage, which pose a major threat to wheat production worldwide. Several stem rust resistance genes including Sr33, Sr35, Sr36, SrCad/Sr42 and Sr43, are effective against race TTKSK. Although Sr36 is ineffective against Ug99 race TTTSK, it is still potentially useful for pyramiding genes to develop germplasm with durable stem rust resistance. For this purpose, we made crosses among RL5405 (Sr33), RL6099 (Sr35), Lang (Sr36), AC Cadillac (SrCad/Sr42), and RWG34 (Sr43) containing the respective Sr genes. A total of 54 doubled haploid (DH) lines were produced from the F1 from AC Cadillac/Lang/RWG34/RL5405, and 82 DH lines were obtained from RW434/RL5405/RL6099. The DH progeny were tested at the seedling stage with race TTKSK and susceptible lines were discarded. We putatively developed 12 genotypes with multiple Sr gene combinations, including Sr33+Sr36+SrCad/Sr42+Sr43, Sr33+Sr36+SrCad/Sr42, Sr33+Sr36+Sr43, Sr33+SrCad/Sr42+Sr43, Sr36+SrCad/Sr42+Sr43, Sr35+Sr33+Sr43, Sr33+Sr36, Sr33+Sr43, Sr36+SrCad/Sr42, Sr36+Sr43, Sr35+Sr33, and Sr35+Sr43, based on positive association with linked PCR markers. Another population with 63 DH lines was derived from (Hoffman*2/RL6099)// (Hoffman*2/Lang) to combine the Fusarium head blight (FHB) resistance of Hoffman (FHB1) with Sr35 and Sr36. We found 17 of 63 DH lines containing both Sr35 and Sr36, based also on linked PCR markers. This indicated that the combination Sr35+Sr36 was pyramided into the Canadian cultivar Hoffman, which will be useful for development of cultivars resistant to Ug99 and FHB in Canada.

Pyramids with Sr33, Sr42

A total of 68 DH plants were produced from the F1 hybrid obtained from crossing AC Cadillac (SrCad/Sr42, Lr34) / Carberry (Lr34 Fhb1) * RL5405 (Sr33) / Carberry (Lr34Fhb1). Two lines contained Sr33, Sr42, Lr34 and Fhb1. These were 16 other combinations of the four genes.

Pyramids involving combinations of Sr33, Sr39, Sr40, Sr42, Sr43

The sources of the genes were Sr33 (RL5405) Sr39 (RWG4-2) Sr40 (RL6087) Sr42 (AC Cadillac) Sr43 (RWG43). Various cross combinations were produced and pyramids recovered in either F2 progeny or doubted haploids. Pyramids with up to four genes were produced eg. Sr33, Sr36, SrCad, Sr43.

S14 HARNESSING GENETIC RESOURCES TO IMPROVE RESISTANCE OF WHEAT TO VIRAL AND FUNGAL DISEASES

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Wheat is of special importance for feeding the earth´s growing population. However, wheat is hit by many pathogens causing severe yield losses. Although wheat breeding successfully improved resistance during the last decades, the appearance of new virulent races necessitates the continuous identification of new sources of resistance followed by marker development and the marker based exploitation of this genetic variation. While in the past marker development was time consuming and laborious, today genomic tools are available facilitating efficient marker development or expression analyses, respectively, even in wild relatives like *Triticum monococcum*. Applying MACE and DArT analyses, differentially expressed genes involved in a race-nonspecific pre-haustorial resistance to *Puccinia triticina* in *T. monococcum* were identified and QTL involved in this pre-haustorial resistance were mapped. By screening genetic resources for resistance to *Zymoseptoria tritici,* resistant genotypes were detected and based on

genotyping DH-lines with the 15k iSelect chip and multi-location trials, QTL involved in this resistance were identified. Besides fungal diseases, viruses, i.e. the leaf hopper transmitted *Wheat dwarf virus* (WDV) and *Soil-borne cereal mosaic virus* (SBCMV) transmitted by *Polymyxa graminis* have gained rising importance during the last decade in Europe. By screening a diverse set of wheat and wild relatives, differences in the reaction to an artificial WDV infection were detected and GWAS will be conducted to identify respective QTL, while with respect to SBCMV closely linked markers have been developed, already. Results presented elucidate, that genomic tools will lead to a faster exploitation of the genetic diversity present with respect to resistances in the wheat gene pool.

Thursday 24 November 2016

Wheat, Health and Misinformation

S15 **IS WHEAT BAD FOR HEALTH?**

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Wheat is the 3rd most consumed cereal in the world. Recently wheat and gluten consumption was suggested as a cause of obesity and diabetes. Social media commentaries mention adverse health effects caused by mechanisms related to hormonal disturbances, leaky gut, brain effects, addiction and overeating. Suggestions that wheat has been genetically modified resulting in compositional changes of the wheat causing obesity and illness cannot be substantiated. Whole wheat related and observed metabolic changes are improved blood glucose control, improved cholesterol levels, reduced blood pressure and lower blood level of markers of inflammation. Individuals that suffer from celiac disease and those who are sensitive to wheat proteins will benefit from avoiding products containing gluten or wheat. Individuals with a hypersensitive gastro-intestinal system (irritable bowel syndrome, prevalence 10-15%) may react positive to avoidance of wheat. Taken all together, the consumption of whole grain wheat foods is associated with significant health advantages in the majority, being at least >90%, of the population. Suggestions that modern bread-wheat contains more gluten than ancient wheat lack evidence. Wheat-containing foods prepared in customary ways (such as cooked, baked, or extruded) and eaten in recommended amounts are, as recently clearly shows in several meta-analysis, associated with a significant reduction type 2 diabetes, heart disease and colon cancer, as well as a more favorable long term weight management.

S16 **NUTRITIONAL VALUE OF CANADIAN HERITAGE AND MODERN WHEAT VARIETIES IS SIMILAR BASED ON GRAIN COMPOSITION ANALYSIS**

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Wheat (*Triticum aestivum* L.) is a major Canadian crop and its grain is part of staple food around the

world. In a wheat grain, carbohydrates including starch and non-starch polysaccharides are the predominant (two-thirds to three-quarters) constituent followed by proteins accounting for one-fifth to one-sixth of grain weight. Minor nutrient components include phenolic compounds in bran, fats, vitamins and minerals that also contribute to the nutritional quality of wheat-based food products and human health. Grain constituents (carbohydrates, proteins and minerals) were analyzed from 37 wheat cultivars belonging to the Canadian Western Red Spring (CWRS) market class the predominant type of wheat grown in Canada, since the turn of 20th century. The selected wheat cultivars included heritage wheats introduced in to Canada in the middle of nineteenth century (cv Red Fife, 1860) to modern varieties that were developed till the beginning of twenty first century (2007). Very little variation was detected in all the grain composition characteristics analyzed. The study suggests that the nutritional composition of the wheat grain, (protein, carbohydrates and minerals) of modern day varieties is similar to that of heritage wheat varieties that were grown in Canada in the middle of nineteenth century.

S17 **CONSUMER TRENDS AND SOLUTIONS IN WHEAT BAKERY PRODUCTS**

Bob Beard

Warburtons Ltd, Hereford House, Hereford St, Bolton, BL1 8JB, United Kingdom

This short presentation will focus on some of the recent consumer trends Warburtons has identified in the UK bakery market, and how we were able to overlay a need to improve the perceived nutrition of bakery products into the launch of a new bakery range incorporating pulse blends from Canada. A rapid journey from developing and health and nutrition strategy, to being first to market in launching a new bakery range of Protein bread onto the UK market.

S18 **ADDRESSING CONSUMER NEEDS: POTENTIAL FOR DEVELOPING WHEAT PRODUCTS WITH LOWER GLYCEMIC RESPONSE**

Nancy Ames and Sijo Joseph

Richardson Centre for Functional Foods and Nutraceuticals, Agriculture and Agri-Food Canada, 196 Innovation Drive, Winnipeg, MB, Canada, R3T 6C5

Diabetes is becoming a global epidemic and has been identified as one of the most challenging health problems in the 21st century. One of the key dietary approaches to prevent/manage diabetes is consuming food with lower glycemic response. Considering the fact that wheat is one of the oldest food crops and serves as a staple food for many nations and cultures, it stands as an optimal vehicle to deliver lower glycemic products. Novel wheat breeding approaches (eg. higher starch amylose content) and processing methods such as milling, sour dough fermentation, freezing of bread, and factors that modify product structure have all been shown to improve glycemic response. Moreover, differences in starch and starch-protein interactions in wheat as well as variations in starch bioaccessibility that can be achieved through cooking and processing methods offer a great platform for developing wheat bread products with lower glycemic response. These strategies either alone or in combination could be used to help attenuate postprandial blood glucose response to consumption of foods made from wheat, and in turn help meet the consumer demand for healthier wheat products.

The Farm Gate and the Export Gate

S19 **FARM DECISION MAKING: WHY WE DO WHAT WE DO**

Kevin Auch

Box 84, Carmangay, AB, Canada, T0L 0N0

Today's farm Managers face dozens of decisions every day, and in terms of their impact on the farm they can range from the insignificant to the profound. "Whenever I can, I always try to look at decisions objectively. While this can be challenging when a farm operation involves people with whom you are interacting on much more than a business basis, it is important not to let emotions guide you into decisions which will not be in the best interests of the family and farm." Kevin will discuss how he makes decisions on his farm in the areas of crop, variety, and input choices; modern farm machine technology usage; equipment sizing; labour and time efficiency; grain storage challenges; and marketing options. At the conclusion of the presentation, the audience will gain a better understanding of farm manager decision making processes and some of the factors that can affect them.

S20 **A VETERAN WHEAT MERCHANT'S PERSPECTIVE ON THE CHANGING MARKET FOR CANADIAN WHEAT OVER THE PAST 25 YEARS**

Rhyl Doyle

Paterson Grain, 22nd floor-333 Main Street, Winnipeg, Manitoba, R3C 4E2, Canada

Over the past 27 years working in the Canadian grain trade with Cargill, the Canadian Wheat Board and Paterson Grain, Rhyl has sold more than two entire crops of Canadian wheat to customers around the world. Over this time the global wheat market has grown and evolved. Canada's customer base has changed and the role of Canadian wheat has also evolved in many markets. Rhyl will reflect back on the last nearly three decades of selling Canadian wheat to a wide range of customers in many different countries and will highlight some of his observations on where we have come from and where we are going in the years ahead.

S21 **WHEAT MARKET SUPPORT: OVERVIEW OF CEREALS CANADA**

Karen Churchill

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Cereals Canada is a relatively new organization formed in support of the cereals industry. It is a broad collaboration of seed and development companies, producer groups, exporter and processors, who share a vision of a dynamic, responsive Canadian cereals industry that brings sustainable profitability to the entire value chain. Cereals Canada's three strategic platforms are to: 1) Build and implement a market development plan for Canadian cereals; 2) Shape the environment for innovation in cereals; and 3) Be a leader for the cereals industry in Canada. The market development pillar includes a number of different initiatives. For example, addressing market access issues such as non-tariff trade barriers, advising on changes to the wheat classification system, and providing information to and receiving feedback from our customers and market development. Cereals Canada in partnership with CIGI, commissioned a marketing study to review the trends in global demand for Canadian wheat to examine potential future shifts in consumption and establish how the Canadian wheat industry can better serve its customers. The report confirmed that Canadian brand does exist and is based on the quality, consistency and cleanliness of Canadian shipments. However, these characteristics are both a strength and a weakness. The quality of CWRS and CWAD make it highly desirable for specific products, whereas our competitors may offer a more diverse range suitable for many products. The challenge for future market plans will be in determining how best to develop our own competitive advantage and respond to changing patterns of global demand.

What's New in Breeding? Part II: Phenotyping

S22 **ABOVE AND BELOW GROUND PHENOTYPING TECHNOLOGIES FOR WHEAT BREEDING**

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Wheat varieties with greater yields arise today mainly by selecting for harvested grain yield in field environments. This approach combines multiple favourable alleles. Gains are slow because the contributions of alleles to yield are largely unknown. The contrasting “pre-breeding” approach aims to introduce a single major enhancing trait (other than yield) into a variety. This approach can take ~20 years from idea to field, and there are few successful examples in wheat (Hall and Richards 2013). Phenotyping may bridge this gap between yield based and single-trait based breeding because multiple traits (alleles) can be measured on one line. Examples are presented where phenotyping technologies quantified shoot and root traits non-destructively on wheats of different genetic and pedoclimatic origins. For early growth traits in controlled conditions: root architecture differed in response to soil water gradients, but shoots did not (Nagel et al., 2015); shoot growth declined in response to reduced N supply, but root growth did not (Gioia et al 2015); and leaf area and water use varied differentially in response to drought (Nakhforoosh et al 2016). Field phenotyping during grain filling has shown that shoot and root development vary independently depending on plant stage, genotype and environment (Severini et al. in prep), and spectral properties of wheat heads and canopy are dynamic, requiring time-lapse systems (Ahrends et al., 2014). Hence phenotyping technologies quantify the high degree of variation at important establishment and grain development stages in wheat, and may increase certainty of incorporating multiple alleles of known effect within breeding.

