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CWFHB • CCF

9th Canadian Workshop on Fusarium Head Blight

9e Colloque canadien sur la fusariose

4th Canadian Wheat Symposium

4e Congrès canadien sur le blé

PROGRAM

Winnipeg

Manitoba, Canada

November 19 - 22, 2018

9th Canadian Workshop on Fusarium Head Blight / 4th Canadian Wheat Symposium Joint Conference

Fairmont Hotel
Winnipeg, Manitoba
November 19–22, 2018

SCIENTIFIC ORGANIZING COMMITTEE

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Welcome

Dear Friends and Colleagues,

Welcome to the first joint conference of the 9th Canadian Workshop on Fusarium Head Blight (CWFHB) and the 4th Canadian Wheat Symposium (CWS), held at the Fairmont Hotel in Winnipeg, Manitoba.

After the consecutive meetings of the 8th CWFHB and 3rd CWS in Ottawa in 2016, we decided on a joint conference format to better showcase the interdisciplinary work and research that both science communities have accomplished to date. With 6 invited plenary and 10 keynote speakers in concurrent sessions, the conference covers a broad range of new developments in, and applications of, transformative technologies.

Recent scientific discoveries in areas such as gene editing, imaging, disease resistance genes, food quality, and new agronomic tools are transforming research capacity around the globe. This 2018 joint conference provides a venue for scientists, industry, and producers to learn and discuss recently discovered technologies, enabling the transformative development of new products that can combat problems caused by *Fusarium* species in cereal crops and in wheat research. The scientific program of the tandem symposia with plenaries, keynote speakers, concurrent breakout sessions, and poster presentations focuses on cutting edge discoveries and state-of-the technologies. The conference goals include building on existing and developing new approaches to more collaborative and interdisciplinary research that will lead to the improvement of quality and the productivity of healthy crops in Canada.

We would like to acknowledge the various sponsors who have been very generous in their financial support of the joint conference. We wish to recognize them for their continued assistance and contributions. We would also like to thank the organizers from SeCan and the scientific organizing committee for the many hours of time invested in preparing and accomplishing this conference. It has been a pleasure to work with such a dedicated and supportive team. We trust you will all have a great, meaningful, and rewarding time in Winnipeg.

Thomas Fetch
Chair, 4th CWS
Brandon Research and Development Centre
Agriculture and Agri-Food Canada

Tom Gräfenhan
Chair, 9th CWFHB
Grain Research Laboratory
Canadian Grain Commission

Welcome from SeCan

Welcome to Winnipeg and the joint 4th Canadian Wheat Symposium and 9th Canadian Workshop on Fusarium Head Blight conference. It is a privilege for all of us at SeCan to have played a part in organizing this event 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.

Wheat is one of the few crops that is grown in every province of Canada, and unfortunately, suffers from increasingly severe Fusarium infestations in all major production areas. This devastating disease has both a dramatic impact on our farm gate income – not to mention food safety concerns for the balance of the food processing value chain. To overcome such tremendous production challenges, we believe both national and international collaboration amongst researchers is necessary.

So, it is against this backdrop of unprecedented opportunities and threats that we welcome you to engage in a very fruitful exchange of knowledge, and build collaborations that will move us ahead in our quest for enhanced productivity and food safety. Again, thank you on behalf of SeCan companies across Canada for the work you do – and for your participation in this important joint conference. 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. Work that is critical to our collective health and prosperity the world over.

Thank you.

Jeff Reid
General Manager

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CMBTC Canadian Malting Barley Technical Centre

CSTA ACCS Canadian Seed Trade Association / L'Association canadienne du commerce des semences

Cigi

9th Canadian Workshop on FHB & 4th Canadian Wheat Symposium

List of Oral Presentations

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S2 **UNLOCKING THE POLYPLOID POTENTIAL OF WHEAT THROUGH GENOMICS;** Cristobal Uauy

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S4 **CANADIAN HERITAGE WHEAT VARIETY ALLELES OF FLOWERING AND PLANT HEIGHT PATHWAY GENES ASSOCIATED WITH LOW FUSARIUM HEAD BLIGHT;** Raman Dhariwal, Maria Antonia Henriquez, Colin Hiebert, Curt McCartney, Robert Graf, and Harpinder Randhawa

S5 **GENOME-WIDE ASSOCIATION STUDY OF A DIVERSE TWO-ROW BARLEY GENOMIC PANEL IDENTIFIES GENOMIC REGIONS ASSOCIATED WITH RESISTANCE TO FHB AND DON ACCUMULATION;** James Tucker, Ana Badea, Aaron Beattie, Colin Hiebert, Bill Legge, Curt McCartney, and Dilantha Fernando

S6 **AN EXPERIMENTAL APPROACH FOR ASSESSING GAIN FROM GENOMIC SELECTION FOR FUSARIUM HEAD BLIGHT RESISTANCE IN WHEAT;** Thomas Miedaner, Cathérine Pauline Herter, Sonja Kollers, Viktor Korzun, and Erhard Ebmeyer

S7 **THE DOT AUTONOMOUS POWER PLATFORM;** Marco Coppola

S8 **RE-EVALUATING THE SEEDING WINDOW OF WINTER WHEAT IN WESTERN CANADA**; Yvonne Lawley and Navneet Brar

S9 **THE INTEGRATION OF SPRING WHEAT GENETICS AND AGRONOMICS TO MITIGATE RISKS ASSOCIATED WITH EARLY PLANTINGS INTO COLD SOILS;** Brian L. Beres, Graham R.S. Collier, Robert J. Graf, and Dean M. Spaner

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S11 **MYCOTOXIN LEVELS IN ALBERTA WHEAT FIELDS IN 2015 AND 2016;** Michael W. Harding, Greg C. Daniels, A. Olubodun, T. Gräfenhan, J. Feng, and T.K. Turkington

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S14 **IMPACTS OF RISK OF FUSARIUM HEAD BLIGHT (FHB) ON THE WHEAT SUPPLY CHAIN;** William W Wilson

S15 **GENETIC ANALYSIS OF OVIPOSITION DETERRENCE TO ORANGE WHEAT BLOSSOM MIDGE;** Curt A. McCartney, Curtis Pozniak, Santosh Kumar, Andrew Burt, Richard Cuthbert, Yuefeng Ruan, Ian Wise, Marjorie Smith, Stephen Fox, and Alejandro Costamagna

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S17 **WHAT WE HAVE LEARNED ABOUT THE WHEAT STRIPE RUST PATHOGEN IN CANADA?;** Gurcharn S. Brar, Sajid Ali, Reem Aboukhaddour, M. Serajazari, A. Navabi, Dinah Qutob, Steve Ambrose, Kun Lou, Ron MacLachlan, Curtis J. Pozniak, Yong-Bi Fu, Andrew Sharpe, and Hadley R. Kutcher

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P33 **ACHIEVING MULTIRUST RESISTANCE: HOW MANY GENES?;** Wentao Zhang, Kerry Boyle, Brittany Polley, Christine Sidebottom, Harpinder Randhawa, Tom Fetch, Randy Kutcher, Brent McCallum, and Pierre R. Fobert

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Abstracts for Oral Presentations

[S1] KNOWLEDGE BASED RESISTANCE IMPROVEMENT OF WHEAT AGAINST FUSARIUM HEAD BLIGHT. Hermann Buerstmayr, Barbara Steiner, Sebastian Michel, Jose Moreno Amores, Marc Lemmens, Christian Wagner, and Maria Buerstmayr. University of Natural Resources and Life Sciences, Vienna, Austria
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Fusarium Fungi are among the most feared pathogens of small grain cereals, particularly wheat. Resistance to Fusarium is therefore a top priority for resistance breeding, and receives high attention in research. The search string: TS=(Fusarium AND resistance AND wheat) in the ISI Web of Knowledge finds in the time frame 2000 -2017 more hits than any other wheat disease. Apart from yield losses, the contamination of the crop with mycotoxins is the major issue associated with Fusarium head blight (FHB). Fusarium is an opportunistic pathogen, which preferentially penetrates and colonizes cereal florets during the flowering period. Environmental conditions which either favor or hamper the fungus and the status of the plant during flowering have therefore a huge impact on disease establishment and development. Resistance to FHB can be classified into passive (morphological and developmental) factors and active (physiological, biochemical) factors, both of which play a role. Typical passive resistance factors are plant height and the extent of anther extrusion during flowering. Based on previous comparative mapping studies we discovered that 1) anther extrusion is a clearly quantitative trait, 2) higher degree of anther extrusion is associated with reduced FHB susceptibility and 3) plant height genes, *Rht-B1b* and even more pronounced *Rht-D1b* are associated with increased FHB susceptibility and reduced anther extrusion, which could partly explain their effect on lowering FHB resistance. The famous FHB resistance allele *Fhb1*, which was discovered in Chinese germplasm, residing on chromosome 3B, most likely has a different function. *Fhb1* has not been linked to height or flowering traits. In our results we always find *Fhb1* associated with increased resistance to Fusarium spreading, and simultaneously to the toxin deoxynivalenol (DON). We could recently show that *Fhb1* improves field resistance to FHB also in durum wheat and in triticale. Further tests on the functional characterization of *Fhb1* in relation to DON detoxification are currently underway. Apart from few large effect QTL for FHB resistance a great proportion of resistance is most likely due to numerous small effect genes. Breeders can make use of these small effect genes as well, using classical phenotypic selection, and since recently using Genomic Selection. Resistance selection utilizes often a skillful combination of phenotypic testing in provocation nurseries and of genome wide selection using genomic prediction approaches.

[S2] UNLOCKING THE POLYPLOID POTENTIAL OF WHEAT THROUGH GENOMICS. Cristobal Uauy[1]. [1]John Innes Centre, Norwich Research Park, Norwich NR4 7UH, United Kingdom
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Several developments over the past 18 months have radically changed the way we work with polyploid wheat. Both hexaploid and tetraploid wheat now have whole genome sequences and reliable gene models. We have developed in-silico mutant resources with over 95% of genes with either a knockout or deleterious allele in both tetraploid and hexaploid wheat. We recently published a comprehensive gene expression atlas in wheat with over 850 RNA-Seq samples along with co-expression and transcription factor target networks. All this data is open-access and displayed at *Ensembl*Plants. Novel strategies have accelerated cloning of disease resistance and other genes. Using accelerated growth conditions (speed breeding), the community now routinely grows wheat in 10-week seed-to-seed cycles compared to the previous 16-20 weeks. All these developments have dramatically lowered the barriers to undertake biological research in polyploid wheat. For many purposes, wheat can now be treated (almost) like a model crop species. The next phase will be to start understanding the biological mechanisms underlying the most important traits in polyploid wheat and to design strategies to ensure this knowledge is quickly transferred to the field. We argue that given polyploidy, breeders have exploited only a fraction of the potential genetic variation in the wheat genome. The recent breakthroughs in wheat genomics now allow us to make a decisive effort towards exploiting this under-utilised variation, thereby unleashing the full potential of the wheat genome.

[S3] GENETICS FOR LOW CORRELATION BETWEEN FHB AND DON IN A BREAD WHEAT POPULATION. Xinyao He[1], Pawan K. Singh[1], and Susanne Dreisigacker[1]. [1]International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico DF, Mexico
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Deoxynivalenol (DON) contamination in food and feed is a major concern in case of Fusarium head blight (FHB) infection in wheat. DON usually shows good correlation with FHB, which makes many researchers believe that DON is merely a consequence of FHB and is heavily dependent on the latter. Here, we report a study in which DON and FHB showed very low correlation (*r* ranged from 0.07 to 0.31), and QTL mapping revealed the largely independent inheritance of the two traits. A population 'NASMA' x 'IAS20*5/H567.71' with 197 recombinant inbred lines was evaluated for FHB and DON in spray inoculated field experiments at CIMMYT-Mexico in 2010, 2013, 2014 and 2017. Genotyping was done with the Illumina 15K wheat SNP chip and SSR markers. QTL mapping results indicated that the field FHB resistance was mainly controlled by QTL at *Rht-D1* and *Vrn-A1*, along with a few minor QTL. As for DON, two major QTL were detected, one of which was located on 3BL (R^2 of 16-24%), showing minor effects on FHB, whereas the other was on 3DL (R^2 of 10-15%), exhibiting effects exclusively on DON. It is likely that both DON QTL are new based on comparison with previous studies. This study indicates a possibility that resistance to DON could be independent to that of FHB, and the utilization of DON QTL in breeding could be helpful in further reducing DON contamination in food and feed.

[S4] CANADIAN HERITAGE WHEAT VARIETY ALLELES OF FLOWERING AND PLANT HEIGHT PATHWAY GENES ASSOCIATED WITH LOW FUSARIUM HEAD BLIGHT. Raman Dhariwal[1], Maria Antonia Henriquez[2], Colin Hiebert[2], Curt McCartney[2], Robert Graf[1], and Harpinder Randhawa[1].
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Fusarium head blight (FHB), caused by mycotoxin-producing Fusarium species, is a devastating disease that reduces yield, quality and marketability of wheat grains. Presence of mycotoxins e.g. deoxynivalenol (DON) in the infected grains is a major food safety issue especially in the export market. The use of resistance cultivars offers the most effective approach to manage FHB in wheat. Therefore, several studies have been conducted to identify FHB resistance QTL in wheat around the globe, however, most of the identified QTL possess a small effect on resistance and a high-level of genotypic x environment interactions. Conversely, several aboveground traits e.g. plant height, canopy and ear related traits have been reported to be associated with low Fusarium infection. Thus, to identify the novel FHB resistance QTL without a possible trade-off with agronomically important traits, a doubled haploid mapping population derived from AAC Innova/AAC Tenacious was utilized. It was phenotyped for different aboveground and FHB resistance related traits during 2015 to 2018 followed by SNP genotyping and QTL analysis. QTL analysis resulted into a flowering pathway gene (*Ppd-D1b*) and two other major QTL/genes (*QFhb.lrdc-2D* and *Rht-B1a*) which were associated with low FHB and derived from the wheat cultivar (cv) AAC Tenacious. Among the three identified major QTL/genes, *Ppd-D1b* (photoperiod sensitive allele) had largest effects on type-I and -II resistance. Haplotype and pedigree analysis showed that *Ppd-D1b* was inherited along with tall allele of *Rht8* through cv Neepawa and traces back to Canadian heritage wheat variety Marquis.

[S5] GENOME-WIDE ASSOCIATION STUDY OF A DIVERSE TWO-ROW BARLEY GENOMIC PANEL IDENTIFIES GENOMIC REGIONS ASSOCIATED WITH RESISTANCE TO FHB AND DON ACCUMULATION. James Tucker[14], Ana Badea[1], Aaron Beattie[2], Colin Hiebert[3], Bill Legge[1], Curt McCartney[3], and Dilantha Fernando[4]. [1]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Rd., Brandon, MB, Canada, R7C 1A1; [2]Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8; [3]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Rte 100 #100., Brandon, MB, Canada, R6M 1Y5; and [4]Department of Plant Science, 205 Agriculture Building, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2
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Fusarium head blight, incited by *Fusarium graminearum* Schwabe, is the most devastating disease associated with barley (*Hordeum vulgare* L.) production in Canada. Mycotoxins such as deoxynivalenol are commonly associated with this disease, rendering grains unsuitable for animal feed and/or the malting and brewing industries. While breeding cultivars with genetic resistance remains the most economical and environmentally-friendly solution, this has been complicated in barley by the lack of resistance sources and the quantitative nature of resistance. Many bi-parental mapping studies have identified resistance QTLs, however these have generally been of small effect, demonstrate environmental specificity and are commonly associated with agro-morphological characteristics. A genome-wide association study was conducted using a diverse genomic panel of two-row barleys (N=400). The germplasm primarily constituted elite breeder lines and cultivars sourced from western Canadian breeding programs. Lines were phenotyped (FHB score 0-5; DON concentration via ELISA technique) in multiple FHB nurseries in Manitoba (Brandon, Carberry and Carman). The panel was genotyped with an Illumina iScan using an Infinium iSelect custom bead array (50K SNP). Significant QTLs were identified at multiple locations of the genome on multiple chromosomes. Annotated SNP effects generally demonstrated potential role in host defence. SNP markers may be useful for further analysis and application in breeding for resistance.

[S6] AN EXPERIMENTAL APPROACH FOR ASSESSING GAIN FROM GENOMIC SELECTION FOR FUSARIUM HEAD BLIGHT RESISTANCE IN WHEAT. Thomas Miedaner[1], Cathérine Pauline Herter[1], Sonja Kollers[2], Viktor Korzun[2], and Erhard Ebmeyer[2]. [1]University of Hohenheim, State Plant Breeding Institute, Fruwirthstr. 21, 70599 Stuttgart, Germany; and [2]KWS LOCHOW GMBH, Ferdinand-von-Lochow-Straße 5, D-29303 Bergen, Germany
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Fusarium head blight (FHB) is of large concern in the European Union due to strict regulations of the mycotoxins deoxynivalenol, zearalenone, T-2 and HT-2 for cereals used for human consumption. FHB resistance is quantitatively inherited by many genes with small effects making marker-assisted selection inefficient. The availability of phenotypes and a high-density marker array in wheat allows to use the information from the whole genome to predict FHB resistance (=genomic selection, GS). We analyzed a training population of 1,120 winter wheat lines for FHB resistance, heading date, and plant height at four locations and genotyped them by a 15k Illumina SNP assay. Mean FHB symptoms varied from 4 to 66% among the lines. From cross validation we calculated prediction accuracies for FHB resistance ranging from 0.74-0.86 depending on the model. For the experiment, a test population of 2,500 progenies was genotyped. To compensate for the significant negative correlation between plant height and FHB resistance, we used a culling level for plant height. From the remaining 1,560 lines we selected genomically the best 10% for FHB resistance and phenotyped them in 2018 in four locations. The realized selection gain for this GS approach for FHB resistance was 10.6 percentage points compared to an unselected sample of the same test population. In conclusion, GS makes FHB resistance selection more efficient, because larger populations can be screened in a shorter period with fewer efforts for phenotypic evaluation.

[S7] THE DOT AUTONOMOUS POWER PLATFORM. Marco Coppola. DOT Technology, #1 South Plains Road West, Emerald Park, SK S4L1C6
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[S8] RE-EVALUATING THE SEEDING WINDOW OF WINTER WHEAT IN WESTERN CANADA. Yvonne Lawley and Navneet Brar. Department of Plant Science, University of Manitoba, 222 Agriculture Building, Winnipeg, MB, R3T 2N2
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Seeding date is one of the key management steps to growing a successful winter wheat crop in Western Canada. Several factors are now limiting the ability of farmers to plant winter wheat within the optimum seeding window. These factors include continuous cropping, limited use of summer fallow, selection of longer season varieties, and the introduction of new late maturing crops, such as soybean and corn. A study was conducted between 2013 and 2017 at 13 sites across the Canadian Prairies (Manitoba, Saskatchewan, Alberta) to re-evaluate the seeding window of winter wheat in light of the recent release of more cold tolerant varieties as well as the introduction of fungicide seed treatments. Winter wheat (cv. Flourish) was planted on five fall planting dates (Sept 1, Sept 15, Oct 1, Oct 15, and Nov 1) over three year at each location in the study. At each planting date, winter wheat treated with a fungicide seed treatment (*Tebuconazole* and *Prothioconazole*) was compared to an untreated control. Weather was less restrictive during late planting dates in all years than initially anticipated. The November 1 dormant seeding treatment (+ or – 4 days) could be planted in 24 out of 29 sites years during the study period. Yield trends were most consistent in Manitoba with yields generally declining with later planting and the highest relative yields occurring when planting winter wheat between Sept 1 and Sept 15. In Alberta and Saskatchewan, yield trends were variable with yields for some site years increasing with later planting while others were unresponsive to planting date. Seed treatment increased spring plant stand and grain yield relative the untreated check when averaged over all planting dates at 8 out of 27 site years. Most of the site years with seed treatment benefits occurred in Manitoba.

[S9] THE INTEGRATION OF SPRING WHEAT GENETICS AND AGRONOMICS TO MITIGATE RISKS ASSOCIATED WITH EARLY PLANTINGS INTO COLD SOILS. Brian L. Beres[1], Graham R.S. Collier[2], Robert J. Graf[1], and Dean M. Spaner[2]. [1] Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, 5403 1st Avenue South, Lethbridge, Alberta, Canada T1J 4B1; [2]410 Agriculture/Forestry Centre, University of Alberta, Edmonton, Alberta, Canada T6G 2P5
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Spring wheat (*Triticum aestivum* L.) is the primary cereal grain grown in western Canada both by area seeded and volume of grain produced. Optimal soil temperature for sowing spring wheat is consistently identified as 20^{o}C; however, conventional practice in western Canada requires seeding prior to reaching this soil temperature due to a relatively short growing season and condensed planting window. Multiple studies indicate yield advantages with early seeding but often fail to determine the point at which this advantage is lost. Field studies were conducted at four locations in Alberta and Saskatchewan, CANADA, from 2015-201, to determine the benefits and risks of ultra-early seeding. This study negates the ambiguity of 'seeding date' by instead using soil temperature to determine seeding time. Multiple seeding times between soil temperatures of 0^{o}C and 10^{o}C were completed (6), investigating the effects of manipulations to the agronomic system including the use of cold tolerant (2 cultivars) and conventional spring wheat genetics (cv. Stettler), seeding rates (200 vs. 400 seeds m^{-2}), and seeding depths (2cm vs. 5cm). Results indicate that grain yield was maximized when seeding occurred at around 2^{o}C soil temperature. The earliest seeding dates, at a soil temperature of 0^{o}C, did not yield significantly lower than seeding dates between 4^{o}C and 10^{o}C. Cold tolerant genetics and conventional spring wheat genetics did not exhibit differential grain yield stability. Manipulations to agronomic management further influenced grain yield – higher seeding rates increased grain yield across seeding times and provided greater system stability over lower seeding rates.

[S10] GENOME WIDE ASSOCIATION STUDIES OF PHOSPHORUS USE EFFICIENCY AND RELATED TRAITS IN SYNTHETIC HEXAPLOID DERIVED WHEAT (*TRITICUM AESTIVUM* L.). Emily Gordon[1] and Alireza Navabi[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Road E, Guelph, ON, Canada, N1G2W1
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Phosphorus (P) is a non-renewable resource and current reserves are becoming depleted due to high demand for fertilizer. Increased fertilizer use over the last several decades has contributed to the pollution of surrounding water bodies. Improving phosphorus use efficiency (PUE) in wheat (*Triticum aestivum* L.) can reduce dependence on P fertilizers. The objective of this study was to identify genomic regions related to PUE under contrasting P amendments. Three field trials were conducted under 0 kg ha^{-1} and 125 kg ha^{-1} of monoammonium phosphate, using a population of 194 synthetic hexaploid derived wheat lines from the International Maize and Wheat Improvement Centre (CIMMYT). Root architecture traits under no phosphorus (NP) and applied phosphorus (AP) were analyzed using a growth pouch phenotyping assay under controlled conditions. Phosphorus use efficiency was assessed through multiple parameters including P deficiency tolerance and P responsiveness. It was determined that variation exists within this panel for P deficiency tolerance and P responsiveness. Using 6 904 SNP markers, 32, three and 7 markers were identified for agronomic traits, average root diameter, and P-use-related traits, respectively, suggesting further evaluation of these genomic regions may uncover genes related to P use. A principle component analysis revealed that several genotypes had high P responsiveness and high grain yield under AP. Selecting for root traits in this population may not be a good indicator of grain yield or PUE. Yield-based selection criteria provided a better estimate of PUE.

[S11] MYCOTOXIN LEVELS IN ALBERTA WHEAT FIELDS IN 2015 AND 2016. Michael W. Harding[1], Greg C. Daniels[1], A. Olubodun[2], T. Gräfenhan[3], J. Feng[4], and T.K. Turkington[5]. [1]Crop Diversification Centre South, Alberta Agriculture and Forestry, 301 Horticulture Station Road East, Brooks, AB, Canada T1R 1E6; [2] Industry Services, Canadian Grain Commission, 600-303 Main Street, Winnipeg, MB, Canada R3C 3G8; [3] Grain Research Laboratory, Canadian Grain Commission, 600-303 Main Street, Winnipeg, MB, Canada R3C 3G8; [4]Crop Diversification Centre North, Alberta Agriculture and Forestry, 17507 Fort Road NW, Edmonton, AB, Canada T5Y 6H3; and [5]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, 6000 C and E Trail, Lacombe, AB, Canada T4L 1W1
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Fusarium graminearum Schwabe is a named pest on Alberta's *Agricultural Pests Act* and traditionally is known to cause head blight in cereal fields in southern Alberta, mainly in Crop Districts 1 and 2. Reports of increasing levels of head blight in wheat fields in central and northern Alberta led to an attempt to characterize the distribution of *F. graminearum* in each county across the Province. Approximately 2% of wheat fields were targeted for surveillance in each county resulting in 910 and 1017 fields sampled in 2015 and 2016, respectively. Approximately 15% of samples tested positive for *F. graminearum* in 2015 while nearly 27% were positive in 2016. Additionally, the proportion of the *F. graminearum* isolates that were the 3-ADON chemotype was 46% in 2015 and 31% in 2016. Grain samples from a subset of these fields were analyzed for mycotoxins and in 2015 there were 51 of 795 samples with detectable levels of deoxynivalenol (DON) with concentrations ranging from 0.5 to 91.4 ppm. In 2016 there were 107 of 809 samples that had detectable levels of DON ranging from 0.5 to 102.4 ppm. Furthermore, there were 14 samples with DON levels ≥ 5 ppm in 2015, but in 2016 there were 37 samples with ≥ 5 ppm DON. Two of these samples each year were from Crop District 4 and always accompanied a high incidence of *F. graminearum.* These results confirmed that *F. graminearum* and DON contamination of wheat grain were a developing issue in Crop District 4.

[S12] LC-MS/MS BASED MYCOTOXIN/DEOXYNIVALENOL (DON) DIAGNOSTIC PLATFORM FOR FHB RESEARCH AND BREEDING PROGRAMS. Lipu Wang[1], Deborah Michel[2], Anas El-Aneed[2], Pierre Fobert[3], Wentao Zhang[3], Irina Zaharia[3], Shawn Clark[3], Bianyun Yu[3], Yuefeng Ruan[4], and Randy Kutcher[1]. [1]Cereal & Flax Pathology Lab, Department of Plant Sciences / Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; [2]College of Pharmacy and Nutrition, University of Saskatchewan, 2D10 HSB, 107 Wiggins Rd., Saskatoon, SK, S7N 5E5, Canada; [3]National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9, Canada; and [4]Agriculture and AgriFood Canada, Gate #3, Airport Road East, Swift Current, SK
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Fusarium head blight (FHB), caused by Fusarium spp., is a destructive disease of small grain cereals, such as wheat, barley, oat and canaryseed. Apart from grain yield losses and reduced baking and seed quality, a major concern with FHB is crop contamination with Fusarium-produced trichothecene mycotoxins, specifically deoxynivalenol (DON), also known as vomitoxin, and its derivatives. These mycotoxins accumulate in the grain making it unfit for consumption by humans and animals. Significant DON contamination may render a crop unmarketable, or reduces the market value by 40-65%. The ultimate goal in FHB resistance breeding is to develop productive cultivars with disease resistance and low mycotoxin contamination despite high infection pressure. At the Cereal Pathology Laboratory, we have established two mycotoxin diagnostic platforms using liquid chromatography coupled with triple quadrupole mass spectrometry (LC-MS/MS) to support FHB breeding and research programs: 1. a rapid, accurate and low cost DON quantification platform for high-throughput DON phenotyping; and 2. a state-of-the-art analytical platform to simultaneously quantify DON and its derivatives: 3-acetyldeoxynivalenol (3-ADON), 15-acetyldeoxynivalenol (15-ADON), and deoxynivalenal-3-glucoside (D-3-G); and the toxins: nivalenol (NIV), HT-2 and T-2.

[S13] TESTING FOR CROSS REACTIVITY IN COMMERCIALLY AVAILABLE KITS FOR DON AND DON-LIKE COMPOUNDS. Kerri Pleskach[1], Tanya Zirdum[1], Richard Blagden[1], Jason Chan[1], and Sheryl A. Tittlemier[1]. [1]Grain Research Laboratory, Canadian Grain Commission, Winnipeg, MB, Canada
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Many cereals are susceptible to F*usarium graminearum* infection, which produces deoxynivalenol (DON) and other DON conjugates, such as 3- and 15-acetyl deoxynivalenol (3-ADON and 15-ADON) and nivalenol (NIV). As a defense mechanism, the plant converts DON to deoxynivalenol-3-glucoside (DON3G). Our lab has evaluated commercially available DON ELISA and lateral flow device (LFD) kits for their cross reactivity towards DON-like compounds. We tested individual standards and mixtures of DON, 3-ADON, 15-ADON, DON3G and NIV at various concentrations to estimate the cross reactivity. It was found that DON3G and the ADONs had an effect on the DON reading; NIV displayed no effect. Matrix matched standards were also tested for wheat and barley, in which we found no difference between the matrices, but found that cross reactivity still occurred. Lastly, we ran a suite of wheat samples that had known amounts of DON and DON-like compounds, previously determined by UPLC-MS/MS. We found that the DON result slightly increased when there was DON-like compounds in the sample. When using the LFDs, there is a positive bias when compared to the UPLC-MS/MS results, which is not due to cross-reactivity. This is important to keep in mind when samples are being tested for DON, that DON3G, and the ADONs can increase the apparent DON as compared to what is actually in the sample.

[S14] IMPACTS OF RISK OF FUSARIUM HEAD BLIGHT (FHB) ON THE WHEAT SUPPLY CHAIN. William W Wilson[1]. [1]University Distinquished Professor and CHS Chair in Risk and Trading, Department of Agribusiness and Applied Economics, North Dakota State University, Fargo, ND 58102
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Fusarium Head Blight (FHB) has led to major economic costs for wheat and barley producers. The purpose of this study was to estimate the economic costs of scab. To do so we developed several economic models, analyzed extensive data and conducted surveys of wheat flour millers, barley maltsters, and grain handlers. The impacts of DON on growers are to increase the probability of DON being excessive, reducing yield and increasing the probability of discounts for excessive DON. Thus, any strategy that reduces DON has the opposite impacts: increasing yield, reducing probability of DON and

associated price discounts. Taken together, DON mitigation strategies have the impact of increasing returns, and reducing risks relative to the technologies not being adopted. The most important direct costs are those related to increased use of fungicide, testing and increased draw areas. While reliance on fungicide is notable, it is risky. The most important indirect costs accrued by the wheat and barley industries were the risk premium paid to induce adoption of DON reducing technologies and the value of yield forgone. The incidence of DON has improved. However, the problems persist and have the implication of adding costs and risks to the supply chain. The impact of these vary through time, and geographically, thus impacting firms differently. There is an indirect cost of reduced production due to DON. The industry accrues an indirect cost of having to pay implicit risk premiums via the market place to induce planting and use of DON reducing technologies. Without these technologies, the cost to the industry would increase substantially.

[S15] GENETIC ANALYSIS OF OVIPOSITION DETERRENCE TO ORANGE WHEAT BLOSSOM MIDGE. Curt A. McCartney[1], Curtis Pozniak[2], Santosh Kumar[3], Andrew Burt[4], Richard Cuthbert[5], Yuefeng Ruan[5], Ian Wise[1,6], Marjorie Smith[1], Stephen Fox[1,7], and Alejandro Costamagna[6]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, R6M 1Y5, Canada; [2]Crop Development Centre, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada; [3]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Brandon, MB, R7A 5Y3, Canada; [4]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, K1A 0C6, Canada; [5]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, Swift Current, SK, S0G 2K0, Canada; [6]Department of Entomology, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada; and [7]DL Seeds Inc., Winnipeg, MB, R6M 1C2, Canada
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Orange wheat blossom midge (OWBM, *Sitodiplosis mosellana* Géhin) is an important insect pest of spring wheat (*Triticum aestivum*) and durum wheat (*Triticum turgidum* var. *durum*) in Canada. OWBM damage reduces both grain yield and grain functional quality. The development of wheat varieties with antibiotic resistance (*Sm1*) or oviposition deterrence to OWBM is an important component of integrated management. We have initiated QTL mapping experiments of oviposition deterrence in four spring wheat populations and one durum wheat population. Results will be presented from the spring wheat cross Superb/BW278. The DH population and checks were evaluated for OWBM kernel damage in six field nurseries over three growing seasons. QTL analysis identified genetic loci for oviposition deterrence on chromosomes 1A and 5A. BW278 contributed oviposition deterrence on chromosome 1A, while Superb contributed oviposition deterrence on chromosome 5A. The 1A QTL was consistent with the major oviposition deterrence QTL previously found in the American variety Reeder. The 5A QTL mapped to the location of awn inhibitor gene *B1*. The additive effects of these QTL explained the improved oviposition deterrence in the Canadian variety Waskada (pedigree: BW278/2*Superb). Candidate genes for the 1A QTL were hypothesized using IWGSC Chinese Spring RefSeq v1.0. The 1A and 5A QTL provide a basis for marker-assisted selection (MAS) of oviposition deterrence to OWBM, which is labour-intensive to assess based upon kernel damage.

[S16] THE RACE AGAINST WHEAT LEAF RUST. Jyoti Saini Sharma[1], Curt McCartney[1], Brent McCallum[1] J. Doležel[2], and Colin Hiebert[1]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 100, Morden, MB R6M 1Y5, Canada; and [2]Institute of Experimental Botany, Centre of the Region Haná for Biotechnological and Agricultural Research, Šlechtitelů 31, CZ-78371 Olomouc, Czech Republic
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The *Aegilops tauschii* Coss (RL5497-1) derived seedling resistance gene *Lr32* confers resistance against wheat leaf rust disease caused by fungal pathogen *Puccinia triticina* Eriks (*Pt*). Our interest is to clone the *Lr32* and develop resources for its future deployment in wheat cultivars. To meet our objectives, two approaches have been adapted: map-based cloning and mutant chromosome sequencing (MutChromSeq). In both approaches plants were phenotypically characterized with *Pt* race MBDS. For map-based cloning, a double haploid population (Thatcher × BW196) was genotyped with 90K wheat single nucleotide polymorphism (SNP) chip, furthermore the *Lr32* region associated 12 SNP's were converted in to Kompetitive allele specific (KASP) polymerase chain reaction (PCR) markers. By

positioning these SNP's on International Wheat Genome Sequencing Consortium (IWGSC) RefSeq v1.0 and *Aegilops tauschii* genome sequence Aet v4.0 chromosome 3D/3, the target genomic region delimited to ~30Mb. This region was fine mapped in an F_2 mapping population (198 plants) with KASP and simple sequence repeats (SSR) markers derived from Aet v4.0. To develop the high-resolution mapping population, 128 recombinants have been selected from 1,440 F_2 plants screened with flanking KASP markers *XKwh142* and *XKwh355*. For MutChromSeq, chromosome 3D was isolated using flow cytometry for five ethyl methane sulfonate (EMS)-derived mutant lines and parents from the mapping population to compare their sequences, which will ultimately identify the candidate gene. Considering that *Lr32* is absent from registered cultivars and is broadly effective against leaf rust, the outcome of current study will contribute to achieving effective resistance.

[S17] WHAT WE HAVE LEARNED ABOUT THE WHEAT STRIPE RUST PATHOGEN IN CANADA?
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Wheat stripe rust is an emerging pest problem in Canada and several epidemics in the past have spurred research on the causal pathogen (*Puccinia striiformis* f. sp. *tritici* - *Pst*) for disease management. To breed for resistance, it is imperative to understand the rust pathogen populations including race dynamics, genetic changes in the races/lineages, and effective resistance genes against prevalent races. Presently, >40 *Pst* races have been characterized from Canada, including six from eastern Canada. The six races from eastern Canada are quite different, in terms of virulence phenotype, from those prevalent in western Canada. Our investigation of the genetic population structure (2009-2013) of the western Canadian *Pst* population using molecular markers and genome re-sequencing, revealed the presence of four divergent lineages with predominantly clonal structure. From a global context, two previously reported lineages were identified: *PstS0* (22%), representing an old Northwestern-European and *PstS1* (35%), an invasive warm-temperature adapted. Additionally, two new, unreported lineages, *PstPr* (9%) and *PstS1*-related (35%), were detected, which produced more telia than other lineages and had double the number of unique recombination events. The *PstPr* was a recent invasion, and likely evolved in a diverse, recombinant population as it was closely related to the *PstS5*, *PstS7*/Warrior, *PstS8*/Kranich, and *PstS9* lineages originating from sexually recombining populations in the centre of diversity. The 2016, the *Pst* population from western Canada belonged to the *PstS1-related* lineage. On the epigenetics side, DNA methylation analysis revealed DNA-methyltransferase1-homologs, providing compelling evidence for epigenetic regulation and as a first report, an average of ~5%, 5 hmC in the *Puccinia* epigenome merits further investigation. This presentation will summarize published and unpublished results from current studies on *Pst* in Canada as well as the future directions we will take.