S23 **DEVELOPMENTS IN WHEAT PHENOTYPING AT ROTHAMSTED**

Malcolm Hawkesford

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S24 **INSIGHTS FROM ABOVE: OVERVIEW OF HIGH THROUGHPUT PHENOTYPING IN THE CORNELL SMALL GRAINS PROGRAM**

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Conventional approaches to phenotyping have stimulated interest in methods that can be used to measure traits on large numbers of plots accurately, rapidly and economically. We work with a company called AgPixel, that flies an airplane at 1,500 ft and uses a Canon EOS Rebel 6D NIR converted camera with 63° field of view. During 2015 and 2016 we flew on 6 dates spanning all stages of development for spring and winter grains nurseries. We calculated Enhanced Normalized Vegetation Index (ENDVI) which uses both the near infrared and the green wavelengths to determine reflectance. ENDVI was useful for measuring winter survival and a strong correlation was observed between reflectance and leaf angle with erect leaves having the highest NDVI. We are also collaborating with CIMMYT to evaluate an A-Series Micro-Hyperspec VNIR hyperspectral camera flown at vegetative and grain filling stages. In this study, 790 wheat lines were grown in 2014 at Ciudad Obregón, Mexico in 4 environments varying in planting date and irrigation. Canopy spectral reflectance was recorded for 250 bands and pedigree and marker genotypes from 4413 genotype-by-sequencing markers were available. Mixed models were fit using the R package “EMMREML” and three relationship matrices: spectral reflectance, pedigree, and genotypes.

Heritabilities for spectral data were consistently 0.1 to 0.2 higher than for grain yield and prediction accuracies for grain yield ranges from 0.6 to 0.7 when multiple flights and all spectral wavelengths were included in the model. These accuracies were consistently 0.2 higher than predictions using pedigree or markers.

S25 **UTILIZING AERIAL IMAGING FROM DRONES FOR WHEAT PHENOTYPING**

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Digital phenotyping of wheat with imagery can be utilized to both serve as a tool to facilitate selection in plant breeding and as a metric for associative genomic selection. Aerial imaging using unmanned aerial vehicles is platform for rapid imaging of wheat breeding plots. The ultimate objective of this research program is to develop field based phenotypic imaging that will contribute useful tools for genetic dissection of complex traits, and as selection tools in breeding programs. However, before this goal can be realized several key questions must be addressed: How precise are multi-scale image-based phenotypes and are they repeatable? Do image-based phenotypes correlate with traditional phenotypes targeted by crop breeders? Can these digital phenotypes, together with measurable environmental factors, be included in genomic selection models to improve selection efficiency in breeding programs? To address these questions, we are developing automated methods of imaging field-expressed phenotypes in wheat. We will first develop and refine procedures for image acquisition using existing and novel imaging, and develop advanced data workflow that are breeder-friendly. These data will be mined for image based phenotypic traits (unique digital phenotypes; UDPs) that will be correlated to field-based performance measures. For this, we will UDPs will be assessed over a three-year period from emergence to harvest with aerial platforms. Characterizing these founder lines and breeding populations will allow identification of the most robust UDPs that we will then apply to the NAM populations in future years with the aim of linking genotypes to UDPs and to improve genomic selection models.

Coping with Abiotic Stresses

S26 **UTILIZATION OF GENETIC DIVERSITY TO ENHANCE TOLERANCE TO ABIOTIC STRESSES IN WINTER AND SPRING WHEAT**

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CIMMYT Global Wheat Program addresses two major wheat producing areas outside of its breeding hub in Mexico: winter wheat in Central and West Asia (12-14 mln ha) and high latitude spring wheat in Northern Kazakhstan and Western Siberia (15-17 mln ha). Both areas are very important for regional and global food security. Winter wheat belt stretching from Turkey in the West to Kazakhstan in the east suffers from frequent droughts reducing grain yield by up to 30-40%. Climate change expressed through higher temperatures in spring and early summer affect grain filling and its size. Cooperative winter wheat breeding program (Turkey-CIMMYT-ICARDA) enhances abiotic stresses tolerance through utilization of

diverse sources of germplasm: modern varieties from the region, Turkish wheat landraces collected recently and hexaploid winter synthetics. Mutlocational breeding framework utilizes key sites in Turkey, Iran and Uzbekistan to select broadly adapted drought and heat tolerant germplasm. Kazakhstan-Siberia Network on Spring Wheat Improvement (KASIB) operated by CIMMYT since 2000 unites 20+ breeding and research programs through cooperative yield trial and shuttle breeding. Moisture stress in this short season wheat represents a major challenge. Though this environment is similar to spring wheat areas of Canada, the avenues for increasing yield and enhancing drought tolerance are quite different. KASIB germplasm maintains tall stature, relatively sensitive to day length and largely lacks 1B.1R translocation. Incorporation of genes from wheat wild relatives to improve rust resistance also contributed to drought tolerance. Future priorities for drought and heat tolerance enhancement are presented.

S27 **IN SEARCH OF MOLECULAR BREEDING TOOLS TO IMPROVE FREEZING TOLERANCE IN WHEAT**

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Lipid composition in plant cells are subjected to a wide range of adjustment when plants encounter unfavorable growth conditions. Great attention has been paid to delineating lipid changes during adaptation to specific stresses, both for seeking novel markers of stress tolerance traits and for exploring the mechanistic details of stress response and adaptation. The level of trans-16:1 fatty acid in phosphotidylglycerol (PG) of cereal leaf tissues during cold acclimation has been found to be associated with capacity of freezing tolerance. Through testing more than 30 wheat cultivars with varying degrees of winter hardiness, we were able to confirm under field conditions a tight correlation between the rate of 16:1 reduction in leaf tissues and Lt_{50}. Focusing on two pairs of NILs that differ only in the VRN1 loci, we conducted transcriptomic and lipidomics profiling on leaf tissues under conditions mimicking cold acclimation. To understand the factors responsible for lipid biochemical changes, we performed lipid-transcript network analysis and focused on subnetworks around PG(16:1) to dissect network connections between individual genes and lipids. We will report findings on novel factors that we hope will provide new insights on how environmental factors trigger glycerolipid pathways response during cold acclimation in wheat.

S28 **IDENTIFICATION OF THE *WAX* AND *INHIBITOR OF WAX* LOCI IN WHEAT – KEY GENES FOR THE GLAUCOUS TRAIT**

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Surface waxes on the cuticle of terrestrial plants function as a protective barrier to environmental stresses – particularly water and heat stresses. In wheat, long-chain β-diketones and their hydroxlated derivatives are major components of surface waxes and their deposition leads to the bluish-white glaucous trait in reproductive-age plants. To reach our goal of discovering markers important to productivity under water stress, we identified the genes responsible for β-diketone wax deposition using four sets of durum lines isogenic for the glaucous trait. Glaucousness in durum is controlled by two major loci, *Waxy 1* (*W1*) and the suppressor *Inhibitor of wax 1* (*Iw1*) on chromosome arm 2BS. In wheat, the D subgenome contains

the paralogs *W2* and *Iw2* on 2DS. Using transient gene knockdowns and expression profiling, we identified *W1* as an uncharacterized carboxylesterase-like protein associated with β-diketone biosynthesis. Further, from the same isogenic lines, we identified the wax inhibitor gene *Iw1*. When *Iw1* was introduced into glaucous wheat, a non-glaucous, β-diketone-depleted phenotype was observed due to down-regulation and silencing of the *W1/W2* genes. Corroborative evidence for *Iw* functionality includes the identification of *Iw2* in *Aegilops tauschii*. Sequence analyses suggest that *Iw* genes arose from gene duplication with subsequent acquisition of expression to generate a mechanism for genetically dominant repression of the glaucous trait.

S29 **HEAT STRESS-RESPONSIVE miRNAs ARE TRANSIENTLY EXPRESSED TO IMPART STRESS TOLERANCE IN WHEAT PLANTS**

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With rising global temperature, understanding plants adaptation to heat stress has implication in plant breeding. The prominent role of miRNA-guided gene expression has been uncovered in several stress responses. In this study, leaf tissues were harvested from four biological replicates of control and heat stressed wheat plants at 0, 1 and 4 days after treatment (DAT). A total of 24 small RNA libraries were sequenced on the Illumina platform, generating 55 million reads corresponding 18 million distinct tags. These tags were mapped to previously annotated miRNA precursors and a total of 208 miRNAs were identified. Forty-seven of these were differentially expressed in response to heat stress. Approximately 63% of the differentially expressed miRNAs were transiently downregulated immediately following the heat stress but their expression levels were similar to control plants four days later. MiRNA downregulated in response to heat stress included miR159, miR169, miR171, miR528 and miR1122 which were predicted to target transcription factors, signal transduction pathways and antioxidant activity. MiR1122 and miR171 were also predicted to target methyl transferases and dicer-like 3, respectively. To verify miRNA-guided cleavage sites, the corresponding 24 degradome libraries were sequenced and approximately 370 million reads were mapped and analyzed using the CleaveLand pipeline. Cleaved targets of miR159, miR169 and miR1122 corresponding to transcripts involved in DNA binding and protein kinase activity were identified in the degradome libraries. Accurate identification and validation of miRNA and their target is essential to develop novel regulatory gene based wheat breeding strategies.

Friday 25 November 2016

The Yield Challenge

S30 **ACHIEVING SUSTAINABLE WHEAT PRODUCTION**

Brian L. Beres

Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South Lethbridge, AB, Canada, T1J 4B1

As soon as a kernel of wheat is planted in the soil the gap forms between its genetic potential and realized yield - it will only widen over the growing season. The role of the agronomist is to occupy that space and develop methods and practices for wheat production that close the gap. How? Agronomy is

the science of integration and by nature a cross-disciplinary science that addresses yield stability and exploitable yield gaps through the holistic application of a set of principles that serve to enhance an entire crop production system. While there are obvious factors contributing to the yield gap in wheat such as water deficits, nitrogen loss, and heat stress/shock, others exist and more will emerge. The development of traits in the future will no doubt increase genetic potential; however, the impact will be less than desirable if factors contributing to the yield gap are not identified and addressed. The aim of this presentation will discuss how the transformative innovation around conservation agriculture laid the foundation on which the agronomist built a truly integrated and sustainable management system for global wheat production, and how this evolving science is critical to addressing the emerging issues and challenges that lay ahead for wheat production.

S31 **KEEPING WHEAT IN THE ROTATION – IF IT DOESN'T YIELD, IT DOESN'T STAY**

Paul Sullivan

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Growing any kind of wheat is not the most glamorous or seriously respected of any field crops in Ontario. Challenges are many if you talk to most cash cropper that grow wheat. The conversation starts out negative and then goes from there. I have the opportunity of working with many cash crop farmers that grow spring and winter wheat in the Upper Ottawa Valley. I believe the main reason most stop growing wheat related to crop yield. If it doesn't yield, wheat doesn't stay in the rotation. I will share production practices from one of my clients Schouten Corner View Farms Ltd, at Richmond, Ontario. In 2011, they won the GFO Spring Wheat Challenge weighing off Sable wheat at 98.4 bushel/acre. In 2012 they had achieved winter wheat yields on a field of over 135 bu/acre and averaged 110 bushel/acre on 350 acres. The common ingredients in their success with wheat are as follows 1. Seed as early as field conditions permit. 2. Manage previous crop residue. 3. Grow wheat on your most productive fields. 4. Aim for even emergence. 5. Use the most adapted and highest yielding genetics. 6. Use 11-52-0 as starter seed place fertilizer. 7. Control all weeds early in crop. 8. Use sulfur fertility for yield and quality. 9. Use a T1 or T2 timing fungicide application and a T3 application. 10. Pre-harvest apply glyphosate and direct combine the crop early.

S32 **IMPROVING AGRONOMIC INPUT EFFICIENCY AND MAXIMIZING YIELD BY MANAGING WHEAT ON A CULTIVAR BASIS**

Sheri Strydhorst[1], Doon Pauly[2], Robyne Bowness[3], Kabal Gill[4], Lori Oatway[5] and Rong-Cai Yang[6]

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Breeders develop wheat cultivars with different genetic traits but producers typically use the same agronomic management regardless of the cultivar's genetic traits. Small plot research trials were conducted to determine the yield and agronomic response of 12 wheat cultivars to either standard or advanced agronomic management. Standard agronomic management received no in-crop nitrogen (N), plant growth regulator (PGR), or fungicide. Advanced agronomic management involved in-crop foliar

applications of: 34 kg N/ha as Urea Ammonium Nitrate (UAN) + Agrotain N stabilizer at Growth Stage (GS) 29; Chlormequat chloride PGR at GS30-31; and two fungicides (pyraclostrobin + metconazole at GS39 and prothioconazole + tebuconazole at GS55). Nine site years of data demonstrate how different cultivars require different agronomic management to optimize input use. AC Foremost yields were significantly increased with advanced agronomic management by 11-36% in 7 of 9 site years while AAC Penhold yields were significantly increased by only 8-15% in only 4 of 9 site years. The yield response of AAC Penhold was found in site years when there was at least 258 mm of growing season precipitation; however, AC Foremost responded even in site years where growing season precipitation was less than 150 mm. Findings from this and associated studies suggest that the genetic disease resistance of AAC Penhold is superior to that of AAC Foremost and therefore different fungicide management strategies must be employed for different cultivars. Future research should be conducted to develop cultivar specific agronomic packages that will maximize the genetic potential of newly registered wheat cultivars and provide the highest returns to producers.