[S18] *YR15*-MEDIATED RESISTANCE AGAINST STRIPE RUST IN WHEAT: EVIDENCE OF AN HR-INDEPENDENT MECHANISM.
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Stripe rust, caused by the biotrophic fungal pathogen *Puccinia striiformis* f. sp. *tritici* (*Pst*), has been recently emerging as a serious threat to wheat production in new areas in North America. Genetic seedling-resistance against stripe rust is often conditioned by the products of the resistance genes that

detect the pathogen and initiate a cascade of signaling events, culminating in the generation of reactive oxygen species (ROS) and hypersensitive response (HR) that eventually suppress the infection. However, our microscopic and transcriptional analyses of the resistant Avocet+*Yr15* near isogenic line (NIL) suggest that defense response against stripe rust in this particular pathosystem is not mediated through the induction of ROS generation and/or HR. In particular, histochemical analysis of ROS generation, using diaminobenzidine tetrahydrochloride (DAB), produced negative results and did not show any difference between mock- and pathogen-inoculated Avocet+*Yr15* plants at several time points post inoculation (dpi). Similarly, no HR-related gene(s) was detected in our RNA-seq-based differential gene expression analysis of Avocet+*Yr15* plants at 3 dpi. Further microscopic analyses revealed that the infectious mycelia of *Pst* was unable to effectively penetrate through the stomata on the surface of Avocet+*Yr15* during early stages of the interaction (until 7 dpi), whereas successful stomatal penetration was seen in the susceptible Avocet -*YrA* NIL plants. Such observation was also confirmed by the RNA-seq results, detecting genes coding for stress-induced stomatal closure to be highly and strongly upregulated in the resistant NIL. Collectively, we hypothesize that unlike the other known stripe rust seedling resistance genes, the pathogen is suppressed at the penetration stage in Avocet+*Yr15* plants, which leads to an HR-independent resistance response.

[S19] NOVEL FHB CONTROL STRATEGY USING THE VOLATILE TRICHODIENE TO REDUCE MYCOTOXINS. Martha Vaughan[1], Santiago Gutierrez[2], Matthew Bakker[1], Robert Proctor[1], and Susan McCormick[1]. [1]Mycotoxin Prevention & Applied Microbiology, US Department of Agriculture, 1815 N University St, Peoria, IL 61604 USA; and [2] Microbiology Department, University of León, Campus de Ponferrada, Av. de Astorga s/n, 24400 Ponferrada, León, Spain
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Fusarium graminearum, the primary fungal pathogen responsible for Fusarium head blight, reduces crop yield and contaminates grain with trichothecene mycotoxins that are deleterious to plant, human and animal health. The first committed step in trichothecene biosynthesis is the formation of trichodiene. Trichodiene is a volatile compound, which suggests it may be useful in chemical communication. However, little is known about the potential function of trichodiene in regulating trichothecene biosynthesis. Our results indicate that fumigating with trichodiene reduces production of trichothecenes by *F. graminearum*, via downregulating expression of trichothecene biosynthetic genes and boosting host plant defenses. The trichodiene synthase gene was transformed into the previously characterized biocontrol fungus *Trichoderma harzianum*, to create a system for delivery of trichodiene in combination with other biocontrol traits. Wheat plants treated with the transformed biocontrol strain (trichodiene +) develop significantly less disease and accumulate less mycotoxin, compared to plants treated with the wild type biocontrol strain (trichodiene -) or plants that receive no biocontrol treatment.

[S20] DEOXYNIVALENOL REDUCTION IN FUSARIUM INFECTED BARLEY BY DENSITY SORTING. Taryn S. Garew[1] and Rex W. Newkirk[1].[1]Department of Animal and Poultry Science, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8
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Deoxynivalenol (DON) produced by *Fusarium graminearum* is a leading concern for barley producers due to toxicity and reduced grain quality. This trial investigated the ability to separate infected barley, with initial DON concentrations 1.80 to 4.04 ppm, by densities, and if these densities affected DON concentrations. Infected barley was separated into seven fractions with a Fractionating Aspirator at speeds of 40%, 50%, 60%, and 70% of fan capacity. The premise of this separation is grain density and DON concentration share a negative correlation while air speed affects the quantity of grain recovery in fractions, therefore affecting DON concentrations. At 40% air speed, Fractions 1 and 2 combined, 3, 4, 5, 6, and 7 had 0.58, 0.81, 1.96, 4.49, 9.40, and 11.20 ppm DON with 7%, 40%, 41%, 9%, 2%, and 1% of grain recovered in fractions respectively. Whereas at 70% air speed, Fractions 1 and 2 combined, 3, 4, 5, 6, and 7 had 0.76, 0.60, 0.63, 1.47, 3.27, and 4.51 ppm DON with <0%, 3%, 10%, 22%, 28%, and 35% of grain recovered in fractions respectively. This showed that higher air speed resulted in higher DON concentrations in Fractions 6 and 7, whereas lower air speed resulted in higher concentrations in Fractions 5 and 6. However, lower air speed resulted in higher proportions of barley recovered <1 ppm

DON. This experiment supports that barley can be separated into low and high DON fractions with air speed affecting the relative DON concentrations and grain recovery in fractions.

[S21] PARTITIONING OF WHEAT CONTAMINATED WITH DEOXYNIVALENOL FROM LOW TO HIGH CONCENTRATION BY AIR FRACTIONATION. M. E. Taylor[1] and R. W. Newkirk[1]. [1]Department of Animal and Poultry Science, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Dr, Saskatoon SK S7N 5A8
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Fusarium graminearum infection of wheat causes the production of the secondary metabolite deoxynivalenol (DON). As the infection progresses grain density decreases, making it possible to partition the grain. Air classification has been used in flour milling to separate particles into the bran and the endosperm. The objective of this experiment was to determine if this technology could be applied to intact wheat. This study was performed with a 3x2 factorial experimental design with three levels of abrasion using a cement mixer and two windspeeds using a Kharkov ISM 10 CSC Fractionating Aspirator which separated into eight fractions of wheat from low to high DON concentration. The abrasion treatments were non-abraded wheat, self abraded wheat, and abrasion with half in gravel. The airspeeds used were 60%, and 80% of fan capacity. The results for the air fractionated non-abraded wheat indicate that at 60% airspeed, DON levels were reduced from 7-10ppm to 1-2ppm for 35-45% of total material, 70-80% of total material was below 5ppm, and 20-30% of total material was 12-70ppm. At 80% airspeed, 35-50% of total material was reduced to below 3ppm, and 50-65% of material was 7.5-73ppm. Both abrasion types caused increased DON levels in all eight fractions. The results from this experiment indicate that it is possible to partition intact wheat contaminated by DON from low to high concentration. Abrading wheat increases DON levels in all fractions of air fractionated material.

[S22] RISK ASSESSMENT AND MANAGEMENT OF FUSARIUM HEAD BLIGHT: LESSONS LEARNED FROM MORE THAN A DECADE OF RESEARCH. P. A. Paul[1], J. D. Salgado[1], K. Ames[2], G. Bergstrom[3], C. Bradley[2], E. Byamukama[5], J. Cummings[3], M. Chilvers[9], R. Dill-Macky[11], A. Friskop[4], P. Gautam[4], N. Kleczewski[6,7], L. V. Madden[1], M. Nagelkirk[9], J. Ransom[4], K. Ruden[5], S. Wegulo[10], and K. Wise [8]. [1]The Ohio State University/OARDC, Wooster, OH 44691; [2]University of Illinois, Urbana, IL 61801; [3]Cornell University, Ithaca, NY 14853; [4]North Dakota State University, Fargo, ND 58102; [5]South Dakota State University, Brookings, SD 57007; [6]The University of Delaware, Newark, DE 19719; [7]University of Maryland, College Park, MD 20742,[8]Purdue University, West Lafayette, IN 47907; [9]Michigan State University Extension, Sandusky, MI 48471, [10]University of Nebraska-Lincoln, NE 68588; and [11]University of Minnesota, St. Paul, MN 55108.
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For more than a decade, field experiments have been conducted through the U.S. Wheat and Barley Scab Initiative to evaluate the effects of fungicide and host resistance on Fusarium head blight (FHB) and deoxynivalenol (DON) and to generate data to fine-tune risk assessment models for FHB. FHB index and DON data were collected from more than 300 wheat trials across 17 U.S. states and meta-analyzed to quantify: 1) efficacy of different fungicide active ingredients; 2) efficacy, additivity, and stability of integrating host resistance and fungicide application; 3) efficacy and economics of integrating in-field and grain harvesting strategies; 4) relative efficacy of fungicide applications before, at, and after anthesis; 5) the effects of Quinone outside inhibitor (QoI) and demethylation inhibitor (DMI) fungicide combinations; and 6) efficacy and economics of two-treatments fungicide programs. Summary results from these studies will be presented and discussed, with emphasis on the influence of study-specific factors such as wheat market class (winter vs. spring wheat) and baseline levels of FHB on the efficacy of different management programs. I will highlight our recent findings on the effects of QoI, with and without an accompanying DMI, on DON. I will also present preliminary results on a new fungicide, Miravis Ace, and discuss options for its use in combination with Prosaro, Caramba, Proline, or Folicur for FHB and DON management. Finally, I will present an update on the national FHB prediction center and discuss our attempt to develop guidelines for its use as a tool for fungicide application decision-making.

[S23] PRODUCER RESEARCH AND FUNDING OBJECTIVES. Harvey Brooks. General Manager, Saskatchewan Wheat Development Commission, #310 – 111 Research Drive, Saskatoon, SK S7N 3R2
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Historically, producers have been very significant funders of wheat research and varietal development. The high returns available to producer investments in research indicate that more investment should be occurring. The formation of Sask Wheat in 2013 created a new opportunity for producers to be a significant player in funding and directing wheat research activities. Sask Wheat has a strategic focus on three research areas including variety development, agronomy, and post production and looks for collaborative efforts to maximize research efforts. In 2017, Sask Wheat was a founding member of the Canadian Wheat Research Coalition (CWRC), along with Alberta Wheat and the Manitoba Wheat and Barley Growers. The CWRC will facilitate a collaborative approach to producer funding of regional and national wheat research on behalf of producers. The CWRC is the proponent on the current Canadian National Wheat Cluster and is leading discussions for successor programming to the Core Wheat Breeding Agreements producers fund with AAFC and western Universities. Producers continue to have strong support for funding wheat research; however, producer objectives are not always aligned with government and industry funders. Creating a shared vision for future research activities will be key to the success of future research funding initiatives.

[S24] CEREAL VARIETY DEVELOPMENT 2.0 – A BRIGHT FUTURE IN VARIETY INNOVATION. Brent Derkatch. CANTERRA Seeds, 201 – 1475 Chevrier Blvd., Winnipeg, MB R3T 1Y7
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CANTERRA SEEDS was founded in 1996 by 9 pedigreed seed growers in Western Canada. Today the business offers a portfolio of top-quality field crop seed cultivated with local investments in plant breeding, access to a global network of germplasm and traits and a commitment to seed that goes back to its' roots as a grower-owned company. In 2015, CANTERRA SEEDS announced two long-term strategic investments in cereal seed breeding. The first was a 4P model (public, private, producer partnership) together with Agriculture and Agri-Food Canada, the Alberta Wheat Commission and CANTERRA SEEDS to support the Canadian Prairie Spring Red breeding program at AAFC Lethbridge. The second was a new joint venture cereal breeding company together with Limagrain and based out of Saskatoon called Limagrain Cereals Research Canada (LCRC). With the need to foster ongoing investment in innovation in cereal crops, new models are being considered to benefit all stakeholders in the value chain.

[S25] AGRICULTURE & AGRI-FOOD CANADA WHEAT SCIENCE STRATEGY. Felicitas Katepa-Mupondwa. Agriculture & Agri-Food Canada- Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK S7N 0X2 Canada
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Canadian wheat research is experiencing a time of rapid change. Evolving production and market challenges, consumer demand, international competition, technology advancements and regulatory change emphasize the need for a coordinated approach across the sector. Agriculture and Agri-Food Canada (AAFC) Science and Technology Branch (STB) wheat science is well positioned to support the growth of Canada's wheat industry. AAFC is using its science capacity to address key challenges including improving profitability for farmers, mitigating climate change impacts, reducing disease and pest pressures, and integrating new transformative science advancements that are now available or on the horizon. Through greater public sector focus on discovery science, encouraging greater and earlier industry engagement, and continued leveraging of national and international partnerships, AAFC's wheat science program will maximize benefits for the wheat value chain.

[S26] SEED INDUSTRY VALUE CREATION – THE PATH TO INCREASED INVESTMENT IN CEREAL R & D. Todd Hyra SeCan, 94 Woodington Bay, Winnipeg, MB, R3P 1M9
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A brief overview of the 10 year process that brought the seed industry to the decision to support a trailing royalty contract, why the seed industry feels the trailing royalty system is the best alterative for value creation in cereals, and how it could work.

[S27] HYPER IMAGING – A VERSATILE TOOL FOR FUSARIUM CELL BIOLOGY. Lewin Günther[1], Michael Mentges[1], Wilhelm Schäfer[1], and Jörg Bormann[1,2]. [1] Dept. of Molecular Phytopathology, Institute for Plant Science and Microbiology, University Hamburg, Hamburg, Germany; and [2] Dept. of Molecular Phytopathology and Cell Biology, University Bremen, Bremen, Germany
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Reactive oxygen species (ROS) are integral components of every aerobic cell's metabolism and are formed as by-products of oxygen-based cellular reactions. While being harmful to the cell structure when accumulating, ROS are also necessary for cellular functions serving as an important second messenger mediating cellular differentiations. In particular, they are essential elements in plant-pathogen interactions, such as fungal infection processes. A combined reverse genetics and fluorescence ratiometry approach was applied to gain further insights into the role of ROS and specific ROS-related enzymes. In total 26 ROS-related enzymes were functionally characterized for their role in virulence, vegetative growth, ROS-sensitivity, ROS-accumulation, and fertility. A relatively low incidence of adverse phenotypes indicates a high resilience of *F. graminearum* against disruptions of its ROS-metabolism. It seems that the ROS-equilibrium which the fungus seeks to maintain during infection is a highly secured system, fortified by a large array of enzymes with redundant function. To visualize ROS-fluctuations in vivo ratiometric ROS-measurements were performed using the genetically encoded H_2O_2 reporter HyPer. HyPer had been expressed in the cytosol of *F. graminearum* (cytHyPer) and anchored to internal membranes by a GPI-anchor. Organelle-specific staining revealed that this modified HyPer (GPI-HyPer) predominantly attaches to the endoplasmic reticulum (ER) and mitochondria. These two reporters enable both global and organelle-specific redox-detections using fluorometry and live-cell imaging.

[S28] FUNTAP: A *FUSARIUM GRAMINEARUM* PROTEIN-PROTEIN INTERACTION NETWORK TO STUDY DEOXYNIVALENOL BIOSYNTHESIS PATHWAYS. Gopal Subramaniam, Ottawa Research and Development Centre – Agriculture Canada
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Protein interaction networks provide insights into complex biological pathways within organisms. These networks help identify proteins that belong to a distinct functional group and establish relationship between the groups. *F. graminearum* is an agriculturally important pathogen infecting wheat and other cereal crops. The infection process requires the production of harmful mycotoxins such as deoxynivalenol (DON). To study the signalling pathways leading to biosynthesis of DON in *F. graminearum,* we constructed the Fusarium Network of Trichothecene Associated Proteins (FuNTAP) based on yeast two-hybrid interactions of proteins potentially involved in DON biosynthesis. The FuNTAP network identified both novel and critical proteins regulating the biosynthesis of DON. The network also provides a base to interrogate gene expression profiles and other regulatory networks that could be used to construct a comprehensive DON metabolic network.

[S29] RESPONSE OF INDIGENOUS FIELD POPULATIONS OF *FUSARIUM GRAMINEARUM* TO FUNGICIDE APPLICATION IN MANITOBA. S. Allen[1, 2], H. Derksen[3], M. Sachs[1, 2], A. Brûlé-Babel[1], and T. Gräfenhan[2]. [1]Department of Plant Science, 222 Agriculture Building, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2; [2]Canadian Grain Commission, 196 Innovation Drive, Winnipeg, MB, Canada, R3T 6C5; and [3] Manitoba Agriculture, 65 3rd Ave NE, Carman, MB, Canada, R0G 0J0
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Fusarium Head Blight (FHB) is an important disease of wheat in Canada. The disease causes direct yield loss and downgrading of grain due the presence of infected kernels and mycotoxins. Application of synthetic

fungicides is part of an integrated pest management strategy; however field efficacies have been variable. The main causal agent of FHB in Canada is *Fusarium graminearum*. This species has multiple characteristics that can drive rapid adaption to the environment. High genetic diversity has been demonstrated in field populations, supporting the species' ability to adapt its phenotype. The high genetic diversity of *F. graminearum* may be a contributing factor in the observed variation in fungicide efficacy. This study aimed to assess the response of indigenous field populations *of F. graminearum* on spring wheat to fungicide application in southern Manitoba. Field trials at two farm locations with four replicated plots of untreated control and fungicide treatments at recommended and late timings were sampled for infected wheat spikes in 2017. An Amplified Fragment Length Polymorphism (AFLP) approach was used to assess the genetic response of *F. graminearum* field populations to fungicide treatment. Fungicide treatment was not a significant source of genetic variation, however, minor genetic variation among fungicide treatments was observed for isolates with the 15-acetyldeoxynivalenol trichothecene chemotype. The genetic data will be complemented with *in vitro* fungicide sensitivity testing. This research will provide an increased understanding of the within-field variability of *F. graminearum* and the field population response to fungicide application.