S33 **THE RESEARCH OF YIELD**

Ellen Sparry

C&M Seeds, 6180 5th Line, Palmerston, ON

What's new in yield research? A summary of work of wheat yield research currently underway around the globe shall be presented. New concepts, new technology, new techniques.

Building Public Trust in Food and Farming

S34 **SOCIAL MEDIA FOR SCIENTISTS: BEST MANAGEMET PRACTICES FOR USING ONLINE NETWORKS**

Lindsay Chichester

University of Nevada Cooperative Extension – Carson City/Storey Counties, 2621 Northgate Lane, Suite 15, Carson City, Nevada, 89706, USA

Sharing information and interacting with the public on social networking sites can be intimidating. In the past, people took to social media to interact with family, share pictures of their kids, or show off hobbies and travel adventures. However, we now see more people taking to social media to obtain news (~62% of U.S. adults) and information. Specifically, the PEW Research Center indicates social media has affected the way people get and share information about health, civic life, news, various communities, teenage life, parenting, and dating; also changing such things as politics and political deliberation and communication patterns. Scientists and agriculturalists make up a portion of the online community, sharing day-to-day activities/events, or celebrating publications and research successes. Because scientists and researchers participate on social networks, members of the public have more access than ever before to information from valued, trusted, and credible sources – the scientists doing the work and the people growing and raising the food first hand. More importantly, online networks can create interactive, genuine, and far-reaching communities, which can provide opportunities for collaboration and scientific inspiration, as well as keeping current and connected to issues or concerns of the general public. This presentation will go through best management practices for scientists or agriculturalists interested in participating in online communities, primarily social networking sites, sharing how to maintain a professional/personal balance, providing insight into social license, and responding to criticism with professionalism.

S35 **BUILDING PUBLIC TRUST IN FOOD AND FARMING**

Kim McConnell

AdFarm, 700-5940 Macleod Trail SW, Calgary, AB, Canada, T2H 2G4

Trust is becoming the defining issue for the success of the entire Canadian food system. Recent research shows that 50 percent of Canadians are unsure about whether our food system is going in the right direction. And with 93 percent of Canadians saying they know little or nothing about farming, determining fact from fiction about our food continues to be a growing issue. Lots of work has been done as part of the "Canadian Journey for Public Trust". Input has been received from 300 plus Canadian agri-food leaders who have developed a "trust framework" that will define roles for industry, governments, academics and individuals. This presentation will provide an overview of the process and next steps in the "journey", as well as ideas on funding public trust initiatives and having those confident conversations with Canadians.

Poster Abstracts

P01 DIVERSITY ANALYSIS OF CANADIAN DURUM WHEAT CULTIVARS USING EXOME CAPTURE

Kirby T. Nilsen[1], Amidou N'Diaye[1], Aron T. Cory[1], P.R. MacLachlan[1], John M. Clarke[1], Krystalee Wiebe[1], Andrew G. Sharpe[2] and Curtis J. Pozniak[1]

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Exome capture is an efficient sequencing approach that targets the protein coding regions of the genome. The aim of this study was to characterize a population of advanced durum wheat *(Triticum turgidum* L. var *durum*) breeding lines and cultivars using exome capture. Using an available 110 Mb liquid capture design, we generated ~ 75 million 2 x 100 bp high quality filtered reads for each cultivar and breeding line, and these were aligned to the wild emmer wheat genome cultivar Zavitan using NovoAlign V3.04.06. Variant calling was performed using Samtools V.1.2. We applied a set of stringent filters (per sample sequence depth >6, phred-scaled quality score > 20, missing data < 30%, minor allele frequency > 5%) to improve confidence in variant calls using in-house PERL scripts. Using this approach, a total of 191,804 high confidence genetic variants survived filtering which mapped to all 14 chromosomes at a rate of 1 variant per 55 kb across the genome. We characterized the variants using snpEff V.4.2, and found that the majority were localized to downstream, upstream and intronic regions of predicted transcripts. In total, 6% of variants were predicted to have high to moderate effect on gene function. The final variant list was analyzed using Bayescan v.2.0 and the adegenet R package to generate diversity summary statistics (Tajima's D and π), and to identify genomic signatures of selection using *Fst*. These identified 70 regions under strong selection pressure on 11 different chromosomes. This study demonstrates the efficacy of exome capture in identifying and classifying variants based on functional effect.

P02 GENOMIC ANALYSIS OF A CANADIAN WHEAT DIVERSITY PANEL REVEALS DISTINCT PATTERNS OF DIVERSITY ACROSS MARKET CLASSES AND KEY TRAIT-ENCODING LOCI

William Hargreaves[1], Amidou N'Daiye[2], Curtis J. Pozniak[2] and Lewis Lukens[1]

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Understanding the structure of genetic diversity among Canadian wheats will facilitate managing the germplasm and identifying the past targets of selection. We used the Wheat 90K SNP iselect assay- to genotype 388 hexaploid wheat cultivars grown in Canada, which yielded 24,841 polymorphic markers with marker allele frequencies >5% and missing rates < 10%. The cultivars were drawn from different market classes including Hard Red Spring (HRS), Hard Red Winter (HRW), and Soft White Spring (SWS). Our results suggest that distinct market classes resulted from selection of allelic variation at different loci throughout the genome, as opposed to selection at different alleles at the same loci. We also investigated if allele frequency differences between phenotypically distinct groups could identify loci that contribute to these differences. Grouping cultivars with grain colour and photoperiod response, both AMOVA and Fst analyses recover loci known to control these traits. However, these analyses also reveal many other loci,

indicating the effects of population history. Finally, we investigate a number of putative inversions within the wheat germplasm which cause the co-inheritance of linked alleles. We anticipate this study will constitute a valuable resource for breeding efforts and for the genetic dissection of important traits.

P03 **GENETIC DIVERSITY OF CAMEROONIAN BREAD WHEAT CULTIVARS (*TRITICUM AESTIVUM* L.) REVEALED BY SSR MARKERS**

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The assessment of genetic diversity is a key prerequisite for studying the adaptation of populations to new environmental conditions, and therefore for the selection of new varieties. Several authors have shown that the narrowness of the genetic diversity of crops could lead to increased vulnerability to disease and pests, as well as the ability of plants to respond to changing environmental constraints. The present investigation aimed to estimate the levels and genetic structure within bread wheat varieties grown in Cameroon. Thus, genetic diversity was assessed in seventeen hexaploid wheat cultivars, using 11 microsatellite markers. Genetic resources were collected at the Nord-Western, Adamawa and Nord regions. All pairs of specific marker loci used gave amplifications with allelic variations of size on all DNA from wheat accessions. A total of 77 alleles were detected among cultivars and the number of alleles per locus ranged from 2 to 13 with an average of 7, comparable to those observed in most previous studies. Gene diversity ranged from 0.46 (Xgdm 125) to 0.90 (Xgwm 177) with an average of 0.88, increasing with the number of alleles. Microsatellites markers used had an average value of PIC (Polymorphic Information Content) of 0.69, indicating that these markers were very informative in our study. Moreover, the cluster analysis has structured all of the 17 wheat accessions in 5 main groups at a genetic similarity of 80%. This high diversity revealed among wheat accessions grown in Cameroon could be useful in the breeding programs.

P04 **EVALUATION OF HEXAPLOID WHEAT (*TRITICUM AESTIVUM* L.) FOR ALUMINUM TOLERANCE**

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Acid soil is a worldwide constraint to wheat production. A lack of essential nutrients in the soil and the presence of the toxic aluminum cation in the plant root zone is the main cause of the acid soil toxicity. A total of 60 bread wheat lines from different countries (South Africa, Egypt, Kenya, Ethiopia, Cameroon, France, Italy) were phenotype under greenhouse sand experiments and the treatments consisted of non-acid soil (pH = 5.7; Al =0 mg/L) and acid soil (pH 4.3; Al= 50 mg/L). Citrate efflux from excised root apices

was measured on individual seedlings using as few as four apices and its concentration was estimated with coupled enzyme assays that detect the production or consumption of NADH. SSR markers Xwmc 331 and Xgdm 125 were used for the molecular selection. The root growth rate of all the genotypes was reduced with the addition of Al to the pots and the Al-sensitive and Al-tolerant wheat genotypes were clearly identified. Genotypes with intermediate Al-tolerance levels showed variable root lengths in response to Al stress. Correlations between root lengths and plant height, fresh biomass of shoot/root, dry biomass of shoot/root, released citrate or tolerance indices in the non-acid soil versus acid-soil experiments were highly significant ($P < 0.01$). So, 22 wheat genotypes were selected for acid soil tolerance under aluminum toxicity conditions. Those genotypes could be useful in the wheat breeding program.

P05 **PHOTOPERIOD SENSITIVITY IS THE MAJOR DETERMINANT OF PLANT PHENOLOGY IN THE FALL-PLANTED WHEAT IN SOUTH WESTERN ONTARIO**

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Flowering and maturity time of wheat (*Triticum aestivum* L.) are important characteristics that govern adaptation to diverse geographical regions and avoidance of abiotic and biotic stresses. The objective of this research was to examine the adaptation of fall-planted wheat in Ontario as influenced by the allelic forms of the major *Vrn* and *Ppd* genes. A diverse panel of 208 winter and spring wheat genotypes, representing a wide range of maturity was phenotyped for the number of growing degree-days (GDD) to reach important phenological stages in fall-planted field trials. The panel was genotyped using allele-specific markers of the major *Vrn* and *Ppd* loci, *Vrn-A1, Vrn-B1, Vrn-D1, Vrn-B3, Ppd-A1, Ppd-B1*, and *Ppd-D1*. The photoperiod-sensitive alleles *Ppd-D1b* and *Ppd-A1b* were present in 127 and 166 genotypes, respectively. Genotypes carrying the photoperiod-sensitive allele at the *Ppd-D1* locus, on average, required additional 43.6, 44.9, 46.2, and 56.5 GDD to reach booting, heading, anthesis, and maturity, respectively, and were 10.7 cm taller. Genotypes carrying the photoperiod-sensitive allele at the *Ppd-A1* locus required additional 33.8, 38.9, and 34.0 GDD to reach booting, heading, and anthesis, respectively. Results are expected to contribute to a better understanding of adaptation of winter wheat genotypes in Ontario, as influenced by *Vrn* and *Ppd* genes.

P06 **HAPLOTYPE ANALYSIS OF QUALITY TRAITS IN ELITE DURUM WHEAT BREEDING LINES**

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Quality traits are important targets for improved pasta manufacture and cooking quality of durum wheat (*Triticum turgidum* ssp. *durum*). The goal of this study was to investigate genomic regions associated with pigment colour traits and gluten strength using haplotype-based on a genome-wide association approach. A total of 169 durum breeding lines were genotyped using the 90K Infinium assay, and 12,234 high quality single nucleotide polymorphisms (SNPs) were generated and used to assess population structure

and the linkage disequilibrium pattern. Based on LD, we clustered SNPs into 406 haplotypes based on the genome-wide estimate of LD decay (5.3 cM) in our material. Genome-wide association analysis was performed using the mixed-linear model (MLM) with Q and K-matrices. For pigment colour traits (pasta a* and b*, semolina a* and b*, semolina pigment and pigment loss), a total of 12 loci were identified, spanning 6 chromosomes, 2A, 3B, 4B, 5B, 7A and 7B. The *Psy1-A1* and *Psy1-B1* loci were in strong LD with the haplotype blocks identified on the group 7 chromosomes. The haplotype block on chromosome 4B associated with pasta a*, pasta b* and pigment loss explained on average 38% of the variation, and was in strong LD with *LpxB1.1*. For gluten strength, a total of 8 loci were detected and all coincided with known QTL. We determined favorable allele combinations for each haplotype which will serve as a useful tool for marker-assisted selection of quality traits in Canadian durum wheat breeding programs.

P07 **DEVELOPMENTAL AND GENE EXPRESSION PROGRAMS IN WHEAT GRAIN**

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Wheat is globally one of the most important crops. Recent advances in genomics based approaches are contributing to development of new tools for applications in several crops. We have used genomics based approaches to advance the understanding of grain development in wheat. Towards this goal, we focused our studies on developmental and gene expression programs of grain from fertilization to maturity in hexaploid, tetraploid and diploid wheat species. These studies include dissection and isolation of tissues from key phases of grain development and detailed analyses of these using Nomarski and electron microscopy, followed by RNA-seq based approaches to profile transcriptomes associated with these tissues. Analyses of the results revealed gene expression programs specific to embryo, endosperm and pericarp compartments as well as dynamic programs that are regulated coordinately between these tissues and different genomes. Comparative expression analysis of A, B and D genomes suggest differential regulation of some of the alleles representing these three genomes. Key findings from these studies and their implications to grain development in wheat will be presented.