[S30] THE ROLE OF THE *FUSARIUM GRAMINEARUM* STE2P RECEPTOR IN THE PATHOGENIC INFECTION OF WHEAT. Pooja Sridhar[1], Daria Trofimova[1], Chris Bonner[2], Dianevys González Peña-Fundora[3], Nora A. Foroud[3], Gopal Subramaniam[2], John Allingham[1], and Michele Loewen[1,4]. [1]Department of Biomedical and Molecular Sciences, Queen's University, 18 Stuart Street, Kingston, ON, Canada, K7L 3N6; [2] Agriculture and AgriFood Canada, 960 Carling Ave, Ottawa, ON, Canada K1A 0C6; [3] Agriculture and AgriFood Canada, 5403 - 1st Avenue South, Lethbridge, AB, Canada T1J 4B1; and [4]National Research Council of Canada, 100 Sussex Drive, Ottawa, Canada, K1A 0R6
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Fusarium Head Blight (FHB) of wheat, caused by *Fusarium graminearum*, leads to decreased grain quality and deposition of harmful mycotoxins. Although there are potential methods of control, none are completely effective, indicating a need for novel approaches and targets for fungal inhibition. It is currently not known what directs the growth of *F. graminearum* to penetrate and infect wheat cells. Recent studies on a related *Fusarium* species demonstrated that catalytic activity of a plant-secreted peroxidase directs the growth (chemotropism) of the fungus towards its host. The chemotropism is mediated by the Ste2p receptor, a pheromone-sensing receptor in fungi. In the present work, we were interested to know if a similar chemotropism mechanism, mediated through Ste2p, is present in *F. graminearum*. By adapting a previously developed chemotropism assay, various stimulants were tested against *F. graminearum,* showing that compounds, including wheat head exudate, induced positive chemotropism in the wild-type strain. Using mass spectrometry and activity assays, the presence of active wheat peroxidases in the exudate was confirmed. Treatment of the wheat exudate with a peroxidase-specific inhibitor resulted in the elimination of chemotropic response, indicating that chemotropism requires a catalytically active peroxidase. Knockout of *ste2* through homologous recombination abolished chemotropism. Thus, Ste2p mediates chemotropic response of *F. graminearum* towards the wheat head in response to the action of a catalytically active peroxidase. Ongoing work includes evaluation the role of MAPK Mgv1 and studies related to mechanism of receptor stimulation.

[S31] CHARACTERIZATION OF THREE CYSTEINE-RICH PROTEINS FROM THE SECRETOME OF *FUSARIUM GRAMINEARUM.* Anas Eranthodi[1,4], Rajagopal Subramaniam[2], Christof Rampitsch[3], Therese Ouellet[2], Kristina Shostak[2], Dianevys González-Peña Fundora[1,5], Elizabeth A. Schultz[4], and Nora A. Foroud[1]. [1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403-1st Avenue South, Lethbridge, AB, Canada, T1J 4B1; [2]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6; [3]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100 Morden, MB, Canada, R6M 1Y5; [4]Department of Biological Sciences, University of Lethbridge, 4401 University Dr W, Lethbridge, AB, Canada, T1K 6T5; and [5]Department of Chemistry & Biochemistry, University of Lethbridge, 4401 University Dr W, Lethbridge, AB, Canada, T1K 6T5
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During infection of its host, *Fusarium graminearum* secretes small cysteine-rich proteins. Cysteine-rich proteins of fungi have been shown to have roles in pathogenicity in plant-pathogen interactions. This study was undertaken to elucidate the role of three cysteine-rich proteins from the secretome of *F. graminearum* in fungal growth and host infection: cerato-platanin (CP; FGSG_10212) and two common in fungal extracellular membrane (CFEM) domain-containing proteins (CFEM1; FGSG_02077 and CFEM2; FGSG_08554). Targeted deletion (KO) and *in locus* overexpression (OX) of these genes in *F. graminearum* were achieved through homologous recombination. When tested for mycelial growth and spore germination, the CP and CFEM transformants grew similarly to the wild-type (WT), except for CFEM1-OX which germinated faster. The transformants also showed similar sensitivity as the WT to various stress agents targeting the cell wall and membranes. CP-OX produced more DON in axenic cultures and also caused higher initial infection in different wheat lines. However, disease spread caused by CP-OX did not differ from the WT. Meanwhile, no differences were observed in the CP-KO strain. CFEM1-OX produced less DON in culture and showed increased disease spread only in a moderately susceptible wheat line, 'Penhold'. It has not yet been determined whether DON accumulation observed in axenic cultures is reflected *in planta*; however, gene expression analysis indicates that trichothecene biosynthesis genes are up-regulated in CP-OX inoculated wheat and down-regulated in CP-KO inoculated wheat. To provide some insights into how CP and CFEM proteins interact with the host, subcellular localization and protein interaction studies in wheat are underway.

[S32] *FUSARIUM* AND THE FUTURE. Keith A Seifert[1]. [1] Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Our understanding of the biology, genetics, chemistry and taxonomy of *Fusarium* has changed significantly over the past thirty years as DNA-based methods and microcomputer-based technologies swept across science. How has this changed the situation for researchers, regulators, farmers, and other parts of the sector? Instead of one disease caused by one fungus, *Fusarium graminearum*, we now have a suite of diseases caused by a complex of closely related but genetically distinct species. Instead of contamination by one mycotoxin, deoxynivalenol, we have isomers, additional trichothecenes, and other non-trichothecene toxins, some produced by other species such as *Fusarium avenaceum*. Studies of population genetics and gene flow reveal the significance of hybrids among species, genetic phenomena such as chemotypes that seem to cross species boundaries, and the potential significance of transferable non-chromosomal elements, all affecting pathogenicity and toxin production. Microgenomic studies reveal the full microbial diversity of plant/soil systems, completely altering the traditional one plant/one pathogen view; they also open a new window on species diversity. How many species of *Fusarium* are there in the world, anyway? This seems overwhelming, but perhaps we are entering a time when our abilities to understand the fine details and complexities of Fusarium head blight will allow more direct and efficient detection of and response to the most significant factors. There are many analogies in medical diagnostics and treatments. Continuing technological developments will remove taxonomic uncertainty from the decision chain and allow all concerned parties to focus on the most important variables affecting crop and public health.

[S33] APPLYING GENOMICS TO CHARACTERIZE AND IMPROVE FUSARIUM HEAD BLIGHT RESISTANCE IN DURUM WHEAT. Ehsan Sari[1,2], Wentao Zhang[1], Peng Gao[1], Kerry Boyle[1], Adrian Cabral[1], David Konkin[1], Maria Antonia Henriquez[3], Andrew Burt[4], Santosh Kumar[4], Randy Kutcher[5], Curtis J. Pozniak[5], Yuefeng Ruan[2], Ron Knox[2], and Pierre R. Fobert[6]. [1] Aquatic and Crop Resource Development Research Centre Canada, National Research Council, 110 Gymnasium Place, Saskatoon, SK, Canada, S7N 0W9; [2] Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road, Swift Current, SK, Canada, S9H 3X2; [3] Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, Canada, R6M 1Y5; [4] Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB, Canada, R7A 5Y3; [5] Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8; and [6] Aquatic and Crop Resource Development Research Centre, National Research Council Canada, 100 Sussex Drive, Ottawa, ON, K1N 5A2
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Canada Western Amber Durum is the second largest class of wheat grown in Canada, supplying more than a third of the world's total exported durum. It is considered the most susceptible wheat to Fusarium Head Blight (FHB) with few effective resistance genes available to durum wheat breeders. Accordingly, the spread of FHB into durum growing areas of the Canadian prairies has created a serious problem for the industry, responsible for the downgrading of a significant amount of the crop and millions of dollars in lost revenue in 2016 alone. To address the challenge of developing of new durum cultivars with desirable FHB resistance, several new initiatives have been launched that exploit modern genetic and genomics approaches. This presentation will highlight recent advances by our group in the following areas: (1) Exploiting known FHB resistance genes, including the fine-mapping of the large genetic intervals underlying priority FHB resistance quantitative trait loci (QTL), the development of new genomics sequence resources, and haplotyping to identify more predictive SNPs as candidates for marker-assisted selection (MAS); (2) Investigating the genetic basis of FHB resistance available in breeding programs, including Genome-Wide Association Studies (GWAS) and Nested Association Mapping (NAM) in breeder assembled panels; and (3) Screening of non-adapted tetraploid wheats as new sources of effective FHB resistance.

[S34] WHOLE GENOME SEQUENCES OF DURUM WHEAT BRING A NEW ERA FOR GENE DISCOVERY AND BREEDING. Sean Walkowiak[1], Ron Knox[2], Ruan Yuefeng[2], Ehsan Sari[3], Pierre Fobert[3], Richard Cuthbert[2], Andrew Sharpe[4], Brook Byrns[1], Jennifer Ens[1], Kirby Nilsen[1], Luigi Cattivelli[5], and Curtis Pozniak[1]. [1]Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8; [2]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, Swift Current, SK, Canada, S9H 3X2; [3]National Research Council, 110 Gymnasium Place, Saskatoon, SK, Canada, S7N 0W9; [4]Global Institute for Food Security, University of Saskatchewan, 110 Gymnasium Place, Saskatoon, SK, Canada, S7N 0W9; and [5]CREA Research Centre for Genomics and Bioinformatics, 302 San Protaso, Fiorenzuola d'Arda, Italy, 29017
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Due to its size and complexity, wheat is one of the last staple food crops to have its genome sequenced. With the recent completion of whole genome sequences for both tetraploid (durum) and hexaploid (bread) wheat, we now have new resources at our fingertips to refine genetic intervals and identify candidate genes for traits of interest. This will not only generate improved markers for breeding, but also help uncover the underlying mechanisms behind key traits needed by Canadian growers. As a result, breeders will be able to make more informed breeding decisions, which will accelerate cultivar development. Unfortunately, the wheat lines whose genome sequences are currently available do not carry some of the alleles of interest to Canadian breeders; therefore, additional genomic resources are required. In our wheat breeding programs at the University of Saskatchewan, we are using the latest sequencing and assembly technologies to generate several whole genome assemblies for both bread and durum wheat, with the goal to uncover the genetic cause of important traits in wheat.

[S35] IDENTIFICATION OF CANDIDATE GENES CONFERRING STEM-SOLIDNESS IN DURUM WHEAT. Kirby Nilsen[1], Sean Walkowiak[1], Daoquan Xiang[2], Teagen D. Quilichini[2], Peng Gao[2], Ian Willick[1], Krystalee Wiebe[1], Jenn Enns[1], Amidou N'Diaye[1], Raju Datla[2], and Curtis Pozniak[1]. [1]Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8; and [2]National Research Council Canada, 110 Gymnasium Place, Saskatoon, SK, Canada, S7N 0W9
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The most effective way to reduce losses caused by the wheat stem sawfly (WSS; *Cephus cinctus* Norton (Hymenoptera: Cephidae) is to grow resistant cultivars that express the solid-stem phenotype. The goal of this research was to identify candidate gene(s) conferring stem-solidness. Towards this, we previously localized a major QTL (LOD = 127, R^2 = 92 %) for stem-solidness, *SSt1,* to chromosome 3BL using a durum mapping population derived from a cross between Kofa and W9262-260D3. The physical interval of *SSt1* in the durum reference sequence (cv. Svevo) spans 2.5 Mb and contains 56 predicted high-confidence genes. To gain insights into any differential gene activity associated with this genomic region, RNA-Seq was performed on a panel of six durum cultivars with varying levels of stem-solidness, including a loss-of-function (hollow-stemmed) mutant line, "Pithless-1", that was generated via EMS mutagenesis of the solid-stemmed cultivar CDC Fortitude. This work identified 31 genes that were expressed within the *SSt1* interval, of which eight were differentially expressed between CDC Fortitude and Pithless-1. Among these, a gene (*TRITD3Bv1G280530*) encoding a putative Dof (DNA-binding with one finger) transcription factor was differentially expressed between contrasting stem types in the RNA-Seq panel. Whole genome sequencing revealed that CDC Fortitude carries multiple copies of *TRITD3Bv1G280530*, whereas the entire gene is deleted in Pithless-1. Copy number variation at *TRITD3Bv1G280530* was investigated using a qPCR assay in a diversity panel of 96 durum cultivars, which showed increased copy number was associated with stem-solidness. The key findings from these studies directly contributed to the development of *SSt1* specific molecular markers that are currently being used in our breeding programs to select for stem-solidness.

[S36] UNIQUE SOURCES OF RESISTANCE TO FUSARIUM HEAD BLIGHT FOR DURUM WHEAT. George Fedak[1], Dawn Chi[1], Danielle Wolfe[1], Sylvie Cloutier[1], Allen Xue[1], and Lianquan Zhang[2]. [1] Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6; and [2]Triticeae Research Institute, Sichuan Agricultural University
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There was a major epidemic of FMB in the durum wheat crop in Canada in 2016. There is not as much variability for FHB resistance in the primary gene pool of *T. durum* as there is in bread wheat.
In a recent screening of synthetic hexaploids and their parents for FHB resistance by point inoculation, a number of *T. dicoccon* accessions appeared to have enhance levels of FHB resistance. The floret infection frequencies ranged from 10-12 % while the values for Langdon durum were 73%. These inoculations were repeated for a second time with similar results. The *T. dicoccon* accessions were accessed from various gene banks. Records indicate that some of these accessions were collected in Russia and Georgia in the 1930s by N. I. Vavilov and deposited in the genebanks. As would be expected from *T. dicoccon* accessions collected in the wild, some are deficient in useful agronomic traits. For example some are very tall and others have smaller spikes. However, such traits could easily be removed by a few backcrosses so as to minimize any linked drag. On the other hand other accessions had very large seeds, a trait that could be an asset to a breeding program. Another potential source of FHB resistance for durum wheat is that found in amphiploid *Triticum durum* x *Hordeum chilense* with the genomes AABBHH. This source of resistance will be more difficult to integrate into durum wheat.

[S37] IDENTIFICATION OF POLYMORPHIC FHB-RESISTANCE GENES TO DEVELOP CISGENIC WHEAT CULTIVAR PASTEUR BASED ON GENOME EDITING. Ajjamada Kushalappa, Russiachand Heikham, and Nancy Soni. Plant Science Department, McGill University, Ste.-Anne-de-Bellevue, QC, Canada H9X 3V9
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Resistance in plants against biotic stress is mainly due to complex metabolites that are deposited to reinforce the cell wall to contain the pathogen to the initial infection area. Based on metabolo-transcriptomics, *Fusarium* head blight (FHB) resistance QTLs (Fhb1, Fhb2, Fhb5, 2DL), breeding source genotypes and susceptible wheat cultivars, several R genes were identified and their resistance functions were proved by silencing the R genes in resistant genotypes. Based on this, a novel concept was developed stating disease resistance is due to hierarchies of metabolite/protein biosynthetic and regulatory genes. Even to produce a single resistance metabolite/protein, several linked genes are needed, meaning, these QTLs or R genes are not independent in conferring resistance. Phenylpropanoid and fatty acid pathway metabolite biosynthetic and regulatory R genes play a significant role in FHB resistance. Some of these genes are polymorphic in Pasteur and other susceptible cultivars, rendering them unable to biosynthesize these metabolites. Replacement of these mutated gene segments in an intermediate susceptible cultivar, such as Pasteur, with functional gene segments from resistant sources, using CRISPR-Cas9 and geminivirus vectors can enable these genes to biosynthesize these metabolites, thereby, improving the ability of Pasteur to resist FHB. Simultaneously several mutated R-genes (r) can be edited in different Pasteur plants and subsequently those genes can be pyramided into one cisgenic Pasteur using marker assisted breeding. Replacement of 4-8 most effective genes should confer high FHB resistance. It is expected that these metabolite R-genes should confer resistance to multiple diseases. This new Plant Breeding Technology once standardised can be used to improve thousands of cultivars around the world.

[S38] TRANSCRIPTOMIC ANALYSIS UNVEILS GENE NETWORKS ASSOCIATED WITH THE FUSARIUM HEAD BLIGHT RESISTANCE TRANSFERRED FROM *TRITICUM TURGIDUM* SSP. *CARTHLICUM* INTO DURUM WHEAT. Ehsan Sari[1], Adrian L. Cabral[1], Brittaney Polley[1], Yifang Tan[1], David J. Konkin[1], Emma Hsueh[1], Ron E. Knox[2], Yuefeng Ruan[2], and P.R. Fobert[1]. [1]Aquatic and Crop Resource Development Research Centre Canada, National Research Council, 110 Gymnasium Place, Saskatoon, SK, Canada, S7N 0W9; and [2]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road, Swift Current, SK, Canada, S9H 3X2
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Fusarium head blight (FHB) resistance in durum wheat gene pool is rare. *Triticum turgidum* ssp. *carthlicum* cv. Blackbird is a relative of durum wheat that offers partial FHB resistance. The objective of this study was to identify candidate regulatory resistance genes of cv. Blackbird and determine the co-localization of these genes with QTL previously identified from a population of cv. Strongfield × Blackbird. Transcriptome analysis was conducted on FHB challenged and unchallenged spikes of Blackbird, durum wheat cv. Strongfield and two doubled haploid transgressive lines derived from Strongfield × Blackbird population. Weighted Gene Network Analysis identified seven gene networks associated with the resistance to FHB spread (Type II FHB resistance) with some showing moderate to high correlation with the plant height and relative maturity traits. Two gene networks showed subtle differences between inoculated and mock inoculated plants, supporting their involvement in basal defense. The candidate regulatory genes were involved in various layers of plant defense mainly including pathogen recognition. Signaling pathways included the abscisic acid and mitogen activated protein (MAP) kinase. Activated downstream defense gene were transcription factors mostly with dual role in defense and development, and regulators of cell death and cell wall reinforcement. The expression of five candidate genes measured by quantitative real-time PCR was correlated with that of RNA-seq, corroborating the technical and analytical accuracy of RNA-seq analysis. Candidate hub genes were identified within the interval of seven reported resistance QTL and the SNP markers associated with them are available for future high resolution mapping studies.

[S39] A GENOME-WIDE ASSOCIATION STUDY OF FUSARIUM HEAD BLIGHT RESISTANCE IN WINTER WHEAT. Harwinder Singh Sidhu[1], Mitra Serajazari[1], Mina Kaviani[1], Curtis Pozniak[2], Matthew Hayden[3], and Alireza Navabi[1]. [1]University of Guelph, Guelph, ON, Canada; [2]Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada; and [3]Agriculture Victoria Research, AgriBio, La Trobe University, Melbourne, Australia
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Fusarium head blight (FHB) caused by *Fusarium graminearum* is one of the most detrimental diseases of wheat (*Triticum aestivum* L.) and has been responsible for significant economic losses. Inadequate disease control strategies render breeding for FHB resistant wheat varieties as a favorable approach. This research aims to identify FHB response associated genomic regions in a Canadian Winter Wheat Diversity Panel (CWWDP; n=450. CWWDP was genotyped using Illumina iSelect wheat 90K SNP beadchip, from which 20K polymorphic markers were used for various analyses. The diversity panel was phenotyped at FHB nursery near Elora, Ontario in 2017 and 2018. After correcting for population structure, genome-wide association studies identified regions associated with FHB incidence on chromosomes 6B, and 7A, with FHB severity on 1A, 2B, and 5A, with FHB Index on 1A, 5A, and 7A, with Fusarium damaged kernels on 1A, and 5B, and with Deoxynivalenol content 1A, and 3A. Genotypes with specific allele combinations across all associated loci showed significant differences for FHB severity and FHB Index. This research enhances the understanding of FHB response in Winter wheat and contributes to breeding for FHB resistance.