P08 **A LARGE-SCALE STUDY OF THE WHEAT TRANSCRIPTOME AND ITS REGULATION**

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Studies of the wheat transcriptome and its regulation have contributed to identifying the genetic bases for trait diversity. Natural variation in gene expression is also central to crop diversification, and positive selection has acted upon gene regulatory loci. Here, we describe a pipeline to identify wheat transcripts, discover the regulatory loci controlling transcript abundances, and test transcripts for evidence of positive selection. We have harvested RNA from 154 genotypes drawn from a doubled haploid population derived from a cross between an early wheat Red Fife and a recent cultivar (Stettler). We are sequencing 30 million 100nt paired end reads from each genotype. Our analysis pipeline first involves TopHat and BowTie for read alignment, transcript identification, and transcript abundance estimation. Given the depth of sequence data in this study, we expect to detect low level transcripts with very high precision. We will use GATK for SNP calling, MadMapper and MSTmap to construct a genetic map, and non-parametric interval mapping to map eQTL. eQTL data will highlight the genetic basis for gene transcript regulatory

control. We expect genetic variation at regulatory factors located at the same loci in different genomes to often act to regulate gene expression levels. We also expect genetically variable transcripts are those that are expressed at low levels and are environmentally responsive. We will also use a novel test for selection on gene regulation by determining if one parent's regulatory loci have consistent effects on gene expression. Finally, we will determine if eQTL overlap QTL for traits including chlorophyll content, leaf area, photosynthesis, respiration, biomass and spectral reflectance.

P09 **HIGH THROUGHPUT SEQUENCING DATA PROCESSING AND SYSTEMS BIOLOGY DATA ANALYSIS**

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Over the last decade, at NRC-ICT, Ottawa, we have established bioinformatics solutions in processing high-throughput sequencing data and subsequent systems biology data analysis leading to discovery of genetic markers. Under the Canadian Wheat Alliance (CWA) collaboration, we have successfully applied these reliable and efficient RNA-seq and DNA methylation processing pipelines to various research projects. These include 1) RNA-seq data pre-processing to determine read counts, 2) data normalization and detection of differentially expressed genes, transcripts or isoforms, 3) data reduction based on statistical significance and research objectives, 4) clustering analysis for identifying gene co-expression/co-regulation patterns, 5) correlation and network analysis for problem-specific molecular marker discovery, 6) identifying landscape and influence of DNA methylation, 7) performing *de novo* assembly and annotation, and other bioinformatics data exploration solutions, such as identification of novel SNPs and copy number variations, and performing small RNA sequencing data analysis and deep machine learning for specific requirements in a project. These pipelines have been tailor-made to support specific objectives of each project and examples of the successful application of these pipelines will be shown in the poster.

P10 **RECENT BREAKTHROUGHS IN ENABLING TECHNOLOGIES PLATFORMS FOR WHEAT**

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Wheat improvement remains focus of many research undertakings. In past, success has been achieved through wheat breeding efforts. Recently, new technology platforms have emerged which hold promise to accelerate the process of developing improved varieties. However, understanding and utilization of these technology platforms has remained challenging in wheat. There are limited examples of success so far. Here we present our experience with three enabling technology platforms – Doubled haploidy system, genome editing and modulation of epigenetics. Recent preliminary results and challenges in the field are discussed.

P11 **DOUBLED HAPLOIDY FOR CANADIAN WINTER WHEAT GERMPLASM**

Alison M.R. Ferrie, Hung-Mei Wang, Jean Enns, Jennifer Brost and Kim Nelson

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Doubled haploid (DH) production is the quickest method for developing homozygous breeding lines. The advantages of using DH plant production in a breeding program include shortening the breeding cycle, easier identification of recessive traits, more efficient mutant selection, and easier genetic manipulation at the haploid level. Currently, the majority of wheat breeding programs in Canada apply interspecific crossing using maize as the pollen source for creating DH lines; however this method is very labour intensive. While anther culture and isolated microspore culture methods have been published, they have detailed a genotype dependent response, low embryogenic efficiency, and high set–up costs. This has resulted in low acceptance of the technology in Canada for practical application. One of the goals of our project is to develop a genotype independent DH protocol for winter wheat that is more efficient than current DH methods. A number of factors influence embryogenesis including genotype, donor plant growth conditions, composition of the culture medium and environmental conditions during culture.

P12 **CHARACTERIZING THE EPIGENOME OF TETRAPLOID WHEAT USING A WHOLE GENOME BISULFITE SEQUENCING APPROACH**

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Epigenetics play an important role in regulating gene expression, chromatin stability, and maintaining genome structure. In particular, DNA methylation is integral in genome stability, regulating gene expression and maintaining allelic balance following polyploidization. Changes in methylation status acquired during an organism's lifespan can be transmitted to progeny, influencing quantitative trait variation in a heritable manner. This study represents the first comprehensive analysis of a polyploid wheat genome at the single base pair resolution. We have used Whole Genome Bisulfite Sequencing (WGBS) to characterize the methylome and RNAseq to assess the transcriptome of leaf and root tissues of wild emmer wheat (WEW; *T. turgidum* ssp. *dicoccoides* (Körn.) Thell.; genome AABB). The paired-end short sequence reads were aligned to the newly assembled emmer genome using either STAR or Bismark v0.16.1 for the RNAseq and WGBS data, respectively. Custom bioinformatics analyses were developed to efficiently interrogate and integrate these data. Comparison between the A and B sub- genomes show that the majority of observed cytosine methylation patterns were conserved among the A and B sub-genomes, but we were able to detect sub-genome specific methylation patterns. We assessed gene expression and DNA methylation levels between homeologous genes and preliminary results suggest differentially methylated regions (DMR) can be associated with variable gene expression. Finally, we identify a number of tissue-specific DMR. We demonstrate that complex polyploid genomes like durum wheat are now amenable to epigenetic analysis and can be characterised and interrogated, opening new avenues of research into the epigenetic control of gene expression and inheritance.

P13 **DEVELOPING A SINGLE CELL SYSTEM FOR EFFICIENT CAS9-GRNA DELIVERY AND EARLY DETECTION OF GENE EDITING EVENTS IN HEXAPLOID WHEAT**

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Single cells like suspension cells, protoplasts or haploid microspores all offer exciting possibilities for conducting cell-based experiments using different molecular, cellular or genomic tools. With single cell analysis, it is also easier to detect a low frequency of mutated cells than it is with a pooled population. Although many successful reports of Clustered Regularly Interspaced Short Palindromic Repeat/ CRISPR-associated endonuclease 9 (CRISPR/Cas9) mediated gene editing have now been published, effective delivery of genome editing reagents and early detection of mutation - two keys to high efficiency gene editing still remain challenging for most plant cells enclosed in cell walls. In our laboratories at the National Research Council of Canada we are evaluating different methods of single cell isolation, transfection/transduction and early detection and screening of effective gene editing events using different CRISPR/Cas9-gRNA constructs. We are also evaluating different methods of sorting and capturing transfected single cells for validation of efficient nuclease activity using either the Fluidigm C1 single cell platform or Fluorescence Assisted Cell Sorting (FACS) system. Preliminary results have confirmed low frequency capture and DNA extraction and amplification using Qiagen Repli-G whole genome amplification single cell kit. Therefore, single cell system could be a reliable method for validation of efficient Cas9-gRNA delivery and early detection of gene editing events in plants.

P14 **TARGETED GENE EDITING USING CRISPR/CAS9 IN A WHEAT MESOPHYLL PROTOPLAST SYSTEM**

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The clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9 system has become a promising tool for targeted gene editing in a variety of organisms including plants. In this system, a 20nt sequence on a single guide RNA (sgRNA) is the only gene-specific information required to modify a target gene. In this project, we are using the CRISPR/Cas9 system to modify three wheat genes identified in previous experiments, including an ABC transporter and the Nuclear Transcription Factor X box-binding-Like 1 (NFXL1), which are associated with FHB susceptibility, and a non-specific Lipid Transfer Protein (nsLTP) which correlates with FHB resistance. Two sgRNAs were designed for each gene and were shown in an *in vitro* CRISPR/Cas9 assay to guide the sequence-specific cleavage of the DNA template with high efficiency. An *in vivo* assay for CRISPR/Cas9 was established by optimization of a wheat mesophyll protoplast isolation and transformation system. Using a GFP construct as a positive control, estimated transformation efficiencies of about 60% are routinely obtained. High throughput sequencing of amplicons including the sequences targeted for gene editing by CRISPR/Cas9 has clearly showed that two of the targeted genes, nsLTP and NFXL1, have been successfully edited in the protoplast system.

P15 **CRISPR BASED AND TARGETED EDITING OF GOLDEN2-LIKE (GLK) TRANSCRIPTION FACTORS TO STUDY THEIR ROLES IN PHOTOSYNTHESIS AND DISEASE RESISTANCE IN WHEAT**

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Golden2-Like transcription factors (GLK1 and GLK2) have been shown to regulate chloroplast development, senescence and disease resistance in Arabidopsis. While GLK1 and GLK2 act in

redundant fashion to regulate chloroplast development in Arabidopsis, their roles in crop plants, such as wheat, are not known. In tomato and peppers, it has been shown that GLK2 but not GLK1 is involved in fruit development. The roles of GLKs in wheat development have not been defined because of the lack of knowledge about these genes and the lack of their knockout mutants for these studies. We have identified at least 3 copies of *TaGLK1* on chromosome 7 corresponding to three genomes of hexaploid wheat (AL, BL, DL) and 3 copies of *TaGLK2* on chromosome 3 (AS, B, DS). We showed that *TaGLK1* can functionally complement the Arabidopsis *glk1glk2* double mutant to restore chloroplast development, suggesting a similar role for *TaGLK1*. We have designed and constructed s*gRNA*s for *TaGLK1*, *TaGLK2* and *TaGLK1:TaGLK2* for CRISPR mediated editing of the *GLKs* to produce loss of function alleles in wheat. Amplicon sequencing analyses of genomic DNA from independent T_0 transformed lines with these constructs identified InDels in the targeted coding regions of *TaGLK1* and *TaGLK2* individually but not for both genes in the lines transformed with *sgRNAs* for *TaGLK1* and *TaGLK2*. Further analyses of more independent transgenic lines and progression of edited lines to subsequent generations to identify phenotypes are being carried out.

P16 **A HIGH-DENSITY SNP-BASED CONSENSUS MAP OF CANADIAN HEXAPLOID WHEAT**

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Consensus linkage maps are valuable tools for QTL and association mapping, comparative genomics, map-based cloning and molecular breeding since among other features, they allow direct comparison of QTL identified in various genetic backgrounds. We have assembled a high- density hexaploid wheat consensus map by integrating data sets from 11 independent biparental populations involving Canadian wheat cultivars and breeding lines. Each population was genotyped using the 90K Infinium iSelect assay, and component maps were built using a common mapping procedure (a two-step mapping strategy using MSTMap and MapDisto) to avoid any technical bias. In particular, we observed significant variation in segregation distortion across populations, and in some cases these were removed to avoid potential bias. The final consensus map spanned 3,080 cM with an average marker density of 0.1 cM/marker. Unlike the individual component maps, all markers localized to 21 linkage groups. Marker order was highly consistent between the component and consensus maps and there was strong collinearity between the marker order and their position on the pseudomolecule sequences of "Chinese Spring (AABBDD)" and "Zavitan (AABB)" wheat. We have found that this consensus map represents additional SNP information not yet localized to published consensus maps and will be a valuable tool for analyzing genome-wide variation of complex traits, particularly in populations with Canadian wheat parentage. In addition, these maps will be useful for anchoring and super-scaffolding of the genome sequences currently being generated for Canadian wheat cultivars.

P17 **CANADIAN WHEAT-NAM (CAN-NAM): A NEXT GENERATION GENETICS PLATFORM FOR**

CANADIAN WHEAT IMPROVEMENT

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The linkage mapping approach to dissect complex traits has high statistical power but low resolution, and can only analyze two alleles. Genome wide association mapping (GWAS), is a complementary approach that has high resolution, gained by take advantage of historical recombination events, and analyze many alleles, but with lower statistical power. Nested association mapping (NAM) is a powerful genetic platform that can dissect complex traits that combines the advantages of both linkage mapping and association mapping. NAM is designed as a structured multiple family approach by crossing a series of diverse founder lines to an adapted local elite line, and each resultant F1 is selfed for several generations to provide homozygous recombinant inbred lines (RILs). NAM is an ideal genetically designed population to identify robust genotype and phenotype associations since such associations can be translated to breeding programs via the utilization of genetic markers to practice marker assisted selection (MAS). Recently, a 5-year Canadian wheat oriented NAM project started, titled “Canadian Wheat-NAM (Can-NAM): Capturing genetic variation for Canadian wheat improvement”. The goal of this large scale project is to develop a NAM based next generation genetics platform for Canadian wheat improvement. To prove the usefulness of this new genetics NAM platform, the project has targeted the high priority trait fusarium head blight resistance of Canadian wheat. Within this poster, we described the project from a strategic level and also explore other opportunities for this NAM based next generation genetics platform for Canadian wheat improvement.