[S40] THE COMPLEXITY OF *FHB1*, IS IT A GENE OR A GENE CLUSTER? Yuanfeng Hao[1], Zhanwang Zhu[1,2], Chunbao Gao[2], Shunhe Cheng[3], Xianchun Xia[1], and Zhonghu He[1,4]. [1]Institute of Crop Sciences, Chinese Academy of Agricultural Sciences (CAAS), 12 Zhongguancun South Street, Beijing 100081, China; [2]Institute of Food Crops, Hubei Academy of Agricultural Sciences, 3 Nanhu Street, Wuhan 430064, China; [3]Institute of Agricultural Sciences of Lixiahe District in Jiangsu Province, 568 Yangtze North Street, Yangzhou 225007, China; and [4]CIMMYT-China Office, c/o CAAS, 12 Zhongguancun South Street, Beijing 100081, China
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Enhancing resistance to *Fusarium* head blight (FHB) has become one of the most important breeding objectives in major wheat-growing regions in China. The prominent locus *Fhb1*, conferring stable FHB resistance with the largest effect, represents the major source of resistance. Haplotype analysis of *PFT* (pore-forming toxin-like), *HC* (HCBT-like defense response protein) and *His* (histidine-rich calcium-binding protein) genes in the target *Fhb1* region on an association panel of 240 wheat cultivars revealed that a combination of *PFT-I* and *His-I* corresponded to the resistant haplotype as opposed to the previously proposed *PFT-I* alone. A number of cultivars with *PFT-I* supposed to be resistant to FHB were not, raising concern about *PFT* as being the sole candidate gene for *Fhb1*. Accumulated evidence indicated that both *PFT* and *His* could be the candidates, perhaps working with other genes to confer the *Fhb1* phenotype. Pedigree information and diagnostic markers developed in this study revealed that *Fhb1* in Chinese wheat was mainly derived from Sumai 3 and Ningmai 9, in which Ningmai 9 was the major donor. In addition to the very low frequency of *Fhb1* in the wheat association panel, five more QTL on 1AS, 2DL, 5AS, 5AL and 7DS were stably identified and explained about 30% of the total phenotypic variation. The resistant lines and molecular markers characterized in the current study will provide important resources for advancing the breeding progress for FHB resistance through marker-assisted recurrent selection or pyramiding of favorable QTL or genes.

[S41] MYTHS AND REALITIES INVOLVING GRAIN FOOD CONSUMPTION: WHAT DOES THE SCIENTIFIC EVIDENCE SAY? Yanni Papanikolaou[1] and Victor L. Fulgoni[2]. [1]Nutritional Strategies Inc., Nutrition Science Research & Regulatory Affairs, 59 Marriott Place, Paris, ON N3L0A3 Canada; and [2]Nutrition Impact LLC. Nutrition Science Research, 9725 D Drive North, Battle Creek, MI, 49014, USA
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Current and previous dietary guidelines routinely identify a healthy dietary pattern to include higher consumption of whole grains, with limited consumption of refined/enriched grains. Concurrently, many children and adults worldwide have low intakes of select food groups that are key contributors to under

consumed nutrients, including vegetables, fruits, whole grains, and dairy products, while intake of added sugar, total and saturated fat remain higher than recommended. A variety of grain-based food products, of which include refined/enriched grains, are sources for several shortfall nutrients identified by the 2015 US Dietary Guidelines for Americans, including dietary fiber, folate, iron, and magnesium. The aim of the current session will provide an overview of current and emerging research on grain-based food consumption and identify whether whole and refined/enriched grains can be part of a healthy dietary pattern in all ages. All evidence presented will consider research in children and adults using data from the National Health and Nutrition Examination Survey. The session will further examine sources of energy and nutrients from all grain foods and by sub-categories of grain foods (i.e., breads, rolls, tortillas, ready-to-eat cereals) and address prevalent myths and realities linked to grain food consumption.

[S42] PLANT BREEDING INNOVATION: WILL THE BENEFITS OF HEALTHIER WHEAT DRIVE MARKET ACCEPTANCE? Krista Thomas[1]. [1]Canada Grains Council, PO Box 53163 Rideau Centre RO Ottawa, ON, K1N1C5
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Genome editing systems like TALEN and CRISPR-Cas9 are being used around the world to develop new varieties of wheat in less time and with more precision than conventional breeding methods. Consumer-focussed and healthier traits feature prominently among the breeding objectives being pursued. High-fibre, disease-resistant, or reduced-gluten wheat will offer tangible benefits to consumers and potentially new opportunities to add value for growers, millers and food companies. In order to realize these benefits, Canada must cultivate a regulatory environment that encourages innovation. At the same time, market access issues are among the most significant challenges facing Canada's grain sector, and many questions remain about consumer acceptance and the global regulatory landscape for plant breeding innovation. Against this backdrop, what are the opportunities for the Canadian grain sector and what must we do to ensure Canadians have access to healthier food, growers have access to innovation and Canada remains a trusted, competitive and reliable supplier of safe, sustainable, high-quality grain?

[S43] LIFE'S SIMPLE INGREDIENT: GROWING THE CANADIAN WHEAT BRAND. Victoria Decker[1]. [1]Alberta Wheat Commission, 6815 - 8 Street NE Calgary, AB T2E 7H7
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Life's Simple Ingredient (LSI) is a consumer campaign that aims to unlock the existing affinity for Canadian wheat with the goal of increasing consumption and promoting the Canadian wheat brand. The concept for LSI is driven by market research trends that revealed that when consumers think of wheat, "health" is top of mind. Primarily, they associate wheat with positivity when it comes to health with the three top word associations including "healthy", "wholesome" and "nutritious". But the wheat industry still faces risk: despite positive perceptions related to health, wheat consumption is declining. LSI aims to leverage existing positivity to wheat to ensure consumption moves in an upward trend.
LSI was initially launched as an Alberta-based pilot project. With metrics that prove the concept, the long-term goal is to develop partnerships and foster a national presence that brands Canadian wheat and drives consumption. In doing so, the next major step is to build a science-based delivery model. How will we do this? Our first steps are to undergo a gap analysis to determine the information needed. We aim to gather research-based evidence to help us in our promotion of wheat as a healthy ingredient. This could include questions such as, what are the gaps in knowledge from the nutrition industry? What qualities resonate with customers? In-turn, the idea is to start a research call that could help drive scientific knowledge related to wheat and its health and nutritional benefits.

[S44] DEVELOPING NOVEL METHODS TO ASSESS THE FOOD SAFETY AND NUTRITIONAL ATTRIBUTES OF WHEAT PRODUCTS. Nancy Ames and Sijo Joseph Thandapilly. Agriculture and Agri-Food Canada, Richardson Centre for Functional Foods and Nutraceuticals, Winnipeg MB
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Canadian wheat is an important staple food and is world renowned for high milling and baking quality. Recent wheat quantity research at Agriculture and Agri-Food Canada has been directed towards ensuring safety and improving nutritional attributes while maintaining traditional quality. This presentation will

discuss current issues related to grain safety including free asparagine (a precursor to acrylamide) content in Canadian wheat and how genotype and growing environment affect the free asparagine levels. Also presented will be new methods to assess the nutritional quality of wheat that are being developed to support breeding programs. These include *in vitro* systems such as cell culture, static and dynamic models to predict human carbohydrate and protein digestibility as well as bioavailability of other wheat-derived bioactive components. New information gained from these techniques can be used to breed for superior quality wheat that meets specific needs of processors and consumers seeking foods with improved nutrition and safety.

[S45] EXPLOITING SPACE TECHNOLOGIES: WHAT SATELLITES CAN TELL US ABOUT CROP DEVELOPMENT. Heather McNairn[1]. [1]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Satellites orbit about 800 kilometres above the Earth and give a unique perspective on the state and changing conditions of both crops and soils. Canada is a world leader in a specific class of satellites, synthetic aperture radars (SARs). Early in 2019, Canada will have access to data from their newly launched constellation of SARs, the RADARSAT-Constellation. Agriculture and Agri-Food Canada (AAFC) has invested in science innovation to develop methods that take image data from SARs and model information on both soils (tillage practices and soil moisture) and crops (type, condition and growth stage). In a currently funded research project, AAFC scientists have integrated data from various geospatial sources, including space-based data, within a prototype webtool that can help the sector understand disease risk. This prototype integrates data to assess risk of Sclerotinia in canola, but the framework would be adapted to monitor risk factors for other diseases. This presentation will give a brief overview of research in this field, and then describe in more detail the work that led to the development of this risk tool.

[S46] REMOTE SENSING: DRONES – APPLICATIONS IN PLANT BREEDING AGRONOMIC RESEARCH AND PRECISION AGRICULTURE. Steve Shirtliffe[1], Hema Duddu, Kevin Stanley, and Ian Stavness. [1]University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8
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Utilizing remotely gathered imagery using drones has become one of the most dynamic areas in potential to revolutionize plant breeding and agronomy. For plant breeding and genomics, phenomics seeks to quantify plant phenotypes and associate these with regions of the genome. UAV based field imagery also has great potential to associate imagery based phenotypes in agronomic research as agronomic plots are well ground truthed. This ground truth data can allow the quantitation and calibration of a crops response to agronomic inputs. We will present several examples of current research utilizing remotely gathered imagery including crop response to nitrogen fertilizer, stripe rust detection, herbicide tolerance, stay-green, spike detection and plant spatial arrangement. We utilized this imagery with a variety of techniques ranging from vegetation index analysis, classic image analysis plant detection for emergence in crops, accessing herbicide damage and deep learning with convolutional neural networks. We will also explore the methodology of gathering imagery and discuss the opportunities for utilizing imagery for site-specific agriculture.

[S47] HISTORY OF FHB RESEARCH IN WESTERN CANADA. Andy Tekauz, AAFC Cereal Research Centre, Winnipeg, MB (Retired).
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Dr. Tekauz will present a brief history of research on Fusarium Head Blight in Western Canada, from the mid 1980's to the present.

Abstracts for CWS Poster Presentations

[P1] SCREENING FOR GENOTYPES IN HARD RED SPRING WHEAT THAT EXHIBIT AUXIN-INDUCED INCREASES IN GRAIN YIELD WHEN EXPOSED TO HEAT STRESS DURING FLOWERING. G.L.D.N. Abeysingha, J.A.Ozga, D. Spaner, and D.M. Reinecke. Plant Biosystems Group, Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5
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Auxins are a class of plant growth hormones that are involved in regulating reproductive organ development in flowering plants. A one- time foliar auxin application at the beginning of reproductive phase of wheat has the ability to increase the grain set and weight under normal or heat stressed conditions. Previous studies from our lab suggest that plant genotype is a critical factor that contributes to auxin-induced reproductive growth-enhancement in wheat cultivars. In order to identify auxin-sensitive genotypes in wheat, we are screening a recombinant inbred (RI) population (163 RI lines) derived from parental lines that segregate for auxin-responsiveness under heat stress for grain yield. Hormone treatments (4-Cl-IAA, 10^{-6} M in an adjuvant or adjuvant only control solution) were applied at an early reproductive stage (BBCH 41-45) and responses were tested under non-stress and heat stress conditions. In a growth chamber environment, heat stress reduced the grain number and grain weight per spike in both parents ('Attila' and 'CDC Go'). 4-Cl-IAA application prior to the heat treatment improved grain set and yield in 'Attila', but not in 'CDC Go'. We are currently determining if specific gene markers within the RIL population are associated with heat stress and auxin effects on grain yield.

[P2] PROTEOGENOMIC SIGNATURES OF PRE-HARVEST SPROUTING RESISTANCE IN WHEAT. Natalia V. Bykova[1], Mark Jordan[1], Nataša Radovanovic[1], Michelle Rampitsch[1], Junjie Hu-Skrzenta[1,2], and Mei Huang[1]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, Canada, R6M 1Y5; and [2]Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8
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Dormancy-associated proteogenomic signatures were identified using white and red seeded hard spring wheat (*Triticum aestivum* L.) DH populations SC8021-V2/AC Karma and RL4452/'AC Domain', 8-plex iTRAQ-based quantitative proteomics, customized EST database, and association with QTL regions. In white seeded population over 6800 proteins were identified with high confidence, of which 62 and 115 proteins showed significant differential expression in dormant phenotypes, and 368 and 1041 unique proteins were dormancy genotype-specific in embryo and aleurone, respectively. In red seeded population over 7200 and 3580 proteins were identified with high confidence in embryo and aleurone, respectively. Proteomic signatures associated with dormancy phenotype were more evident in white seeded population, whereas genotype-specific and after-ripening induced changes were found in both populations. In dormant embryos, significant phenotype-specific changes were found for proteins involved in redox controlling system, signaling associated with flowering, phytohormones and lipid second messengers, development and growth repression, cell cycle control and epigenetic regulation of gene expression, translational dynamics, cell wall metabolism, vesicle transport, and ubiquitin 26S proteasome pathway. In embryos with non-dormant phenotype energy metabolism showed high capacity for the provision of NADPH reducing equivalents, pyruvate and TCA cycle intermediates for biosynthetic processes. Pathways for energy provision in non-dormant aleurone showed increased flux through the glycolytic pathway, high metabolic network flexibility, and an important role of inorganic pyrophosphate metabolism as an alternative energy donor. Further analysis of the iTRAQ-identified differentially expressed proteins in known QTL regions for PHS tolerance revealed potential candidate genes underlying the QTLs.

[P3] DEVELOPMENT AND APPLICATION OF HIGH THROUGHPUT KASP PLATFORM FOR WHEAT BREEDING. Xinmin Chen[1], Awais Rasheed[1],Yuanfeng Hao[1], Xianchun Xia[1], and Zhonghu He[1,2]. [1]Institute of Crop Sciences, Chinese Academy of Agricultural Sciences,12 Zhongguancun South Street, Beijing 100081, China; and [2]International Maize and Wheat Improvement Center (CIMMYT), CIMMYT China Office, c/o CAAS,12 Zhongguancun South Street, Beijing 100081, China.
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Functional markers (FMs) are the most valuable markers for crop breeding. Low-cost and high-throughput genotyping for FMs could provide an excellent opportunity to effectively practice marker-assisted selection in breeding. Based on FMs, we developed and validated kompetitive allele specific PCR (KASP) assays for genes that underpin economically important traits in bread wheat including adaptability, grain yield, quality, and biotic and abiotic stress resistances. Finally, a KASP platform with a robust marker toolkit for high-throughput and cost-effective screening of 90 functional gene/loci in wheat was developed. It has three advantages: (1) high-throughput, 1536 cultivars can be genotyped with 142 available markers in 2-3 days; (2) low-cost, 9 cents USD per data point including DNA extraction; (3) good quality, highly consistent with normal PCR markers. It has potential application in wheat breeding to accelerate the characterization of crossing parents and advanced lines for marker-assisted selection of known genes. Further, we included all these KASP assays into our new 50K wheat TraitBreed Affymetrix SNP array, which has significant potential to apply for academic wheat research and applied breeding.

[P4] APPLICATION OF AERIAL AND GROUND-LEVEL PHENOTYPING TOOLS IN BREEDING FOR WINTER-HARDY WINTER WHEAT. Yi (Andy) Chen[1], Harwinder Singh Sidhu[1], Mina Kaviani[1], Curtis Pozniak[2], and Alireza Navabi[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON, Canada, N1G 2W1; and [2]Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8
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The harsh winters in Canada leads to high risk of winterkill for winter wheat (*Triticum aestivum* L.). This emphasizes the need for genetic markers that can assist in selection for winter-hardiness to reduce winterkill incidents. The objectives of this research were to optimize and apply high-throughput, unbiased method to estimate winter-survival and to identify genetic factors that are important for winter-survival of winter wheat in Eastern Canada, which produces more than 65% of the Canadian winter wheat. A diversity panel of 450 winter wheat genotypes from Canada, with varying levels of winter-hardiness, was planted in October 2016 and 2017. Normalized difference vegetation index (NDVI) of each individual plot was extracted from multi-spectral imagery captured by unmanned aerial vehicle (UAV) as a measurement for winter-survival. Genome-wide association (GWAS) study was conducted using this data. Two major quantitative trait loci were detected on chromosome 5A to have significant effect on winter-survival in Eastern Canada. The diversity panel was then genotyped for allele variation of candidate genes that have been mapped close to the identified QTLs. This includes *Vernlaization-A1* (VRN-A1), *C-Repeat Binding Factor* (CBF)-*12* and -*15* on chromosome 5A. In this study, we optimized a high-throughput UAV-based method to measure winter-survival quantitatively and demonstrated that it is sensitive enough to be used in quantitative genetic studies. In addition, we have demonstrated that having the frost tolerant haplotype at the CBF region and higher number of copies of VRN-A1 (3) will contribute to higher winter-survival of winter wheat in Eastern Canada.

[P5] IDENTIFYING AND TRANSFERRING GENETIC DIVERSITY FROM THE WILD TO IMPROVE WHEAT. Sylvie Cloutier[1], Sridhar Ravichandran[1], Tara Edwards[1], Brent McCallum[2], Maria Antonia Henriquez[2], Gavin Humphreys[1], Wen Cao[1], George Fedak[1], Curtis Pozniak[3], and Frank M You[1]. [1]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6; [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100 #100, Morden, MB, Canada, R6M 1Y5; and [3]Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8
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Bread wheat is a polyploid crop that arose from ancient natural hybridizations. Subsequent selection, domestication and breeding have resulted in today's adapted elite varieties. However, these events have

also narrowed the genetic diversity of modern wheat. Broader genetic diversity exists in the wild; for example, roughly half of the ~75 leaf rust genes identified to date came from such germplasm. Today, the challenging identification of beneficial genetic diversity from the wild and its transfer are facilitated by genomics. One of the most efficient transfer methods is the use of synthetic hexaploid wheat (SHW) created by crossing *Triticum turgidum* (AB) to *Aegilops tauschii* (D), thereby re-creating the original hybridization that produced bread wheat (ABD), but using more diverse AB and D genome donors. Exome sequencing is a genomic technique that captures the DNA sequence of most of the protein-coding genes. To uncover the genetic diversity of the progenitor gene pools, exome sequencing was performed on a collection of *T. turgidum*, *Ae. tauschii*, their SHW-derived lines, and Canadian elite bread wheat varieties. More than 3 billion 100-bp sequencing reads were aligned to the exome design reference sequence. Sequences encoding disease resistance, photoperiod sensitivity, vernalization and grain quality genes were extracted to determine allelic diversity for these important traits. Comparisons with the elite germplasm revealed the novel and potentially valuable genetic diversity from the progenitor species. Our results also illustrate the promise for SHWs as shuttle germplasm for wheat improvement and the power of genomics-assisted pre-breeding.

[P6] IMPORTANCE OF MULTIPLE LOCATIONS IN BREAD WHEAT REGISTRATION TRIALS: A GXE STUDY OF DOUGH STRENGTH. Brigitte Dupuis[1], Kun Wang[1], Richard D. Cuthbert[2], and Bin Xiao Fu[1]. [1]Grain Research Laboratory, Canadian Grain Commission, Winnipeg, MB, Canada; and [2] Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, Swift Current, SK, Canada Correspondence to: brigitte.dupuis@grainscanada.gc.ca

Bread wheat quality improvement is an important goal of breeding in Canada. Dough rheological testing has been an essential part of quality evaluation of Canadian wheat breeding trial entries. Two of the four check varieties included in these trials, Carberry and Glenn, reflect the floor and ceiling, respectively, of dough strength within which new lines should be targeted. For each trial, check varieties and lines are grown at twelve or more locations and a small quantity of wheat of each check variety is assessed to determine an overall composite formulation for subsequent large scale quality evaluation of all checks and lines. A recently developed small-scale rapid screening protocol has made it possible for us to test the limited quantities of wheat from each location to study the impact of environment on dough strength. Our results confirm that strength is a result of genetics, environment and GxE interactions. However the range of strength between the floor and ceiling check varieties changes with location. In some locations there is a switch in ranking between check varieties based on dough strength. These results confirm the importance for registration trials of growing check varieties and new lines of bread wheat in multiple locations and evaluating composites from multiple locations to ensure a representative ranges and values for strength. Further research is underway to investigate the contribution of gluten composition to the fluctuations in strength observed between locations.

[P7] QUANTITATIVE PROTEOMICS IN THE WHEAT-LEAF RUST INTERACTION. Ursla Fernando, Mei Huang, Xiben Wang, Natalia Bykova, and Christof Rampitsch. Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Rte 100, Morden MB, Canada, R6M 1Y2 Correspondence to: chris.rampitsch@agr.gc.ca, natalia.bykova@agr.gc.ca

A quantitative proteomic approach was used to study the effector- triggered defense responses of wheat cultivar Thatcher LR2a to *Puccinia triticina* (*Pt*) races 9 and 161 in compatible and incompatible interactions respectively. Both pathogen and host proteomes were quantitatively characterized by 8-plex iTRAQ LC-MS. The Mass Spectrometry data were queried against an in-house customized EST wheat and race-specific *Pt* databases for protein identification followed by validation and quantitative analysis with Scaffold Q+ and MaxQuant. Approximately 3000 high confidence proteins were identified at each sampling point (48 h and 5 d post-inoculation (PI). Of these, 58 and 183 wheat proteins showed significant differential expression in the incompatible and compatible interactions respectively at 48 h PI. After 5 d a larger number of unique wheat proteins were identified with 170 in the incompatible and 314 in the compatible interaction with altered abundance. At 48 h PI, of the wheat proteins that were significantly increased, 35% were stress and redox related proteins. There were no significant *Pt* proteins until 5 d PI, when 135 and 219 were differentially expressed in the incompatible and compatible

interaction respectively. This study aims to unravel the function of these proteins to understand the events unfolding in wheat-*Pt* interactions to facilitate resistance breeding strategies in wheat.

[P8] THE CHANGING VIRULENCE OF STRIPE RUST IN CANADA. Kaveh Ghanbarnia[1], Eric Amundsen[1], and Reem Aboukhaddour[1]
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The virulence of 88 different isolates of *Puccinia striiformis f. sp. tritici* (Pst) was tested on 18 near-isogenic wheat lines in the Avocet background. These isolates are part of a collection obtained mainly from western Canada before and after the year 2000. Twenty seven isolates were collected before the year 2000 and 61 isolates were collected in a period from 2015 to 2017. The seedlings were inoculated with a spore/talc mixture (ratio 1:20) and infection types (ITs), on the second leaf, were recorded 18–21 days after inoculation based on a scale of 0–9. In total, 39 different virulence patterns were observed. Near-isogenic wheat lines with resistance genes *Yr1*, *Yr5*, *Yr15* and *Yr76* remain effective against all tested isolates since 1984, and the line harboring YrSp was defeated infrequently by new and old isolates. Lines possessing *Yr6*, *Yr8* and *Yr9* genes were effective against most Pst isolates between 1984-1994, but were defeated by most recent isolates maybe due to worldwide use of these genes in commercial cultivars. This study shows wide spectrum of virulence in recent isolates, and a major shift in virulence in Canadian stripe rust populations over the years.

[P9] PREDICTING AGRONOMIC PERFORMANCE IN CANADIAN WINTER WHEAT USING HIGH-THROUGHPUT PHENOTYPING AND PLANT PIXEL AREA. Gavin Humphreys[1], Claire Gahagan[1], Andre Kalikililo[1], Pouria Sadeghi-Tehran[2], Malcolm Hawkesford[2], and Malcolm Morrison[1]. [1]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6; and [2]Rothamsted Research, Harpenden, United Kingdom AL5 2JQ
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Effective high-throughput phenotyping of wheat lines is desirable to improve breeding selection efficiency and to facilitate the use of whole genome based selection methods. Green pixel area (GPA), expressed as a proportion of the total pixel number in photographs of yield plots, has been used previously as a measure of plant establishment, growth and vigor. In this study, three phenomics factors were used: (1) plant pixel area (PPA) which is a measure of green pixel area in a yield plot filtered to remove weed plants, (2) active canopy coverage (ACC) which is defined as mean growing degree days above 50% canopy, (3) linear senescence rate (LSR) which is the rate of loss of PPA after maximum canopy coverage is attained. The purpose of this research was to investigate the relationships between PPA, AAC and LSR with important agronomic traits. In 2017, mean phenomics parameters were determined from weekly green pixel area estimates in two advanced Canadian winter wheat yield trials (EA and MT). In both trials, ACC and LSR was significantly ($P<0.05$) correlated with grain yield. LSR was also significantly correlated with test weight and seed mass. AAC was significantly correlated with test weight and seed mass for MT. PPA was significantly correlated with heading date and plant height for MT but was not significantly correlated with grain yield in either trial. In this study, LSR which is possibly an estimate of “stay-green” potential was the most promising predictor of grain yield, test weight and seed mass.

[P10] IMPROVED MARKERS AND CANDIDATE GENES FOR PRE-HARVEST SPROUTING QTL IN WHEAT. Mark C. Jordan[1], and Frank You[2]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, Canada, R6M 1Y5; and [2]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Pre-harvest sprouting (PHS) is a condition where warm, wet and humid weather conditions cause germination of the grain to begin while still on the mother plant prior to harvest. QTLs for sprouting index were found on wheat chromosomes 3B, 4A and 7D in the AC Domain x RL4452 bi-parental mapping population (Cabral et al. 2014, BMC Plant Biology 14:340) which had been genotyped and mapped using single nucleotide polymorphism (SNP) markers. The 7D QTL corresponded to a maturity QTL and is

associated with variation in the coding sequence of Vrn-D3 a gene known to affect flowering time. The 4A gene was found to be a MAPKK gene (Torada et al. 2016, Curr. Biol. 26:782). The 3B QTL flanking markers define a region of 185 Mbp in the wheat RefSeq 1.0 genome sequence containing over 1180 annotated high confidence genes. The genomic region between flanking markers was used to identify SNPs between the parental genotypes in a sequence database derived from exome capture sequencing of Canadian wheat genotypes. 1492 SNPs were identified in 288 annotated genes. These genes were examined for expression and genes with expression in developing seeds identified. This further narrowed down the list of candidate genes. These SNPs will be useful to further narrow down the QTL region and provide robust markers for selection of lines with increased tolerance to pre-harvest sprouting. Markers for the chromosomes were used to genotype a collection of Canadian wheat lines to identify elite breeding material carrying PHS tolerant alleles.

[P11] CREATING HYPOMORPHIC MUTATIONS AT THE PDHK LOCUS THROUGH GENOME EDITING IN SPRING WHEAT. Palak Kathiria[1], Binod Pageni [1], John Laurie[2], Harpinder Randhawa[2], and Elizabeth-France Marillia[1]. [1]National Research Council Canada, 110 Gymnasium Place, Saskatoon SK S7N 0W9 Canada; and [2]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South, Lethbridge, AB T1J 4B1, Canada
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The reduction in the mitochondrial Pyruvate Dehydrogenase Kinase (mt PDHK) activity results in higher yield (Harvest Index) and early maturity (precocious flowering), as previously seen in several Brassica species. In this project, we are testing the hypothesis that increased productivity can also be obtained in wheat, through the down-regulation of the PDHK gene expression. To that end, we are deploying a gene editing technology platform in the spring wheat variety AC Andrew to generate mutations of the target gene for induced repression. Optimization of the genetic transformation and tissue culture pipelines are necessary and crucial steps for the success of the project and we report here our recent progress made on technology development.

[P12] HAPLOTYPE, COPY NUMBER AND ALLELIC VARIATION OF PHOTOPERIOD GENES OF CANADIAN WINTER WHEAT AND THE IMPACT ON FLOWERING TIME. Mina Kaviani, Yi Chen, Harwinder Singh Sidhu, and Alireza Navabi. Department of Plant Agriculture, University of Guelph, 50 Stone Rd East, Guelph, ON, Canada, N1G 2W1
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As a crop that is planted in all continents, except Antarctica, wheat (*Triticum aestivum* L.) owes its wide adaptability, at least in part, to the genes that control photoperiod sensitivity. Photoperiod sensitivity is an important physiological trait that influences the phenology of wheat, and the *Ppd-1* (Photoperiod-1) genes on group 2 chromosomes are significant regulators of this process. To identify the impact of genetic variation of *PPD-1* genes on winter wheat flowering time and adaptation in high latitude wheat growing areas in North America, we used a diverse panel of winter wheat varieties, the Canadian Winter Wheat Diversity Panel (CWWDP; n=450), which is a collection of heirloom winter wheat varieties as old as 1830s, winter wheat varieties registered in Canada since the early 1900s, and the breeding materials from eastern and Canadian breeding programs. The CWWDP was genotyped using Illumina *iSelect* wheat the 90K SNP chip, from which 20K polymorphic markers was used for various analyses. The diversity panel was also phenotyped near Elora, Ontario in 2017 and 2018 for different agronomic and yield related traits. We observed allelic variation for *PPD-D1* and *PPD-A1* genes. The allelic, haplotype, and copy number variation at the *PPD-1* group (*PPD-A1*, *PPD-B1* and *PPD-D1*) and the association between these genotypic variations and different phenological and agronomic traits will be presented. The frequency distribution of *PPD-1* genetic variants are expected to relate to the geographical origin of the wheat accessions, which for the most part presents possible adaptation patterns.

[P13] GENETIC DIVERSITY AND POPULATION STRUCTURE OF A NEPALI SPRING WHEAT (*Triticum aestivum* L.) DIVERSITY PANEL. Kamal Khadka[1], Davoud Torkamaneh[1], Francois Belzile[2], and Alireza Navabi[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Road E. Guelph, ON, Canada, N1G 2W1; and [2]Department of Plant Science, Université Laval, 1030, avenue de la Médecine, Québec QC Canada G1V 0A6
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Precise information about genetic diversity and population structure has a key role to play in improving the efficiency of plant breeding. Here, we adopted a genotyping-by-sequencing (GBS) approach to characterize a panel of 318 spring wheat (*Triticum aestivum* L.) accessions from Nepal. Using this approach, we identified 95K high-quality SNPs that were used for genetic diversity and population structure analysis. The STRUCTURE analysis suggested the presence of four distinct sub-groups in this panel, which is in agreement with the results of principal component analysis (PCA) and distance-based clustering. The largest number of SNPs (48,235) were from the B-genome, accounting for more than 50% of all SNPs. We also observed a significant difference in nucleotide diversity in the three sub-groups of accessions based on their sources. These results constitute a useful resource for the Nepali wheat breeding community, provides the foundation for conducting genome-wide association studies, and will accelerate future breeding efforts.

[P14] MOLECULAR CHARACTERIZATION OF ISOGENIC LINES OF HEXAPLOID WHEAT THAT DIFFER IN GRAIN YIELD. Dhouha Kthiri[1], Sean Walkowiak[1], Kirby Nilsen[1], Raju Datla[3], Jatinder Sangha[2], Richard Cuthbert[2], and Curtis Pozniak[1]. [1]Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8; [2]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, Swift Current, SK, Canada, S9H 3X2; and [3]National Research Council, 110 Gymnasium Place, Saskatoon, SK, Canada, S7N 0W9
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Understanding the genetic architecture of grain yield potential in wheat (*Triticum aestivum* L.) is key to meet the world's growing food demands. In the present study, we characterized a set of five F_6 derived F_8 lines (B1018-LN04C01, B1018-LN04C02, B1018-LN04C03, B1018-LN04C04 and B1018-LN04C05) of spring wheat derived from a three-way cross of the hard red spring wheat lines BW928/BW431//Carberry. These isogenic lines differed in their yield profiles and yielded higher than their parents in replicated field trials over multiple years. DNA from the three parental lines as well as the five isogenic lines were genotyped with the wheat iSelect 90K assay. Lines were enriched for coding regions using the wheat exome capture array and sequenced using an Illumina Hiseq2500 platform. Processed reads were aligned to the recently published reference genome sequence of Chinese Spring (RefSeq v1.0) to identify potential allelic variants regulating grain yield. Predictions of the effect of the variants on gene function were determined within high confidence gene models by SnpEff and were associated with gene expression networks derived from RNASeq of the sister lines. The results from the present study will be useful to develop DNA markers to select novel allelic combinations to enhance grain yield in wheat.

[P15] GENETIC MAPPING OF ADULT PLANT LEAF RUST RESISTANCE IN SPRING WHEAT LINE BW278. Mallorie Lewarne[1], Brent McCallum[2], Colin Hiebert[2] and Curt McCartney[2]. [1]Department of Plant Science, University of Manitoba, 66 Dafoe Rd., Winnipeg, MB, Canada, R3T 2N2; and [2]Morden Research and Development Center, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, Canada, R6M 1Y5
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Leaf rust caused by *Puccinia triticina* is a widespread disease of wheat that affects both yield and quality. The preferred method of leaf rust control is through genetic host resistance as it provides protection throughout the growing season without additional costs to the producer and environment. To date there are over 70 characterized leaf rust resistance genes, the majority of which are race-specific and condition resistance to only a single, or a few *P. triticina* races. *Lr46,* a non-race specific adult plant resistance (APR) gene located on the long arm of chromosome 1B, is thought to be present in spring wheat line BW278. A doubled haploid (DH) population (Superb/BW278) and a recombinant inbred line (RIL)

population (BW278/AC Foremost) were inoculated under field conditions with an epidemic mix of *P. triticina* races, as well as indoors with *P. triticina* race TJBJ. Initial results suggest that a single leaf rust (Lr) APR gene is segregating at the adult plant stage in both populations. The objectives of the current study include: (i) confirm the presence of *Lr46* in BW278, (ii) genetically map the resistance and identify closely linked genetic markers and (iii) screen a panel of Canadian wheat cultivars to determine the distribution of *Lr46.*

[P16] MAPPING QTLs FOR PRE-HARVEST SPROUTING RESISTANCE IN RED SPRING WHEAT. M. M. Uzzal A Liton[1], Mark C. Jordan[2], Curt A McCartney[2], Colin Hiebert[2], and Belay T. Ayele[1]. [1]Department of Plant Science, University of Manitoba, 222 Agriculture Building, 66 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2; and [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Rte 100#100, Morden, MB, Canada, R6M 1Y5
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Wheat is the most important cereal crop in Canada and second most-produced cereal worldwide. Pre-harvest sprouting (PHS) significantly reduces the grain yield and quality of wheat. Therefore, identifying quantitative trait loci (QTL) for PHS resistance and determining their effects is important for facilitating marker-assisted breeding of PHS resistant cultivars. A double haploid population of 330 lines derived from a cross between 'Roblin' and RL4137 was studied to identify PHS resistance QTLs. Roblin is susceptible to PHS and RL4137 is strong source of PHS resistance used in wheat breeding programs. The mapping population was genotyped using a 90 K Infinium iSelect Custom Wheat Beadchip and seeds of the population grown under greenhouse conditions were phenotyped for their germination index. The linkage map consisted of 8751 loci. Among them, the highest number of loci (4720) was mapped on B genome followed by the A genome (2886). A total of 1145 loci were distributed across the D genome. A genetic map of 21 chromosomes was constructed with a total of 1499 SNP markers. Map construction and identification of QTLs are in progress and the result will be presented at the symposium. The QTLs to be identified will be used for further identification of candidate genes underlying these QTLs and development of KASP markers for future genetic studies and marker-assisted selection.

[P17] AGRONOMIC MANAGEMENT TO REDUCE LODGING RISK FOR SPRING WHEAT IN WESTERN CANADA. Amy Mangin[1], Yvonne Lawley[1], Anita Brûlé-Babel[1], Don Flaten[2], and Jochum Wiersma[3]. [1]Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2; [2]Department of Soil Science, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2w; and [3]Department of Agronomy and Plant Genetics, University of Minnesota, Crookston, MN, USA
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Lodging in spring wheat commonly results in reduced yield and grain quality. New high yielding wheat varieties require higher rates of nitrogen fertilizer to achieve their yield potential. This leads to increased risk of stem and root lodging under some growing conditions. The objective of this study was to investigate the most effective agronomic strategies to manipulate crop canopy structure to decrease lodging risk without taking resources away from the developing grain. This was investigated through two field experiments during the 2018 growing season at two locations in Manitoba, Canada. The first evaluated nitrogen (N) fertilizer management (reduced rate, split application and controlled release urea), plant growth regulator (PGR) application and their interactions across three common high yield spring wheat varieties. A second study investigated the interactions between plant densities, N application timing, and PGR application across a single spring wheat variety. Dry matter partitioning data were collected at anthesis and physiological maturity to determine the influence of combinations of management strategies on alterations to crop canopy structure and resulting lodging risk. These data will provide agronomy management recommendations to reduce the risk of lodging without sacrificing grain yield and quality.