P18 **NEXT GENERATION PLATFORM FOR GERMPLASM ENHANCEMENT AND GENETIC DISSECTION OF COMPLEX TRAITS IN WHEAT**

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Wheat is an important staple crop and most widely grown cereal in the world. However, loss of genetic diversity in elite wheat breeding populations has limited future genetic gain on wheat improvement. Introducing the targeted trait from the synthetic hexaploid wheat (SHW) donor into adapted germplasm and generating novel recombinant genotypes to widen the existing primary gene pool of bread wheat has proven to be a practical strategy to incorporate allelic diversity into modern wheat. In this study, we describe the development of a large bread wheat nested association mapping (NAM) population that is designed to incorporate novel genetic diversity and take advantage of both linkage analysis and association mapping for dissection of complex quantitative traits. Fifty genetically diverse founder lines including 25 SHW and 25 elite lines were crossed to a common elite wheat line. This will allow the

identification of valuable alleles “left behind” in elite cultivars due to minor effect that is difficult to detect and novel favorable alleles from SHW sources as well. The resulting population will provide a useful resource for not only dissection of genetic architecture of complex traits with higher statistical power and higher resolution but also identification of pre-breeding germplasm for future wheat breeding program.

P19 **GENOMIC SELECTION ACCURACY FOR GRAIN YIELD AND GLUTEN STRENGTH TRAITS IN TWO DURUM WHEAT POPULATIONS**

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Yield and quality traits are important selection criterion in durum wheat (*Triticum turgidum* L. ssp. *durum*) variety development. Due to their complexity of inheritance, genomic selection (GS) could be a viable alternative to improve selection efficiency. Here we evaluated the utility of GS models for practical application in durum wheat breeding. Five GS models were applied for predicting grain yield (YLD), gluten index (GI), and alveograph measures: extensibility (L), tenacity (P) and strength (W) in a breeding panel (BP) and a double haploid (DH) population. Both populations were genotyped with the Infinium iSelect 90K SNP assay, and resulted in 9752 and 5153 polymorphic for BP and DH, respectively. We observed that an increase in the training population size resulted in an increased prediction accuracy. On the other hand, increasing the number of markers beyond 2000 did not show significant increase in accuracy for any of the traits. The mean accuracy for all traits was comparable between the two population types except for GI, which was better in the BP. We evaluated five prediction models and all resulted in comparable accuracies in both populations except BayesB (BB) which better predicted GI and W in the DH population. The joint prediction of traits was also compared with the single trait prediction. Prediction accuracies reported here are comparable with previous reports indicating that GS could be applied to hasten the selection cycle in durum wheat breeding programs for yield and grain quality traits. To our knowledge, this is the first study presenting accuracy of GS models for grain yield, and quality in durum wheat.

P20 **GENOMIC SELECTION FOR WHEAT BREEDING: EMPIRICAL EVIDENCE**

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Genomic selection (GS) is a novel approach which has been suggested as a complementary tool to phenotypic selection to improve genetic gain of quantitative traits. However, there is still limited empirical evidence on the practical application of GS for wheat breeding. The objectives of this study were i) to evaluate the potential of single and multiple-trait GS prediction models for wheat breeding ii) to examine improvements in prediction accuracy when modelling genotype x environment (GxE) interactions. This

study was based on >230 wheat lines that were phenotyped for a number of agronomic and end-use quality traits in ten environments. The lines were also genotyped using the wheat 90K iSelect assay, which generated polymorphic single nucleotide polymorphism (SNP) markers. Several single-trait (RR-BLUP, G-BLUP, BayesA, BayesB, BayesCπ, BRR, BL, and RKHS) and multiple-trait (MT-BayesA, MT-BayesA-matrix, and MT-BayesA-scalar) models were generated to predict yield and other traits. The effect of modelling GxE interactions on GS model prediction accuracy was assessed using a marker x environment (MxE) interaction model. The average prediction accuracies ranged from 0.5 to 0.8 for the various traits and models. Prediction accuracy for single trait prediction models was similar to that when multiple trait prediction models were used. For some traits, multi-trait prediction accuracy was lower to single trait prediction, but this was dependent on the inter-trait correlation. However, in nearly all cases, modeling GxE interactions improved prediction accuracy. Results obtained from this study are encouraging but further research is still required to fully implement GS for wheat breeding.

P21 **SYNERGISTIC EFFECTS OF GENE COMBINATIONS WITH *Lr67* AND *Lr34***

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The leaf rust resistance gene *Lr34* is likely the most important resistance gene in Canadian wheat. It conditions effective resistance to leaf rust, stripe rust and stem rust. It is thought to interact with other resistance genes in a synergistic manner in which wheat lines with a combination of *Lr34* and another gene are much more resistant than would be expected if the resistance in a given line was only as good as the most effective gene. Resistance gene *Lr67* was recently discovered and has not been deployed in Canadian agriculture. It is also a multi-pest resistance gene with resistance to leaf rust, stripe rust and stem rust, similar to *Lr34*. Our objective was to determine if *Lr67* interacted synergistically with other resistance genes as does *Lr34*. We developed doubled haploid populations of the crosses *Lr34*/*Lr13*, *Lr34*/*Lr16*, *Lr34*/*Lr32*, *Lr67*/*Lr13*, *Lr34*/*Lr16*, and *Lr34*/*Lr32*. The parents of the crosses were the Thatcher near isogenic lines carrying each of these genes, with the exception of *Lr32* which was in a Katepwa background. *Lr34* interacted synergistically with *Lr13*, *Lr16* and *Lr32*, in that the resistance of lines with both genes combined was more resistant than lines with either gene alone. *Lr67* interacted synergistically with *Lr16* and *Lr32* but not with *Lr13*. These results indicate that while *Lr67* is similar to *Lr34* there may be some differences in the way the two genes interact. Overall, *Lr34* also conditioned a much better level of resistance than *Lr67* so it is the more effective gene to use in breeding programs. However, since *Lr34* is already present in most Canadian wheat lines, the addition of *Lr67* to these lines would be expected to have positive effects beyond its own resistance, because of the synergistic interaction with other resistance genes.

P22 **CHARACTERIZATION AND MAPPING OF GENES FOR LEAF RUST RESISTANCE FROM UNCHARACTERIZED SOURCES OF DURUM WHEAT**

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The emergence of highly virulent races of *Puccinia triticina* Eriks in Mexico and the USA Great Plains makes leaf rust a rising threat to durum wheat production in Saskatchewan. This study aimed to map genes for leaf rust resistance from uncharacterized sources of durum wheat and to develop molecular markers useful for marker assisted breeding and gene pyramiding. Four segregating populations involving the resistance sources Geromtel_3 (ICARDA), Tunsyr_2 (ICARDA), Amria (INRAM-Morocco)

and Byblos (France), crossed to the susceptible line Atil*2/Local Red, were evaluated for their reaction to the Mexican race BBG/BP. Genetic analysis indicated that resistance in these genotypes were based on single seedling resistance genes. Allelism tests support that Amria and Byblos carry allelic or closely linked genes. The resistance in Geromtel_3 and Tunsyr_2 also appear to be allelic. Selective genotyping using the Infinium iSelect 90K SNP array identified two locations for the resistance: 6BS for Geromtel_3 and Tunsyr_2 and 7BL for Amria and Byblos. Polymorphic SNPs were converted to KASP assays and used to genotype the complete RILs populations. KASP markers *usw215* and *usw218* mapped within 1 cM from the resistance in Geromtel_3 and Tunsyr_2 while *usw255*/*usw260* were closely linked to the resistance in Amria and Byblos. DNA sequences associated with these SNP markers were anchored to the "Zavitan" reference sequence of tetraploid wheat, which identified several putative genes coding for NBS-LRR, RGA2, RPM1 and RPP13-like proteins. The molecular markers reported here will be useful for pyramiding these resistance genes into adapted, elite durum wheat cultivars.

P23 **GENETIC MAPPING OF LEAF AND STEM RUST RESISTANCE IN SPRING WHEAT LINE KU168-2**

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Finding and using new resistance genes is helpful in wheat breeding and disease control. Leaf rust, caused by *Puccinia triticina Eriks*., is a worldwide disease of wheat. There are currently over 70 recognized leaf rust resistance (*Lr*) genes/alleles, many of which have been utilized in wheat breeding. However, most *Lr* genes are race-specific, conditioning resistance to only some races *P. triticina*. Stem rust, caused by *Puccinia graminis* Pers.:Pers. f.sp. *tritici* Eriks. & Henn., is a disease of wheat that can cause severe grain yield losses. The use of resistant cultivars has controlled stem rust for many years. However, the discovery of Ug99, a broadly virulent stem rust race discovered in Uganda in 1999, has renewed efforts to find new stem rust resistance genes. In this study, we will map the resistance genes in the wheat line KU168-2, which is resistant to both leaf and stem rust. A DH population of the cross KU168-2/RL6071 was generated and evaluated for leaf rust resistance in a field test and stem and leaf rust resistance in seedling tests. The adult field test was inoculated with an epidemic mixture of virulence phenotypes found in Canada during the previous year and segregation for resistance was observed. The parents and the progeny will be evaluated for seedling resistance to different leaf and stem races, and genotyped with the 90K wheat iSelect SNP genotyping platform.

P24 **INHERITANCE OF RESISTANCE TO UG99 STEM RUST IN NAPOLEON DURUM WHEAT**

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Stem rust is the most feared disease of wheat worldwide due to the explosive nature of epidemics that can completely destroy a healthy-looking crop in a few weeks. Stem rust is typically managed using host resistance, but a strain known as Ug99 arose recently with virulence on most stem rust resistance (Sr) genes. A previous examination of Canadian durum wheat germplasm found that cultivar 'Napoleon' is highly resistant to the Ug99 race group. A Rusty/Napoleon doubled haploid (DH) population was developed to study the inheritance and map the gene(s) conditioning resistance to Ug99. A population of 143 DH lines was inoculated at the seedling stage (8d-old) using race TTKSK and evaluated for infection type (IT) at 14d post-inoculation using the 0-4 Stakman scale. An IT≥ 3 indicated susceptibility, and IT<3 indicated a resistant reaction. The Napoleon parent and resistant lines displayed seedling ITs from 0; to

12, while the LMPG parent and susceptible lines displayed ITs from 3^- to 4. Chi-square analyses indicated a single gene conditioned seedling resistance to race TTKSK, with 78 resistant:65 susceptible progeny (X^2=1.18, P=0.28). Parents and DH lines were genotyped using a custom 90K iSelect SNP array. Preliminary linkage mapping suggest that the Sr gene conferring seedling resistance to Ug99 is located on the long arm of chromosome 6A and could be *Sr13*. Since the field response of Napoleon is much lower (1R-5R) compared to the *Sr13* differential line (30I-50S), there likely is another gene present, conferring adult plant resistance to Ug99 in the field.

P25 **A MAJOR QTL FOR STRIPE RUST AND LEAF RUST RESISTANCE MAPPED TO CHROMOSOME 2A IN ADAPTED CANADIAN WHEAT CULTIVARS AC CADILLAC AND STETTLER**

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Stripe rust (*Puccinia striiformis*) and leaf rust (*P. triticina*) are devastating diseases of common wheat (*Triticum aestivum* L.). The objective was to identify quantitative trait loci (QTL) associated with resistance to leaf rust and stripe rust contributed by adapted Canadian cultivars. Two doubled haploid populations, Vesper/Stettler (94 lines) and Carberry/AC Cadillac (775 lines), were evaluated for stripe rust in six and leaf rust in four environments in Canada, Mexico, Kenya and New Zealand. The populations were genotyped using the 90K iSelect SNP assay, high density maps constructed, and QTL analysis performed using MapQTL. A stable QTL, *QYr.spa-2A,* associated with stripe rust resistance, which mapped to chromosome 2A in both DH populations, derived from Stettler and AC Cadillac. *QYr.spa-2A* in Stettler was co-localized with the powdery mildew resistance (*QPm.spa-2A*) and expression of leaf tip necrosis (LTN) (*QLtn.spa-2A*). The *QYr.spa-2A* locus in AC Cadillac is allelic or closely linked with the leaf rust QTL *QLr.spa-2A* and LTN QTL *QLtn.spa-2A*. The *QYr.spa-2A* locus explained from 14.7 to 37% of the phenotypic variance for disease severity in the Vesper/Stettler population and 5.1 to 25.9% of the variation in the Carberry/AC Cadillac population. The SNP marker *BobWhite_c6356_87* was the most stable marker associated with *QYr.spa-2A* in Stettler, whereas *BS00041816_51* was the most stable marker associated with *QYr.spa-2A* in AC Cadillac. Because the 2A locus is effective against a wide range of YR races across continental regions and apparently having pleiotropic or linked effects against other fungal diseases, it should be useful in resistance breeding of wheat.

P26 **IDENTIFICATION AND CHARACTIZATION OF NEW STRIPE RUST RESISTANCE SOURCES IN SPRING WHEAT**

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Wheat stripe rust or yellow rust (YR), caused by *Puccinia striiformis* Westend. f.sp. *tritici*, is a devastating foliar disease of wheat. With the occurrence of new virulent races, deployed resistance genes are rapidly rendered ineffective. Continuous identification, characterization and deployment of new resistance sources are essential to minimize economic losses due to YR. To identify novel sources of YR resistance, fourteen recombinant inbred line (RILs; 9 $F_{4:5}$ and 5 $F_{6:7}$) and five doubled haploid (DH) populations were developed using different sources of resistance including Sadash and AAC Innova (both registered cultivars) and several uncharacterized germplasm lines of spring wheat. These populations were screened in stripe rust disease nurseries under natural infection from 2013 to 2016. Phenotypic data showed the presence of either a single or two major genes (in addition to minor additive genes in some populations) in the RILs, which are being advanced to develop homozygous populations. Two DH populations segregated for two major genes while the other three segregated for one major and a set of two minor additive genes. DH populations Sadash/AAC Proclaim and Sadash/P2711 were genotyped using the 90K Infinium iSelect SNP Assay and 15K SNP Assay, respectively. High density genetic linkage maps were constructed followed by QTL analysis, which identified one major QTL for each DH population and other minor QTLs. Both major QTLs were detected over environments. These new sources of stripe rust resistance will be an asset to wheat breeding programs.

P27 **GENETIC MAPPING OF STRIPE RUST RESISTANCE IN SPRING WHEAT**

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Stripe rust caused by *Puccinia striiformis* West. f. sp. *tritici*) is a very devastating foliar disease of wheat and has caused substantial yield and quality losses in wheat across much of western Canada in at least four of the past 12 years. Growing resistant cultivars is the most economical and environmentally safe approach to reduce the use of fungicides and to minimize crop losses due to this disease. Continuous identification and characterization of new resistance genes is essential as the deployed resistance genes can be rapidly rendered ineffective due to the occurrence of new virulence. The introgression of stripe rust resistance into new wheat cultivars through marker assisted breeding (MAB) is a priority in many breeding programs. In order to identify novel sources of resistance to stripe rust and facilitate their utilization through MAB, we developed two doubled haploid (DH) populations in spring wheat using Isolated Microspore Culture (IMC) method. These populations were derived from crosses FL62R1/Muchmore and FL62R1/Stettler. Muchmore and Stettler are both registered CWRS cultivars and the source of resistance. The populations were screened in a stripe rust disease nursery under natural infection during 2015 and 2016. Both populations were genotyped using the 90K SNP Infinium iSelect assay to map genes on wheat chromosomes. QTL analysis was performed and significant QTL identified from both years of field testing. The results of genetic analysis of these populations for stripe rust resistance will be presented.

P28 **GENETIC ANALYSIS OF RESISTANCE TO STRIPE RUST IN DURUM WHEAT (*TRITICUM TURGIDUM* L. VAR. *DURUM*)**

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Stripe rust, caused by the fungal pathogen *Puccinia striiformis* f. sp. *tritici* (*Pst*), is an important disease of durum wheat (*Triticum turgidum* L. var. durum) worldwide. Use of resistant cultivars is generally accepted as the most effective approach for managing stripe rust. In an association mapping (AM) study, field trials and growth chamber experiments were performed on a core collection of 92 diverse cultivars and breeding lines collected from major durum breeding programs globally. The 92 lines were genotyped using 13,539 polymorphic single nucleotide polymorphism (SNP) markers. A major QTL was identified on chromosome 7BL. In a complementary linkage mapping study, a doubled haploid mapping population consisting of 155 durum lines from the cross Kofa (susceptible) x W9262-260D3 (moderately resistant) were evaluated for stripe rust resistance in both field and growth chamber. Mendelian analysis revealed the presence of at least two resistance genes. Subsequent QTL analysis was performed using a genetic map consisting of 4,251 polymorphic markers spanning all 14 chromosomes. Two significant QTLs were identified on chromosome 5BL (*QYr.usw-5B*) and 7BL (*QYr.usw-7B*) that explained 10.7 and 30.4% of the phenotypic variance, respectively. *QYr.usw-5B* and *QYr.usw-7B* are complementary genes and act together to condition resistance. Both QTLs attributed to the moderately resistant parent W9262-260D3. The QTL located on chromosome 7BL, identified by linkage analysis, is located in the same genetic interval as that identified by AM. These insights into the genetic basis of stripe rust resistance can be applied to enhance resistance to stripe rust in durum wheat.

P29 **INCREASED EXPRESSION OF STOMATAL ION CHANNELS INCREASES STRIPE RUST RESISTANCE AT THE APPRESORIAL DEVELOPMENT STAGE**

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One interesting difference between the stem, stripe and leaf rusts of wheat is that stem and stripe rusts only penetrate the plant through open stomata, while leaf rust requires closed stomata. We are investigating the mechanisms mediating these differential interactions at the pre-penetration stage. Here our inadvertent production of transgenic *Brachypodium dystachion* plants with increased expression of two stomatal ion channels, including Quick Activating Channel 1 (QUAC1) and Slow Activating Channel 1 (SLAC1) is described. Characterization of these plants by stomatal closure assays showed a small increase in the number of closed stomata with the over expression of QUAC1 and SLAC1, as expected based on the known role of these channels in mediating stomatal closure. Subsequent evaluation of the

formation of stripe rust appresoria over stomata showed a significant decrease in appresorial formation on the transgenic plants, compared to Wild Type plants. At the same time a qualitative phenotypic evaluation of stripe rust infection on leaves also showed a decrease in stripe rust infection of the transgenic Brachypodium plants compared to Wild Type. Together these data show that stomatal closure can inhibit stripe rust appresorial formation and infection, and highlights that modulation of stomatal function may represent a useful road forward in the development of rust resistant wheat or novel crop applications more broadly.

P30 **MOLECULAR MAPPING OF QTL FOR LEAF SPOT DISEASE COMPLEX RESISTANCE IN SPRING WHEAT**

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The leaf spot disease complex (LSDC) (tan spot, septoria leaf blotch complex and spot blotch) is one of the most prevalent and widespread wheat diseases in Western Canada, reducing test weight and limiting production. Genetic resistance to LSDC is essential to reduce losses of grain yield. This study was conducted to identify DNA markers for LSDC resistance in adapted germplasm of spring wheat. A doubled haploid population of 180 lines was developed from the cross of LSDC moderately resistant to moderately susceptible commercial cultivars Vesper and Carberry. The population and parental controls were field evaluated near Morden and Brandon MB for LSDC response. Continuous distributions of disease reaction in both locations indicated quantitative inheritance. Based on a linkage map that consisted of 6212 SNP markers (Infinium iSelect 90k SNP wheat array), Multiple QTL mapping (MQM) analysis revealed a significant resistance QTL on chromosome 7D detected in both locations, and a significant resistance QTL on chromosome 2D detected only in the Brandon environment. The level of phenotypic variation explained by the 7D resistance QTL was 10.8% in Brandon and 26.4% in Morden. The level of phenotypic variation explained by the 2D resistance QTL was 9.8% in Brandon. Vesper carried the favourable allele associated with LSDC resistance on chromosome 2D, while the chromosomes 7D favourable allele was derived from Carberry. The SNP markers associated with resistance QTL could be utilized to facilitate combining the QTL and to accelerate the development of LSDC resistant adapted wheat cultivars.

P31 **GENE EXPRESSION PROFILING IN HOLLOW VS SOLID-STEMMED DURUM WHEAT**

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Solid-stemmed wheat cultivars are resistant to damage caused by the wheat stem sawfly *Cephus cinctus* L. The solid stem trait is controlled by a major locus on chromosome 3BL in combination with several other minor QTLs distributed throughout the genome. Little is known about the underlying biological mechanisms involved in conferring stem-solidness. The aim of this research was to develop a gene expression profile of the stem of hollow vs. solid-stemmed durum wheat cultivars, and to identify differentially expressed genes (DEGs) between cultivars expressing the two contrasting phenotypes. We isolated RNA from the pith of solid cultivars CDC Fortitude, Golden Ball, and Langdon-Golden Ball 3B, and the hollow control Langdon. Tissue enriched RNAseq libraries were prepared and sequenced on an Illumina HiSeq 2500 (2 X 100 bp) platform. A total of 1330, and 1867, DEGs were identified in pairwise comparisons between Langdon x Golden Ball, and Langdon x Fortitude, respectively; 560 DEGs were co-expressed between the two comparisons. The largest proportion of genes upregulated in Langdon was involved in the regulation of transcription, whereas the genes upregulated in solid cultivars were involved in cellulose biosynthesis, response to ethylene and salicylic acid, and cell wall organization. We found a strong correlation (r = 0.88) between the gene expression levels of co-expressed DEGs, which suggests that the solid-stemmed cultivars Golden Ball and Fortitude may share a common mechanism conferring this phenotype. This research provides an intriguing new insight into the genes and biological processes potentially involved in conferring stem-solidness.

P32 **HIGH DENSITY MAPPING OF THE MAJOR STEM-SOLIDNESS LOCUS *SST1* IN DURUM AND COMMON WHEAT**

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Breeding for solid-stemmed durum *(Triticum turgidum* L. var *durum*) and common wheat (*Triticum aestivum* L.) cultivars is one strategy to minimize yield losses caused by the wheat stem sawfly (*Cephus cinctus*) Norton. Major stem-solidness QTL (*SSt1*) have been localized to the long arm of chromosome 3B in both wheat species, but it remains unclear whether the two QTL share a common genetic interval. In order to further the genetic characterization of the *SSt1* locus, we have improved the resolution of the 3B QTL in durum (Kofa/W9262-2690D3) and common wheat (Lillian/Vesper) mapping populations using the 90K SNP array. Coincident QTL (LOD = 77 - 127, R^2 = 70 - 92 %) were localized near the telomere of chromosome 3BL in both mapping populations. According to the current chromosome 3B emmer genome assembly, the markers mapping within the QTL intervals anchored to an approximate 10 Mb interval in Lillian x Vesper, and 12 Mb interval in Kofa x W9262-260D3. In addition, minor QTL were identified on chromosomes 2A, 2D, 4A, and 5A that were found to synergistically enhance expression of *SSt1* to increase stem-solidness. These results also suggest that developing new wheat cultivars with improved stem-solidness is possible by combining *SSt1* with favorable alleles at minor loci within both wheat species.

P33 **EVALUATION OF SELECTED SPRING WHEAT LINES FOR FUSARIUM HEAD BLIGHT (FHB) AND OTHER AGRONOMIC CHARACTERISTICS**

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Fusarium head blight (FHB) significantly influences wheat yield and quality, and might also have a negative impact on the grain chemical properties like phenolic and antioxidant content. Non- conventional colored wheat varieties (*e.g.,* purple wheat) present a huge market opportunity as functional food ingredients, as their high phenolic and antioxidant content can positively contribute to human health. However, little information exists on purple colored spring wheat with resistance to FHB. The aim of this study was to identify high yielding varieties of colored spring wheats (white, red and purple) with good resistance to FHB, grain quality and other agronomic characteristics. A set of 36 lines (25 selections and 11 registered varieties) of hard spring wheat was harvested in 2015 and 2016 in two locations (Elora and Ottawa) with an additional trial at FHB nursery at Ontario Research and Development Center (ORDC). Yield ranking remained relatively consistent between the two sites. In general, test weights were lower at Elora (-8 kg/hL) than those observed in Ottawa. The average days to heading were similar between the two sites. FL62R1, a line from Ste-Foy, QC was the most resistant to FHB in both sites. Flowering date was negatively correlated with FHB incidence ($r=-0.433$, $p<0.01$), and FHB index ($r=-0.387$, $p<0.01$), while incidence and FHB index values were positively correlated ($r=0.319$, $p<0.01$). Flour yield was generally lower (~5 – 10% lower) for all selected purple lines with a higher ash content (+12%), indicating that the bran may be more friable during milling. In addition, the protein content was on average ~0.60% lower for all flour samples of purple lines, indicating a higher bran contamination of the wheat flour. Based on their color (red, white, purple), yield, disease ratings and protein content, and antioxidant activities, a set of 10 lines with appropriate commercial controls (red, white, or purple) was selected for further grain quality testing.

P34 **GRAIN QUALITY EVALUATION OF SELECTED SPRING WHEAT LINES CARRYING RESISTANT GENE TO FUSARIUM HEAD BLIGHT FROM OTTAWA RESEARCH AND DEVELOPMENT CENTRE**

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The fight against Fusarium Head Blight (FHB) *Fusarium graminearum*, is a major focus in spring wheat breeding programs (Gilbert & Tekauz 2000; McCaig & DePauw, 1995). The fungus is prevalent in areas of high humidity during high precipitation periods. It attacks wheat spikes and in some cases the stems at the heading stage. Infected plants are characterized by dark purple, brown, or black lesions of the glume and florets, deformed awns with bleaching of spikes and poorly filled grains. During the recent years a selection (FL62R1) from the Ste-Foy, Quebec breeding program has been used as a source of resistance to FHB which has a moderated grain quality. The objective of this experiment was to compare the quality and characteristics of a series of lines resistant to FHB in order to find suitable line(s) for future crossing. FL62R1 rank the best for FHB index followed by MAJOR, ECSW60, 12NQW-1017, 12NQW-1018, 12NQW-436, 13NQW-1554, ECSW38 - (2.3, 6.0, 13.3, 13.3, 13.3, 15.0, 15.0, 15.0). Among the resistant

lines, 12NQW-436 and ECSW60 had a comparable grain and flour quality to checks (Major, Roblin, AC Foremost).