[P18] LEAF RUST IN ONTARIO AND QUÉBEC: *PUCCINIA TRITICINA* VIRULENCE AND RESISTANCE GENES IDENTIFICATION IN WINTER WHEAT. Brent D. McCallum[1], Silvia Rosa[2], and Ljiljana Tamburic-Ilincic[3]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Rte 100 #100, Morden, MB, Canada, R6M 1Y5; [2]CÉROM, Centre de recherché sur les grains, 740 Chemin Trudeau, Saint-Mathieu-de-Beloeil, QC, Canada, J3G 0E2; and [3]University of Guelph, Ridgetown Campus, 120 Main St E, Ridgetown, ON, Canada, N0P 2C0
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Breeding for leaf rust resistance is required to monitor changes in the *Puccinia triticina* population and to identify the genes present in the germplasm. The aim of this study was to understand the recent shifts in *P. triticina* population in Ontario and Québec, comparing with the virulence in the prairies; and to identify the resistance genes in a population between Ontario winter wheat cultivars 'Vienna' (moderate susceptible) and '25R47' (moderate resistance). The virulence of *P. triticina* collected in Ontario, Quebec and the prairies from 2001 to 2017 was analyzed using 17 standard differential lines in 'Thatcher' background. Differences in the virulence among the regions in the 2017 isolates were evident in specific resistance genes. The Eastern provinces showed higher virulence than the prairies on *Lr11* and *Lr18*, but lower virulence on *Lr9, Lr16, Lr24* and *Lr21*. Quebec presented higher virulence in *Lr2a, Lr2c, Lr26*, while Ontario was more similar with the prairies on those genes. The most effective resistance genes in Quebec and Ontario are *Lr9, Lr16, Lr24, Lr18* and *Lr21*. The 'Vienna/25R47' population was evaluated in greenhouse and in the field under natural infection in Ontario (Centralia in 2011 and Ridgetown in 2011 and 2012). It was determined the presence of at least four seedling resistance genes segregating in the population after artificial inoculation with BBBD, TDBG, TBBG and MBDS races. A QTL on chromosome 1B was significantly associated with leaf rust resistance in Ontario, with maximum explanation of 30%. *Lr24* was identified as a possible gene in Vienna.

[P19] HAPLOTYPE LOCI UNDER SELECTION IN CANADIAN DURUM WHEAT GERMPLASM OVER 60 YEARS OF BREEDING: ASSOCIATION WITH GRAIN YIELD, QUALITY TRAITS, PROTEIN LOSS AND PLANT HEIGHT. Amidou N'Diaye[1], Jemanesh K. Haile[1], Kirby T. Nilsen[1], Sean Walkowiak[1], Yuefeng Ruan[2], Asheesh K. Singh[3], Fran R. Clarke[2,4], John M. Clarke[1], and Curtis J. Pozniak[1]. [1]Department of Plant Sciences and Crop Development Centre, University of Saskatchewan, Saskatoon, Saskatchewan; [2]Agriculture and Agri-Food Canada, Swift Current Research and Development Centre, Swift Current, Canada; [3]Department of Agronomy, Iowa State University, Ames, IA, USA; and [4]Retired
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Durum wheat was introduced in the southern prairies of western Canada in the late 19th century. Breeding efforts have mainly focused on improving quality traits to meet the pasta industry demands. For this study, 192 durum wheat lines were genotyped using Illumina 90K Infinium iSelect assay, and resulted in a total of 14,324 polymorphic SNPs. Genetic diversity changed over time, declining during the first 20 years of breeding in Canada, then increased in the late 1980s and early 1990s. We scanned the genome for signatures of selection, using the total variance Fst-based outlier method (Lositan), the hierarchical island model (Arlequin) and the Bayesian genome scan method (BayeScan). A total of 407 outliers were identified and clustered into 84 LD-based haplotype loci, spanning all 14 chromosomes of the durum wheat genome. The association analysis detected 54 haplotype loci, of which 39% contained markers with a complete reversal of allelic state. This tendency to fixation of favourable alleles corroborates the success of the Canadian durum wheat breeding programs over time. Twenty-one haplotype loci were associated with multiple traits. In particular, *hap_4B_1* explained 20.6, 17.9 and 16.6% of the phenotypic variance of pigment loss, pasta b* and dough extensibility, respectively. The locus *hap_2B_9* explained 15.9 and 17.8% of the variation of protein content and protein loss, respectively. All these pleiotropic haplotype loci offer breeders the unique opportunity for further improving multiple traits, facilitating marker-assisted selection in durum wheat, and could help in identifying genes as functional annotations of the wheat genome become available.

[P20] QUANTITATIVE TRAIT LOCI (QTL) MAPPING FOR AGRONOMIC AND QUALITY TRAITS IN A DOUBLED HAPLOID WINTER WHEAT POPULATION. Anjan Neupane[1], Ljiljana Tamburic-Ilincic[2], Anita Brûlé-Babel[1], and Curt McCartney[3]. [1]Department of Plant Science, University of Manitoba, 222 Agriculture Building, Winnipeg, Manitoba, Canada R3T 2N2; [2]University of Guelph, Ridgetown Campus, Ridgetown, Ontario, Canada N0P 2C0; and [3]Morden Research and Development Centre, Agriculture and Agri-Food Canada, Unit 101 Route 100, Morden, Manitoba, Canada R6M 1Y5
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Wheat (*Triticum aestivum* L.) is a major staple food crop of the world. Winter wheat breeding for improved grain yield, and end-use quality is a major challenge. The objective of this project is to identify QTL associated with agronomic (plant height, anthesis date, maturity date, yield) and quality characteristics (protein content, test weight and thousand kernel weight). A doubled haploid population consisting of 103 lines from the cross of a soft red and a hard red winter wheat was used in this study. The agronomy trials were conducted using two-replicate randomized complete block experiments grown in three locations in Canada in 2016 and 2017, and one location in 2018. Agronomic data including plant height, days to heading, days to 50% anthesis were recorded in the field and yield was measured from collected grain. Test weight, thousand kernel weight and protein content were measured on the grain samples. The parents differed for all agronomic traits measured and the DH population segregated for these traits. Genotyping of the population was performed using the 90K Illumina Infinium iSelect single nucleotide polymorphism array. Linkage mapping and QTL analysis is in progress. Significant agronomic and seed quality QTL identified from this project will be used in marker development. Further, superior progenies identified using both phenotypic and marker assisted selection will be incorporated in future breeding programs.

[P21] IDENTIFICATION OF PUTATIVE MARKERS FROM WITHIN A CHROMOSOME 3D STEM-SOLIDNESS QTL IN SPRING WHEAT. Isabelle Piché[1], Richard Cuthbert[1], Ron Knox[1], Yuefeng Ruan[1], Brad Meyer[1], Curtis Pozniak[2], and Kirby Nilsen[2]. [1]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, Box 1030, Swift Current, SK, Canada, S9H 3X2; and [2]Crop Development Centre, Department of Plant Sciences, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8
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The wheat stem sawfly, *C. cinctus* (Norton), is a major insect pest of wheat (*Triticum* spp.) causing economic losses through reduction in yield. A common strategy to mitigate yield loss is to grow solid-stemmed wheat varieties. Establishing and maintaining good stem-solidness in hexaploid wheat is an important yet challenging component in the development of new solid-stemmed varieties. At SCRDC, a doubled haploid (DH) breeding population was generated from the cross of Concord and Hughes where Sst1 (the most common source of stem-solidness) was fixed and an alien source (3Ag) was introduced from Concord. 204 DH lines were genotyped with the Infinium iSelect 90K wheat assay and a subset of lines (135) was phenotyped for stem-solidness from two locations during the 2016 growing season. Composite interval mapping analysis (CIM) revealed a QTL with major effect for stem-solidness on chromosome 3D. The QTL, contributed by AAC Concord accounted for 49.4% of the total phenotypic variation. Putative KASP markers have been developed from within the QTL interval. Upon validation the markers should be a convenient tool to assist with selection of improved stem solidness and sawfly resistance.

[P22] MOLECULAR AND GENETIC DIFFERENCES BETWEEN A MODERN AND HISTORICAL SPRING WHEAT CULTIVAR. Elie Raherison[1], Mahdi Majidi[1], Roos Goessen[1], Nia Hughes[1], Richard Cuthbert[2], Ron Knox[2], and Lewis Lukens[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Road E, Guelph, ON, Canada, N1G2W1; and [2]Agriculture and Agri-Food Canada, 1 Airport Road, Swift Current, SK, Canada, S9H 3X2
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Plant improvement often occurs within a circumscribed germplasm to maintain desired traits, and new germplasm is introduced to provide novel, positive alleles. For example, Red Fife (RF) is an ancestor of Stettler (S), a modern spring wheat cultivar. Both cultivars have good bread-making and milling qualities,

yet Stettler is shorter, higher yielding, and more disease resistant. In this work, we investigate both the molecular differences that distinguish historical and modern cultivars, and the genetic bases for the cultivars' trait differences. Using RNA-seq, we identify over 22,000 SNPs between RF and S. We classify 17% of the genome, containing 25% of the expressed genes, as identical by descent (IBD). These regions likely share the core, grain quality genes. Deleterious mutations may accumulate in germplasm that has not been widely exposed to selection. Consistent with this idea, IBD region SNPs change amino acid sequences at significantly higher frequencies than do non-IBD region SNPs. We map 30 QTLs using a population of 156 doubled haploid lines for 14 early and late physiological and agronomic traits. Many traits are genetically correlated, including those measured late and early in development, suggesting pleiotropy is an important component of gene improvement. Most QTL explained between a small or moderate proportion of traits' genotypic variation. However, the Rht-B1 dwarfing allele in Stettler has a major effect on plant height as well as on other traits. In summary, our results pinpoint the genomic regions maintained between a historical and a modern cultivar and suggest that Rht-B1 is the one key, genetic difference between historical and modern cultivars.

[P23] NOVEL SOURCES AND THEIR GENETIC RELATIONSHIP OF ADULT PLANT RESISTANCE TO WHEAT RUSTS. Y. Rauf[1], C.X. Lan[2], R. P. Singh[2], M. N. Rouse[3], M. Imtiaz[4], and J. A. Anderson[1].
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The rapid appearance of new races of rust pathogens with virulence for the major seedling resistance genes in wheat has intensified the focus to discover adult plant resistance (APR) genes in wheat and utilize them in breeding programs for sustainable wheat production. The experimental breeding line 'Copio' developed by the International Maize and Wheat Improvement Centre (CIMMYT) in Mexico has exhibited high levels of APR to all three rusts including the African stem rust Ug99 race group. To dissect the mechanism of APR in Copio it was crossed with APAV#1, which is susceptible to all three rusts and a population of 176 F_4:F_5 recombinant inbred lines (RILs) was developed at CIMMYT. Both parental lines were found to be susceptible (IT >3) at the seedling stage to races TTKSK and TKTTF, which ensures the field data from Africa will be applicable for APR mapping. Both parents were also tested for the known APR genes *Lr34/Yr18*/*Sr57*, *Lr46/Yr29/Sr58*, *Lr67/Yr46/Sr55* and *Sr2/Yr30* using molecular markers and results indicate that APAV#1 does not carry any known APR genes, while Copio might have *Lr46* and *Sr2.* This population was tested in four field environments (US, Pakistan, Mexico and Kenya) for leaf, stem and yellow rusts during 2015-16 and 2016-17. Disease severity distributions of all three rusts for the RILs across all environments were continuous, suggestive of quantitative and polygenic resistance. Genotyping by sequencing (GBS) was used as a genotyping platform and preliminary mapping results suggest that the resistance might be unique.

[P24] BRAZILIAN SPRING WHEAT GERMPLASM AS SOURCE OF GENETIC VARIABILITY. Silvia Rosa[1], Linda Langille[2], Gavin Humphreys[2], Brent McCallum[3], Tom Fetch[4], Harpinder Randhawa[5], Maria Antonia Henriquez[3], Harvey Voldeng[2], Allan Cummiskey[6], Barbara Blackwell[2], Pedro Scheeren[7], Igor Valerio[8], and Camila Turra[8]. [1]CÉROM, Centre de recherché sur les grains, 740 Chemin Trudeau, Saint-Mathieu-de-Beloeil, QC, Canada, J3G 0E2; [2]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6; [3]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Rte 100 #100, Morden, MB, Canada, R6M 1Y5; [4]Brandon Research Station, Agriculture and Agri-Food Canada, 2701 Grand Valley Rd, Brandon, MB, Canada, R7C 1A1; [5]Lethbridge Research Centre, Agriculture and Agri-Food Canada, 5403 1 Ave S, Lethbridge, AB, Canada, T1J 4P4; [6]Crops & Livestock Research Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PE, Canada, C1A 4N6; [7]EMBRAPA Trigo, Rodovia BR 285, Km 294, s/n, Passo Fundo, RS, Brazil, 99050-970; and [8]OR Sementes, Av. Rui Barbosa, 1300, Passo Fundo - RS, Brazil, 99050-120
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As part of a Canada-Brazil germplasm exchange, 106 modern and ancient Brazilian spring wheat cultivars have been genotyped and phenotypically evaluated in Canada since 2014. There were four cultivars that exhibited adult plant resistance to leaf rust, and the absence of *Lr34* was confirmed in two with molecular markers. Forty-eight cultivars were resistant to leaf rust at the seedling stage to six predominant Canadian races. In Alberta, 55% of the cultivars had severity to stripe rust lower than 30%, while to leaf rust scored in Manitoba, it represented 98% of the collection. There was 76% of the cultivars with severity of 30% or less to powdery mildew, and 57% with resistance to stem rust. The Brazilian collection was evaluated for agronomic suitability and many cultivars showed good adaptability in the Eastern provinces with high yield potential, but low grain protein. The germplasm is a source of gibberellin-insensitive reduced height (*Rht*) genes, and almost all lines had the reduced height allele at either the *Rht-B1* or *Rht-D1* marker. In Fusarium head blight (FHB) nurseries in Manitoba and Ontario, 20% of the cultivars had FHB index lower than 30%. Seventy-nine cultivars were genotyped for FHB QTL, and none of the lines with low FHB scores carried Frontana (3A, 5AS) or Sumai 3 (3BS, 6BS) haplotypes. Additional DNA marker screening will be completed to postulate the genes in the germplasm. Brazilian material is a valuable resource to increase the genetic variability of Canadian wheat and has resistance to various pathogens.

[P25] DIFFERENCES IN LEAF STOMATAL TRAITS IN AN ELITE DOUBLE HAPLOID BREAD WHEAT POPULATION ASSOCIATED WITH TOLERANCE TO DROUGHT STRESS AND YIELD STABILITY. Jatinder S. Sangha[1], Prabhath Lokuruge[1], Ron E. Knox[1], Richard D. Cuthbert[1], Samia Berraies[1], Yuefeng Ruan[1], and Vijai Bhadauria[1]. [1]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, Swift Current, SK, Canada
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Stomata are microscopic structures on the surface of plant leaves that contribute significantly to photosynthetic efficiency and water loss. Between 2014 and 2017, physiological traits were studied in a doubled haploid (DH) bread wheat population derived from Carberry/AC Cadillac, under rainfed and irrigated conditions, to determine drought tolerance mechanisms and relationship with grain yield. Principal component analysis of grain yield under different growing environments (4 years and 2 water regimes per year) explained over 92% of variance to the first five principal components (PCs), 69% of variance to the first two PCs, and 54% of variance to the first PC, with irrigated environments as the main contributors. Notable wheat lines with consistently higher grain yield were B0767&AG075 (registered as AAC Goodwin), B0767&AX125 and B0767&BF109. Data collected with leaf porometer on flag leaves of wheat lines with contrasting grain yields reveal lower stomatal conductance in these three accessions under water stress. Normalized difference vegetation index and chlorophyll measurements also differed among genotypes suggesting for a possible relationship with grain yield. Results indicate that altering stomatal conductance and density through physiological breeding could improve drought tolerance in wheat. Since the majority of water loss from plants occurs via transpiration through leaf stomata, selecting traits such as stomatal number and size per unit area to limit transpiration rate could provide opportunity to grow wheat in dry environments without grain yield penalty. Physiological understanding of stomatal

numbers and function in wheat will be a focus of future studies targeting yield stability under drought stress.

[P26] HOST-PATHOGEN INTERACTION IN THE WINTER WHEAT-STRIPE RUST PATHOSYSTEM IN ONTARIO. Mitra Serajazari[1], Brett Hilker[1], Harwinder Singh Sidhu[1], Joanna Follings[2], and Alireza Navabi[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Rd E., Guelph, ON, Canada, N1G 2W1; and [2]Ontario Ministry of Agriculture, Food and Rural Affairs, 63 Lorne Avenue E., Suite 2B, Stratford, ON, Canada, N5A 6S4
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In recent years, stripe rust, caused by *Puccinia striiformis,* has been spreading to new areas in North America with record-high severity in Ontario winter wheat reported in 2016. The objectives of this research were to monitor the geographical spread and virulence pattern of stripe rust in Ontario and to examine seedling and adult-plant response of diverse winter wheat germplasm, in search of resistance genes. From 2016 to 2018, 80 stripe rust samples were collected from Ontario. Virulence analysis using a set of 42 differential lines, which includes the Avocet near isogenic lines indicated that stripe rust isolates from Ontario resemble races from central and eastern regions of the USA. Results also suggest that the seedling resistance genes *Yr1*, *5*, *10*, *15, 24, 26* and *28* are effective against the current prevalent races in Ontario. Seedling infection analysis of a Canadian Winter Wheat Diversity Panel (CWWDP; *n*= 430) indicated that only less than 5% of the panel carry effective seedling resistance against the Ontario isolates. Priesley is the only commercially available variety that carries seedling resistance in Ontario. However, field evaluations at the adult stage showed that more than 50% of Ontario commercial varieties possess varying degrees of adult-plant resistance against stripe rust. Results highlight the importance of introgression of effective seedling and adult plant resistance genes in Ontario winter wheat germplasm.