P35 **IMPROVEMENT OF FUSARIUM HEAD BLIGHT RESISTANCE IN WINTER WHEAT**

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Fusarium head blight (FHB) is a destructive disease of cereal crops such as wheat and barley. FHB is particularly prevalent in areas where warm temperatures and high relative humidity at flowering exist (e.g. eastern Canada). AC Morley, an eastern Canadian hard red winter wheat variety, is known for its high grain yield combined with high protein content, good winter hardiness and moderate resistance to FHB. Emerson, a western Canadian hard red winter wheat variety, has high grain yield, a resistant rating to FHB and superior milling quality. Although these two cultivars have been widely used in breeding for improved FHB resistance, the genetic nature of their FHB resistance is not well understood. In order to characterize FHB resistance in these two varieties, this study has the following objectives: i) to develop a doubled haploid (DH) population from the cross AC Morley x Emerson, ii) to genotype the DH population using single nucleotide polymorphism (SNP) markers, iii) to phenotype the DH population for FHB resistance including deoxynivalenol (DON) levels and iv) to develop a high-density map to identify quantitative trait loci (QTL) for FHB resistance. For this study, phenotyping of the DH population will be conducted at three different locations: AAFC-Ottawa and University of Guelph in Ontario, Canada and Yangzhou University in China. Genotyping will be conducted using the 90K Illumina Infinium assay at AAFC-Morden, Manitoba.

P36 **STRATEGY IN HOST-PATHOGEN DUAL GENOME RNA-SEQ DATA PROCESSING**

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The plant pathogen *Fusarium graminearum* (Gibberella zeae) is the predominant causal agent of Fusarium head blight (FHB) in Canada and in most other parts of the world. It is not only a major constraint to wheat yield, but also results in the production of mycotoxins that affect human health and livestock feed. In the Enhanced Fusarium and Rust Tolerance (EFRT) pillar of the Canadian Wheat Alliance, we analyzed two RNA-seq datasets of Fusarium-challenged wheat lines to identify differentially expressed genes (DEGs) in the resistant and susceptible wheat lines in order to discover the molecular mechanism of FHB resistance. In contrast to the single-genome RNA-seq data processing procedure, these data contain a mixture of reads from both pathogen and host - two reference genomes have to be involved in the alignment process, either sequentially or simultaneously. In such circumstance, the sequential order of alignment to the host and the pathogen genomes, or simultaneous alignment to both genomes will result in difference in read counts of some genes, especially at the advanced infection stages. Therefore, it is crucial to have an appropriate alignment strategy. We did a comparison of the

different schemes and found that an alignment to a “pan” genome consisting of both the host and the pathogen genomes improved the mapping quality. We believe this strategy is universally applicable to other pathogen-host dual-genomes systems.

P37 **DEVELOPMENT OF BLUE WHEAT DERIVED FROM WILD SPECIES *THINOPYRUM INTERMEDIUM***

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Blue wheat has blue pigments located in the aleurone layer of wheat grains. Previous research has shown that blue wheat contains high levels of anthocyanins. Anthocyanins have been recognized as health-enhancing substances due to their antioxidant activity, anti-inflammatory, anticancer, and hypoglycemic effects. The objective of this study was to develop novel germplasm using wide crosses between *T. aestivum* L. and *Th. intermedium*. The cross Crocus / 08-47-50 was made at the Ottawa Research and Development Centre. Crocus is a hexaploid wheat with genome AABBDD, while 08-47-50 is a partial amphiploid with genome AABBEE, generated by crossing durum wheat (AABB) with *Th. intermedium*. The F_1 hybrid was advanced to F_4 generation using a single-seed descent (SSD) method, and 155 lines were obtained. At the F_4 generation, a wheat plant with a mixture of blue and red colour kernels was found. Sixty blue color seeds were selected from this wheat plant and advanced to the F_7 generation. Twenty-one F_7 lines with blue colour kernels were selected based on fertility and evaluated for leaf rust, stem rust, and stripe rust resistance. The results indicated that five out of 21 lines were resistant to stem rust race TTKSK (Ug99) and five lines were resistant to stripe rust race YR6. None of them were resistant to leaf rust. Cytological study indicated that the blue color lines all had 42 chromosomes. The long-term goal is to release blue coloured wheat germplasm with multiple disease resistance for use in wheat breeding programs.

P38 **GRAIN QUALITY OF SELECTED ADVANCED SPRING WHEAT LINES FROM OTTAWA RESEARCH AND DEVELOPMENT CENTRE**

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Twenty-three hard red spring wheat (*Triticum aestivum* L.) advanced lines from the Ottawa Research and Development Centre (ORDC) Spring Wheat Breeding Program were selected from several populations tested in 2014 and 2015 at ORDC based on resistance to Fusarium head blight (FHB), grain yield, and other agronomic characteristics in comparison to several named cultivars. These lines were assessed for their end-use qualities, alongside four established check cultivars. The objective of this experiment was to identify those lines displaying similar or superior quality performance to Scotia, Carberry, Norwell and Sable, with the goal of pursuing recommendation for entry into further regional trials. Using material harvested during the 2015 growing season, all twenty-three advanced lines and four check cultivars were assessed for grain protein content, and dough quality strength using the 35-

gram mixograph procedure. Experimental lines 13BW0426, BH33-47-4, and ECSW05 displayed similar or superior performance in dough strength characteristics in comparison to the check cultivars. Based on the obtained results, lines 13BW0426, BH33-47-4, and ECSW05 will be tested further in several regions using replicated trials.

P39 **REGULATION OF THE EXPRESSION OF STARCH-DEGRADATION GENES DURING SPROUTING IN WHEAT**

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Preharvest sprouting promotes the activity of hydrolytic enzymes that degrade starch and ultimately lead to substantial reduction in grain yield and quality. The activity of starch degrading enzymes is regulated by several intrinsic and extrinsic factors. Plant hormones such as ethylene are among the classical plant hormones that regulate starch degradation and germination. This study examined the effect of reducing ethylene level, through seed treatment with ethylene biosynthesis inhibitor, amino-ethoxyvinylglycine (AVG), on starch degradation in wheat seeds by examining the expression patterns of genes encoding hydrolytic enzymes such α-amylase and α-glucosidase, and growth of radicles and other post-germinative seedling parts. It appears from our data that AVG treatment resulted in decreased expression of genes encoding α-amylase and α-glucosidase at different time points during the pre-germinative and post-germinative phases, suggesting repression of starch degradation in AGV treated seeds. Consistent with this result, the repressions in the expressions of α-amylase and α-glucosidase genes was associated with inhibition in the growth of radicles, coleoptiles and seminal roots during the post-germinative growth phase.

P40 **CANDIDATE GENES FOR PRE-HARVEST SPROUTING TOLERANCE ON WHEAT CHROMOSOME 4A**

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A major QTL was identified on chromosome 4A for dormancy and pre-harvest sprouting (PHS) tolerance in the cross RL4452 x AC Domain. Genetic markers suitable for breeding purposes spanning the QTL region have been produced. Lines in the population that are recombinant between the markers were assessed for dormancy. Lines carrying the AC Domain allele at both markers were the most dormant. Lines carrying the AC Domain allele at one marker and the RL4452 allele at the other were intermediate and lines carrying the RL4452 allele at both markers were the least dormant. The region contains several candidate genes including a plasma membrane protein identified in Australian wheat (Barello et al. 2015) and a gene encoding the transcript with the highest differential expression between dormant and non-dormant lines of the population in a microarray assay. It was determined that AC Domain carries a large deletion in this gene. The evidence supports the theory that more than one gene in the 4A QTL contributes to the enhanced dormancy of AC Domain. The line RL4137 appears to be the source of the dormant haplotype at the first marker allele in Canadian germplasm while the second dormancy related allele has been present in Canadian wheat since Red Fife. Reference: Barello, JM et al. Genome Biology 16:93.

P41 **REGULATION OF SEED DORMANCY BY ABSCISIC ACID METABOLIC GENES OF WHEAT**

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Abscisic acid (ABA) regulates the induction and maintenance of seed dormancy over a wide range of plant species. The present study identified the three homeologues of genes encoding 9-cis-epoxycarotenoid dioxygenases (NCED) and ABA 8'-hydroxylase (ABA′8OH), which are the key regulators of ABA biosynthesis and catabolism, respectively, from wheat, cv. AC Domain. Phylogenetic analysis of the three homeologues of *NCED* revealed that they belong with other previously reported NCED and ABA′OH genes showed that they belong to the monocot NCED2 subgroup, resulting a designation of *TaNCED2* while the homeologues of *TaABA'8OH* belong to the *ABA'8OH1* group. Analysis of the expression patterns of *TaNCED2* and *TaCYP707A1* in different wheat tissues revealed that these genes are mainly expressed in seeds. Our result shows differential expression of *TaNCED2* and *TaCYP707A1* between dormant and non-dormant seeds, implying their role in the control of seed dormancy and germination. Furthermore, ectopic expression of the A genome copy of *TaNCED2* and B genome copy of *TaCYP707A1* of wheat cv. AC Domain in seeds of model diploid species led to increased and decreased level of dormancy, respectively.

P42 **INTEGRATED PROTEOGENOMICS APPROACH TO REVEAL SOURCES OF PRE- HARVEST SPROUTING RESISTANCE IN CANADIAN WHEAT**

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The integration of multiple measurements in proteogenomics provides a powerful approach to capture functional modules that discriminate between the sources for pre-harvest sprouting resistance or susceptibility. We analyzed dormancy-imposing processes in embryo and aleurone tissue-specific proteomes and redox metabolomes using spring wheat (*Triticum aestivum* L.) doubled haploid hybrid lines with marginal dormancy phenotypes, comparative iTRAQ-based protein quantitation, fluorescent labeling and 2DE-based thiol redox proteomics, and redox metabolite measurements. iTRAQ-based approach resulted in over 6800 high confidence protein identifications, of which 62 and 115 unique proteins showed significant differential expression in dormant phenotypes, and 368 and 1041 unique proteins were dormancy genotype-specific in embryo and aleurone, respectively. In dormant embryos, significant alterations were found for protein translation, folding, transport and degradation, DNA-repair, and mRNA surveillance, oxidative and nitrosative stress response. Potentially critical for imposing dormancy and after-ripening regulation, changes were found in cell cycle control, epigenetic regulation of gene expression, arrest of development and growth. Proteins responsible for natural defences against pathogens were up-regulated in dormant aleurone. Corresponding genes on chromosome arms where QTL for sprouting tolerance had been previously identified were further analysed to compare their location in the QTL region. The level of total glutathione was significantly higher in dormant embryo tissues, and the capacity for GSSG disulfide regeneration decreased dramatically upon after-ripening. In dormant embryos, the concentration of total and reduced ascorbate increased 2-3 folds during after-ripening indicating high capacity for ascorbate regeneration, which reveals different roles of ascorbate and glutathione in redox control of dormancy.

P43 **PHENOTYPING OF A NEPALI SPRING WHEAT (*Triticum aestivum,* L.) DIVERSITY PANEL FOR PHYSIO-MORPHOLOGICAL TRAITS ASSOCIATED WITH DROUGHT TOLERANCE**

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Most of the modern wheat (*Triticum aestivum*, L.) varieties are highly responsive to inputs such as water, pesticides and fertilizers. However, impact of rapidly changing global climate on wheat production has been observed in the recent years. Consequence of climate change with regard to wheat production is predicted to be more severe in the rural and marginal areas of developing nations. Thus, phenotyping of wheat genotypes for traits associated with stress tolerance is becoming critical while developing high yielding varieties. We have phenotyped a diversity panel of 320 spring wheat genotypes: Nepali Wheat Diversity Panel (NWDP), for various physio-morphological traits that are critical for drought tolerance at Elora research station, University of Guelph, Ontario. Details of the phenotyping protocol and the results will be presented.

P44 **COMPUTATIONAL DISCOVERY OF MOLECULAR MECHANISMS IN WHEAT COLD RESISTANCE FROM RNA-SEQ DATA**

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Canada is suffering from frequent extreme weathers. As a staple food source for the world population, the quality and yield of Canadian wheat are severely affected by drought and cold conditions. Therefore, identifying cold responsive genes and developing cold resistant cultivars are of key importance to sustain food supplies to Canadians and secure Canada's impact in global businesses in the long term. Applying high-throughput RNA sequencing platform to a variety of wheat lines provides us with an opportunity to push forward this study. The main objective of this project is to identify key biomarkers for wheat cold tolerance that can be translated to breeding program for next generation of cold tolerant resilient cultivar. We constructed an efficient and effective pipeline for the comprehensive analysis of RNA-seq data that includes triplicates from four wheat cultivars (manitou, winter manitou, norstar and spring norstar) treated with cold paired with control. In this presentation, we will show that, through clustering analysis, correlation analysis, and gene ontology enrichment analysis, interesting winter acclaimed patterns and genes are identified.

P45 **EVALUATION AND VALIDATION OF HOUSEKEEPING GENES AS REFERENCE FOR GENE EXPRESSION STUDIES IN WHEAT (*TRITICUM AESTIVUM*) UNDER PHOSPHOROUS STRESS CONDITION**

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Improving Phosphorous (P) use efficiency of wheat (*Triticum aestivum* L.) is important in sustainable use of P resources. Studying the expression pattern of genes for the P signaling network will help to breed wheat with improved P use efficiency. In order to do the gene expression analysis using quantitative real-time PCR (qRT-PCR), the results need to be normalized due to the high sensitivity of the method and also to eliminate technical variation. Normalization against a reference gene that is constitutively transcribed and has minimum variation among samples is the ideal method. To identify stable

housekeeping genes as a reference for expression analysis under phosphorous stress conditions in wheat, the relative expression variation for 10 commonly used housekeeping genes (translation elongation factor alpha, actin, ADP-ribosylation factor, ubiquitin, Glyceraldehyde-3-phosphate dehydrogenase, 18S subunit ribosomal protein, 28S subunit ribosomal protein, cell division control protein, alpha tubulin, RNase L inhibitor like protein) will be studied in root and leaves tissues of *Triticum aestivum* cv. Chinese Spring. The relative quantification of these genes according to the internal controls (most stable, least stable, and combination of most stable and least stable housekeeping genes) will be presented. The identified and validated housekeeping genes are expected to facilitate gene expression studies under phosphorous stress.

P46 **MYCORRHIZAL COLONIZATION IN SPRING WHEAT: PHENOTYPIC AND GENOTYPIC ANALYSIS**

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Wheat (*Triticum aestivum* L.) is the second most important cereal crop planted over one sixth of the global cultivated farmlands, providing 40% of the world grain production. Several biotic and abiotic challenges limit its production, including soil salinization. According to recent statistics, more than 77 million hectares of global cultivated land is under different levels of salt erosion; this is especially concerning in arid and semiarid regions. Many approaches had proved to be beneficial to plants in enhancing their tolerance towards salt stresses and one of the most potential approaches is the use of mycorrhizae. Mycorrhizal-colonization in roots had been studied in different plants (ex. rice, pepper, citrus, etc.) and had proved to benefit host plants in various aspects, such as increasing water absorption, enhancing mineral uptake and so on. The objective of this project was to investigate the influence of four mycorrhizal strain colonizations on four selected spring wheat genotypes under three salt concentrations. The results demonstrated that mycorrhizal strains *Funneliformis mosseae* and *Rhizophagus irregulare* increased plant biomass and improved root structure. Wheat inoculated by these two mycorrhizae had higher yield, higher root to shoot ratio and stronger root systems than non-inoculated wheat lines. Salinity had no effect on most variables except root surface area and root dry weight.

P47 **GENOME-WIDE IDENTIFICATION AND ANALYSIS OF MITOGEN ACTIVATED PROTEIN KINASES (MAPKS) IN WHEAT**

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The sessile nature of plants exposes them to a multitude of abiotic stresses that differ both in quality and quantity. MAPKs are a critical component of the signalling mechanism that perceives the threat stimuli and initiates a defense response. MAPKs have been shown to participate in various abiotic defense responses. The research progress on MAPK signalling in wheat, however, is meagre as compared to other plant species, which is largely due to the lack of information on MAPKs in this species. Our analysis of the wheat (*Triticum aestivum*) genome data has identified various single MAPKs (TaMPKs), double MAPKs (TaMAPKKs) and triple MAPKs (TaMAPKKKs) on different chromosomes. Homologous sequences were also identified in the ancestral genomes of bread wheat: *Aegilops tauchii* and *Triticum*

urartu. A comprehensive list of their DNA and protein sequences with correct annotation of names has been developed. The interaction, observed through yeast two-hybrid assays, among certain TaMPKs and TaMAPKKs is reminiscent of the MAPK signalling cascade for the defense activation mechanism present across the plant kingdom. Phylogenetic analysis of conserved motifs revealed a tendency of diversification from other plant MAPKs. The presence of multi-variants of several MAPKs could be an outcome of a complex genome formed through integration of A, B and D genomes during evolution. Differential expression of various MAPKs in different types of tissues indicates their specific or preferential role in wheat plant biology. This work builds a platform that would help accelerate MAPK signalling research to better understand the abiotic stress response in wheat.

P48 **PHENOTYPIC EVALUTATION OF A DIVERSE PANEL OF SYNTHETIC HEXAPLOID WHEAT DERIVATIVES GROWN UNDER DIFFERENT PHOSPHORUS CONDITIONS**

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Phosphorus (P) is a non-renewable resource, where current high quality reserves have approximately 60 to 130 years remaining based on current removal rates. Agricultural production worldwide harvests 12 MT of P annually for fertilizer use. Not only are current removal rates unsustainable, fertilizer application from agriculture production is a major source of P loading into water bodies around the world. Developing more P efficient crops through genetic improvement may improve the P balance efficiency of the entire cropping system by preventing dissolved P from being lost, exported and accumulated in the field. As a major cereal crop worldwide, wheat has the potential to be improved in terms of its genetic diversity for P use efficiency (PUE). We hypothesize that synthetic hexaploid wheat (SHW) derivatives contain significant variation for desirable quantitative traits, including P uptake and P utilization efficiency, that can be used for breeding purposes. To investigate this, 194 SHW accessions from the International Maize and Wheat Improvement Centre (CIMMYT) were grown under 0 kg P/ha and 120 kg P/ha in a low P field near Elora, Ontario. P uptake efficiency was estimated as the total P content per unit of P available in the soil and P utilization efficiency was estimated as the grain yield per unit of total P. Additionally, harvest index, plant height, days to anthesis, days to maturity and chlorophyll content were used to phenotype the lines. The results from one growing season will be presented.

P49 **BALANCING THE COST AND UTILITY OF ADDING YIELD TESTING FIELD SITES IN A WHEAT BREEDING PROGRAM**

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Plant breeding is the scientific application of genetic principles to improve plants for human benefit. Successful breeding programs continuously invest in efficiency both attempting to increase genetic gain and to balance budgets. The Canadian Western Red Spring (CWRS) wheat breeding program for the northern prairies develops germplasm with early maturity and high yield for the Peace River and Parkland regions of Western Canada. While multi-location testing is exceedingly important to successfully identify superior genotypes in light of highly significant genotype by environment interactions, a breeding program must balance the need for additional yield test locations with the reality of limited resources. In recent years, privately contracted yield trials have become significantly more expensive and represent an increased proportion of the total program budget. Site regression models were created using historical data from several years of advanced yield trials. These models are used as the basis to discuss the utility

of privately contracted yield trials and the return on investment provided by these locations.

P50 **IMPROVEMENT IN WHEAT CARBON FLUX FOR INCREASED YIELD AND HARVEST INDEX**

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With an increased global demand due to a growing world population, more productive wheat varieties that can efficiently metabolize more carbon fixed through photosynthesis are now needed. Previous studies in Arabidopsis have shown that reduced activity of the mitochondrial pyruvate dehydrogenase complex kinase (mt PDHK), the negative regulator of the mt PDH, resulted in increased carbon flux toward the seed and eventually higher yield (push/pull effect). In addition, the strong correlation between increased mt PDH activity and elevated CO2 fixation translated into a higher photosynthetic rate and seed filling via increased cellular respiration rates. Here, we propose to validate this concept in wheat and increase productivity by exploiting the effects of reduced mt PDHK activity on enhanced respiration and increased CO2 fixation for higher photosynthate production and consequent increases in seed size/weight. To that end, we designed a gene editing strategy to reduce the expression of the wheat PDHK gene(s) by introducing small nucleotide mutations in the coding sequence (indels). This novel molecular, potentially non-GMO, approach combined with double haploid (DH) technology has the potential to accelerate the production of genetically improved lines to be transferred into existing commercial cultivars through conventional breeding. We present here our first results on the development of an optimized embryogenesis platform, the characterization of several nano-complexes formed with different classes of transfection agents as well as the optimization of a gene-gun mediated embryo bombardment method, all necessary steps toward the development of an efficient platform for the delivery of gene editing tools in wheat.

P51 **THE EFFECTS OF FOLIAR APPLICATION OF PLANT HORMONES AT THE BOOTING STAGE ON WHEAT (*TRITICUM AESTIVUM* L.) YIELD COMPONENTS**

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The grain number is one of the most important components in final harvested yields of wheat and it is closely related to the number of florets initiated during stem elongation and number of survived florets before anthesis, especially at booting stage. A split-plot experiment using a randomized complete block design with three blocks was used to study the effects of different plant growth regulators [3-Indoleacetic acid (IAA), 6-Benzyalaminopurine (6-BAP) and IAA × 6-BAP] compared with control on two wheat genotypes (Sivand and Pishtaz) at booting stage. This study was conducted at the Campus of Agriculture and Natural Resources of Razi University during 2012-2013. The results showed that there was not a significant difference between the genotypes for the yield and yield components of wheat, however the effects of hormones were significant on grain yield, number of grains per spike and harvest index. The application of IAA × 6-BAP had the greatest effect on these traits, however, the interaction effect between the genotypes and hormones was not significant for traits. The number of grains per spike had a positive and significant correlation with the wheat grain yield. The increase in the grain yield could be attributed to increasing of grain numbers per spike that had been earned by the application of two growth hormones (IAA × 6-BAP) at booting stage.

P52 **TIMING AND RATES OF NITROGEN FERTILIZER APPLICATION ON WHEAT YIELD AND LODGING RESISTANCE**

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Lodging, which is the permanent displacement of crop plants from vertical, is a leading cause of yield loss and quality reduction for wheat production. Nitrogen (N) management strategies are of importance to ensure optimum wheat yields when sustaining a high lodging resistance for wheat (*Triticum spp.*) production. Field experiment was conducted in Ottawa to determine the impact of different rates and timing of application of N fertiliser on wheat yield and lodging risk of two varieties, and to determined which kind of lodging (stem or root lodging) was more prevalent. Treatments included factorial combinations of five rates of N as urea (46% N) and timing of application (pre-plant only or preplant plus side-dressed applications). At maturity, the stems underwent a three point bending test, while the roots underwent a root lodging test and had their morphological traits analyzed. The results showed that side-dressed N application resulted in significant improvements in seed yield and lodging resistance over equivalent preplant-only applications. Wheat yield increased with increasing N rates, but the significant increases were only found between zero-N and N application treatments. Meanwhile, lodging risk significantly increased with increasing N rates due to an increase in self-weight moment and a decrease in stem bending strength. Root lodging was more prevalent than stem lodging. Present study implies that root lodging should be targeted as the priority to increase lodging resistance through breeding selection for a high rigidity root system, especially when plants was subject to high nitrogen condition in eastern Canada.

P53 **EVALUATION OF DIFFERENTIAL HERBICIDE SENSITIVITY IN CHINESE WINTER WHEAT VARIETIES UNDER MESOSULFURON-METHYL STRESS**

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Mesosulfuron-methyl, also known by its product name 'Sigma', is a sulfonylurea herbicide commonly used for weed control in China. However, it appears that mesosulfuron-methyl can have harmful effects on some winter wheat cultivars. Subordinate function analysis was applied to seven wheat varieties for their tolerance to Sigma herbicide and different sensitivity levels were observed. Varietal sensitivities ranked as follows (ranging from lowest to highest): Shannong129 > Yanmai19 > CA0547 > 040542 > Changzhi9578 > Fengyu3 > Shunmai1718. Two winter wheat varieties, Shannong129 and Shumai1718, with contrasting seedling herbicide sensitivities (lowest and highest sensitivity, respectively) were selected. These varieties were further evaluated for their responses to Sigma herbicide. Wheat seedlings of both varieties were subjected to twice the recommended dose (80ml/m^2) of Sigma and the following parameters were measured: seedling height, root length, root number, seedling fresh weight, seedling dry weight, active oxygen and malonaldehyde (MDA) levels as well as superoxide dismutase (SOD) and peroxidase (POD) activities. Shunmai1718 had a much greater decline in seedling height, root length, seedling fresh and dry weights compared to its untreated control than Shannong129. Similarly, Sigma treatment had little effect on root number for Shannong129 compared to its untreated control; whereas, Shunmai1718 exhibited significantly lower root number compared to its untreated control. Sigma treatment resulted in higher levels of active oxygen and MDA and increased activity of SOD and POD, the largest increase was observed for the active oxygen levels of Shunmai1718 and its accumulated

activity of protective enzymes compared to its untreated control.

P54 **AGRONOMY AND QUALITY CHARACTERISTICS OF HARD RED WINTER WHEAT BREEDING LINES IN ONTARIO IN 2014 AND 2015**

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Hard red winter wheat grown in Ontario typically has lower yield and higher protein compared to soft red winter wheat. Generally, more nitrogen needs to be applied in hard red winter in order to achieve higher protein levels. Experimental plots of fifty four hard red winter wheat breeding lines were planted in 2013 and 2014 at Ridgetown. Hard red winter wheat cultivars commercially grown in Ontario were included in tests as checks. Each cultivar had four replications, and plot size was 1.15 m by 4.0 m. Winter survival, heading date, plant height and disease severity (0-9 scale) for powdery mildew and *Septoria tritici* blotch were estimated. Grain was harvested by a small plot combine and yield was reported at 14% moisture content. After harvest, quality characteristics which included test weight (TW), thousand kernel weight (TKW), grain protein and hardness, flour protein and yield, and dough strength were performed. Averaged TW and TKW were higher in 2014 than in 2015 (80.0 kg/hl and 36.8 g vs. 74.5 kg/hl and 35.2 g), but lower grain protein level was in 2014 (11.9%) than in 2015 (13.3%). Breeding lines with the highest grain protein level were Ca33-18 in 2014 (16.3%) and Ca17-4 in 2015 (15.7 %). Together with lines with high yield and good diseases resistance, they will be tested again across Ontario and used as parents in new crosses.
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