[P27] GENETIC DIVERSITY IN THE CANADIAN WINTER WHEAT. Harwinder Singh Sidhu[1], Mina Kaviani[1], Curtis Pozniak[2], Matthew Hayden[3], and Alireza Navabi[1]. [1]University of Guelph, Guelph, ON, Canada; [2]Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada; and [3]Agriculture Victoria Research, AgriBio, La Trobe University, Melbourne, Australia
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Realizing a species' genetic diversity and genome wide linkage disequilibrium is central to identifying genomic regions associated with phenotypes through genome wide association studies. In this study we studied the linkage disequilibrium, population structure, and selection signatures across the genome of wheat in Canadian Winter Wheat. A Canadian Winter Wheat Diversity Panel (CWWDP; n = 450) was assembled, including registered varieties, as old as 1830s, current breeding material from breeding programs in Canada, and key genotypes from the ancestors of Canadian winter wheat. The CWWDP was genotyped using Illumina iSelect wheat 90K SNP beadchip, from which 20K polymorphic markers were used for various analyses. Linkage Disequilibrium analysis confirmed the presence of linkage blocks across all chromosomes, some chromosomes *e.g.,* 1A. 1B, 2B and 6A carrying large fixed blocks. STRUCTURE analysis carried out on 1923 markers obtained by LD pruning identified 7 subpopulations. Canadian market classes of wheat such as soft red winter (SRW) and hard red winter (HRW) were clearly differentiated by some subpopulations. The largest subpopulation consisting primarily of SRW wheat had the highest expected heterozygosity between individuals. Allele frequency divergence ranged from 0.11 to 0.31 among subpopulations. The first five principal components (PC) of a PC analysis on 20K markers accounted for 24.1% of the variation. This study contributes to the understanding of genetic diversity in the Canadian winter wheat and provides crucial information for genome wide association studies for important traits.

[P28] CONTROL OF STRIPE RUST IN ONTARIO WINTER WHEAT IN 2017. Ljiljana Tamburic-Ilincic[1] and Albert Tenuta[2]. [1]University of Guelph, Ridgetown Campus, 120 Main St E, Ridgetown, ON, Canada, N0P 2C0; and [2]OMAFRA, 120 Main Street E, Ridgetown, ON, Canada N0P 2C0
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Stripe rust (*Puccinia striiformis* f. sp. *tritici* Erikss.) was the most important disease in Ontario winter wheat in 2016 when high yield losses were reported. The disease was not an issue in Ontario for couple of

decades. Breeding resistant cultivars and fungicides application are considered the most effective ways to control the disease. The objectives of this study were: 1) to evaluate the effect of different fungicides for stripe rust control in cultivars with different level of resistance, 2) to evaluate the effect of seeding rates. The experiment was conducted at Ridgetown in 2017. The winter wheat cultivars were: Gallus (resistant to stripe rust), UGRC Ring (moderately resistant), OAC Flight (moderately susceptible) and Venture (susceptible). The fungicides azoxystrobin plus propiconazole (Quilt), trifloxystrobin plus propiconazole (Stratego) and prothioconazole plus tebuconazole (Prosaro) were tested in four replicates in a randomized complete block design, using 400, 500 and 600 seeds/m^2. Stripe rust severity (scale 0-9), yield, and test weight were recorded. The highest yield and test weight, and the lowest stripe rust severity, across the cultivars and seeding rates, were recorded after Prosaro applications. UGRC Ring has the highest yield, while Gallus had the lowest stripe rust severity and the highest test weight, across the fungicides and seeding rates. Seeding rate did not influence stripe rust severity in 2017. The experiment was repeated in 2018 at two locations. The results from this study will help growers to have the best management strategies for stripe rust including fungicides, seeding rate and resistant cultivars.

[P29] IDENTIFICATION OF QTL_S AND CANDIDATE GENE FOR ESSENTIAL YIELD COMPONENTS IN AN INTERNATIONAL COLLECTION OF HEXAPLOID WHEAT (*TRITICUM AESTIVUM* L.). Honoré Tékeu[1,2,4], Eddy Ngonkeu[3,4], Alireza Navabi[5], Pierre Djocgoué[4], Sébastien Bélanger[1, 2], Marc-André Lemay[1,2], Amina Abed[1,2], Brian Boyle[1,2], Wuletaw Tadesse[6], Martine Jean[1,2], and François Belzile[1,2]. [1]Département de Phytologie, Université Laval, Quebec City, QC, Canada; [2]Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Quebec City, QC, Canada; [3]Institute of Agricultural Research for Development, PO Box 2123, Yaoundé, Cameroon; [4]Department of Plant Biology, University of Yaoundé I, PO Box 812, Yaoundé, Cameroon; [5]University of Guelph, Canada; and [6]International Center for Agricultural Research in the Dry Areas (ICARDA), Beirut, Lebanon
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Grain size is a key agronomic trait that contributes to grain yield in wheat. Grain length and width were evaluated in a collection of 170 wheat accessions including cultivars of different geographic origin from Africa and Mexico, across four environments. These accessions were genetically characterized using a genotyping-by-sequencing (GBS) protocol that produced 73,784 single nucleotide polymorphism (SNP) markers. We also genotyped 12 plants of Chinese Spring (CS) and compared the GBS-derived genotype calls to the CS reference genome; among the resulting 1.2M genotype calls, 99.9% were in agreement. This indicates that GBS can yield a large amount of highly accurate SNP data to study genetic diversity and perform genome-wide association studies in hexaploid wheat. The genetic diversity analysis performed using this set of SNP markers revealed the presence of six distinct groups within this collection. A genome-wide association study was conducted to uncover genomic regions controlling variation for grain length and width. In total, seven SNPs were found to be associated with both traits, identifying three quantitative trait loci (QTLs) located on chromosomes 1D, 2D and 4A. In the vicinity of the peak SNP on chromosome 2D, we found a promising candidate gene (D11), whose orthologous had previously been reported to be involved in the regulation of grain size in rice. These markers will be useful in breeding for enhanced wheat productivity.

[P30] MARKER DEVELOPMENT FOR GLUTEN SUBUNITS AFFECTING GRAIN QUALITY IN ELITE CANADIAN WHEAT. Jacob Toth[1], Cherilyn Babel[1], and Santosh Kumar[1]. [1]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Brandon, MB R7A 5Y3
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Canadian hexaploid spring wheat (*Triticum aestivum* L.) is renowned for its superior baking quality. Breeding for high quality wheat can be difficult due to expensive phenotyping, environmental influences, and due to the need for large samples sizes for quality testing. Molecular markers offer a cost-effective, efficient, and easily scalable method of testing. The Canada Western Red Spring wheat combines high yield with high protein and strong gluten strength. In the bread wheat, most storage proteins belong to the glutenin and gliadin class. The glutens can be monomeric (gliadin) which exhibit viscous behavior whereas the polymeric glutens (glutenin) provide elasticity. The variations in quantity and quality of polymeric glutenins dictate the break making attributes. Markers for superior glutenin and gliadin subunits that are polymorphic in Canadian wheat germplasm will allow for enrichment of these proteins in early

generations of breeding populations where the grain samples are limited. In a large set of diverse homozygous breeding lines at F_9 generation, we found correlations between various grain quality attributes and the marker loci 7BxOE, GluA3-1, GluA3-3, GluB3-3, and Gli-D1. We also found that the released cultivars were enriched with favourable alleles of the above mentioned markers. Further diversity in gluten subunits was discovered in Canadian wheat varieties within various quality classes. The markers, genotypic and phenotypic information presented will allow for early generation selections of lines with high gluten strength.

[P31] ADAPTIVE RESPONSE OF WHEAT TO EXCESS MOISTURE IS MEDIATED BY THE PLANT HORMONES ETHYLENE AND AUXIN. Pham Anh Tuan[1], Tran-Nguyen Nguyen[1], Shalini Mukherjee[1], and Belay T. Ayele[1]. [1]Department of Plant Science, 222 Agriculture Building, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2
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Excess moisture is one of the major abiotic stress factors that negatively affect the growth and development of wheat crop, leading to significant reduction in yield. Adaptation of crops to excess moisture condition involves root morphological and anatomical changes. To understand the roles of ethylene and auxin in the regulation of changes in root morphology and anatomy under excess moisture, this study investigated changes in the expression patterns of ethylene and auxin metabolic and transport genes, and the level of auxin in wheat root and stem node tissues. Excess moisture inhibited axile root elongation and lateral root formation but promoted the development of axile roots, and the formation of surface adventitious roots and aerenchyma. These effects of excess moisture are associated with the enhanced expression levels of ethylene biosynthesis genes, *ACS7* and *ACO2*, in both root and stem node tissues. Inhibition of axile root elongation is also associated with increased root indole acetic acid (IAA) level, which appears to be regulated by enhanced expression of auxin biosynthesis (*TDC* and *YUC1*) and transport (*PIN9*) genes. In addition, emergence of adventitious roots from excess moisture stressed stem nodes is accompanied by increased IAA level and up-regulation of *TDC*, *YUC1* and *PIN9*. These results suggest that modulation of ethylene and auxin levels in root and stem node tissues play crucial roles in mediating adaptive response of wheat root to excess moisture.

[P32] A SMALL-SCALE RAPID SCREENING PROTOCOL FOR QUALITY TRAITS OF HARD RED SPRING WHEAT. Kun Wang[1], Brigitte Dupuis[1], Richard D. Cuthbert[2], and Bin Xiao Fu[1]. [1]Grain Research Laboratory, Canadian Grain Commission, Winnipeg, MB, Canada; and [2]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, Swift Current, SK, Canada
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Effective and efficient selection of key quality traits for early generations is crucial to develop new wheat varieties with improved end-use quality. This research proposes a screening protocol for wheat flour yield, flour water absorption and gluten strength based on limited grain samples of early generation testing in wheat breeding programs. A modified Quadrumat Junior (QJ) milling protocol was developed to predict flour yield as compared to the standard Bühler test mill. The resulting flour (8 g) was tested with the GlutoPeak to predict flour water absorption. Gluten strength was assessed with the GlutoPeak and a rapid extensograph method. Significant correlation ($r = 0.90$, $p < 0.001$) was shown for QJ flour yield in comparison with the yield obtained with a Bühler test mill. GlutoPeak torque was highly correlated with farinograph water absorption ($r = 0.91$, $p < 0.001$). Significant correlations ($r > 0.91$, $p < 0.001$) were found for both GlutoPeak strength index and rapid extensograph R_{max} with the R_{max} value of modified extensigraph method used in the evaluation of breeder line dough properties. Additionally, the mixing parameters obtained during dough preparation for rapid extensigraph provided further information about dough strength and mixing requirement. The proposed combination of QJ mill/GlutoPeak/Rapid Extensograph requires as little as 200 g of wheat for predicting water absorption and gluten properties. With a four-fold increase in throughput and much reduced sample size, the new protocol can be widely adopted for screening flour yield, water absorption capacity and gluten properties in breeding programs.

[P33] ACHIEVING MULTIRUST RESISTANCE: HOW MANY GENES? Wentao Zhang[1], Kerry Boyle[1], Brittany Polley[1], Christine Sidebottom[1], Harpinder Randhawa[2], Tom Fetch[3], Randy Kutcher[4], Brent McCallum[5], and Pierre R. Fobert[6]. [1]Aquatic and Crop Resources Development, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9, Canada; [2]Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, 5403 1st Avenue South Lethbridge, AB T1J 4B1, Canada; [3]Agriculture and Agri-Food Canada, Brandon Research and Development Centre, Brandon, MB R7A 5Y3, Canada; [4]Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; [5]Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Route 100, Morden, MB R6M 1Y5, Canada; and [6]Aquatic and Crop Resources Development, National Research Council of Canada, 100 Sussex Drive, Ottawa, ON, K1A 0R6, Canada
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Rust diseases, including leaf, stripe and stem rusts, are the most widely occurring diseases of wheat worldwide. Pyramiding multiple resistant genes has been proposed as the most effective way to control these diseases in wheat. However, to practise this approach, one must know the most effective gene combinations from the pool of more than 200 genes that bring resistance to the three rust diseases. Deployment the most effective/or optimal gene pyramids will ensure the maintenance of durable rust resistance within Canadian wheat cultivars, thus avoid production losses from rust epidemics. Moreover, the optimization will minimize the yield penalty of resistance genes, as well as improve breeding efficiency in the development of new cultivars. Here, we explore the most effective/optimal gene pyramids for rust resistance from a well-known CIMMYT line, Parula, which has durable resistance to multiple rust types. Our analysis found that the leaf rust genes *Lr34/Yr18/Sr57*, *Lr46/Yr29/Sr58*, *Lr-7BS*, *Lr68* from Parula conferred an almost an immune response to leaf rust. *Lr34/Yr18/Sr57* has the largest effect, followed by *Lr68* and *Lr46/Yr29/Sr58*. For stripe rust, *Lr34*/*Yr18/Sr57*, *Lr46/Yr29/Sr58* and *Lr27/Yr30/Sr2* contributed the largest portion of the resistance, respectively. For stem rust, *Lr27/Yr30/Sr2* conferred the largest resistance effect, while the genes *Sr-5A* and *Lr34/Yr18/Sr57* from Parula and *Sr12* from Thatcher act *synergistically with Lr27/Yr30/Sr2 to increase stem rust resistance.* Based on these findings, we propose that 2-3 R genes added to a foundational multi-APR cassette of *Lr34/Yr18/Sr57*, *Lr46/Yr29/Sr58*/ and *Lr27/Yr30/Sr2* will achieve desirable and durable resistance to all 3 rusts in Canadian wheat.

[P34] GENOMIC SCREENING FOR MOLECULAR SIGNATURES OF SELECTION DURING WHEAT IMPROVEMENT. Wentao Zhang[1], Bianyun Yu[1], Emma Hsueh[1], Christine Sidebottom[1], Peng Gao[1], David Konkin[1], Ron Knox[2], Curtis Pozniak[3], Richard Cuthbert[2], Yuefeng Ruan[2], Brent McCallum[4], Maria Antonia Henriquez[4], Kerry Boyle[1], P.R. Fobert[5], and Andrew Sharpe[1]. [1]Aquatic and Crop Resources Development, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9; [2]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, Post Office Box 1030, Swift Current, SK, S9H 3X2; [3]Crop Development Centre, University of Saskatchewan, Agriculture Building, 51 Campus Drive Saskatoon, SK, S7N 5A8 Saskatoon, SK, S7N 5A8; [4]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, R6M 1Y5; and [5]Aquatic and Crop Resource Development Research Centre, National Research Council Canada, 100 Sussex Drive, Ottawa, ON, K1N 5A2
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Since the advent of Canadian wheat breeding in 1886, the crop has undergone intensive selection by breeders and led to the release of a large number of locally adapted modern cultivars with high yield, better disease resistance, improved agronomics, and enhanced end-use quality. Genetic contributions play an important role in these improvements; however, little is known about the underling genomic changes. To identify these genomic changes underlying Canadian wheat, we performed population level genetic analysis using a large dataset generated by a deep re-sequencing of a diverse accession of wheat. These accessions include Canadian heritage and elite cultivars, USA cultivars, cultivars from other counties, landraces, and newly synthesized hexaploid wheat. In total, we identified 3.1 million single nucleotide polymorphisms (SNPs), with an almost equal number of variants across A, B and D genomes (averaging approximately 1 variant in every 100 bp). Diversity analysis revealed that there is almost no mixture between Canadian wheat lines and lines from other countries. We also observed a dramatic reduction of diversity in Canadian wheat from ~1930 (the release of Thatcher). The nucleotide diversity (*pi*; π) showed an elevated level of diversity in D genomes from synthetic hexaploidy wheat. The negative

Tajima's D value indicates an intensively directional selection on Canadian wheat. Cold spots of recombination were identified linkage disequilibrium analysis and a greatest extend LD block was observed on 7A. We will present our findings focusing on signatures of selection in Canadian wheat as well as their implications in wheat breeding.

Abstracts for CWFHB Poster Presentations

[P35] AAC GOLDMAN – A CULTIVAR WITH LOWER DEOXYNIVALENOL CONTENT HOLDS PROMISE FOR MALTING AND BREWING. Ana Badea[1], Bill Legge[1], James Tucker[1], Adam Carter[1], Christian Azar[2], Peter Watts[3], and Yueshu Li[3]. [1]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Rd., Brandon, MB, Canada, R7C 1A1; [2]La Coop Fédérée, 19235, avenue Saint-Louis Ave., Saint-Hyacinthe, QC, Canada, J2T 5J4; and [3]Canadian Malting Barley Technical Centre, 303 Main St., Winnipeg, MB, Canada, R3C 3G7
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AAC Goldman is a two-row, malting barley cultivar widely adapted to western Canada. It was developed at Agriculture and Agri-Food Canada Brandon Research and Development Centre (AAFC-BRDC) from the cross TR04282/Newdale by isolated microspore culture. TR04282 is an elite line developed at AAFC-BRDC from the cross Harbin/TR253//TR253. Harbin is a two-row accession from China used as the FHB resistance source. When evaluated in FHB nurseries in Manitoba, AAC Goldman has consistently displayed 35% less deoxynivalenol than the well-known malting cultivar AC Metcalfe.
The license for AAC Goldman was awarded to La Coop Fédérée in 2017 and received registration from the Variety Registration Office, Canadian Food Inspection Agency in 2018.
In collaboration with the Canadian Malting Barley Technical Center, malting and its first detailed brewing analyses and sensory evaluation were conducted alongside AC Metcalfe (malt quality standard), on grain samples grown by La Coop Fédérée and AAFC-BRDC at three locations in 2017.
The overall malt quality for AAC Goldman was good (very good values in friability, extract yield, soluble protein, and enzymes; however, lower FAN levels). Under the brewing conditions used, on average, AAC Goldman showed quicker conversion time, produced wort with higher pH, comparable colour and higher attenuation limit than AC Metcalfe. The sensory evaluation of finished beers made from these two cultivars observed intensities of 38 flavours and aromas and are presented for each variety.
These preliminary analyses indicate that, soon, the Canadian farmers and barley industry will have another good choice available when it comes to malting barley.

[P36] PROSPECTING FOR MICROBIAL TRANSFORMATIONS OF TRICHOTHECENES. Matthew Bakker[1] and Susan McCormick[1]. [1]Mycotoxin Prevention & Applied Microbiology, US Department of Agriculture, 1815 N University St, Peoria, IL 61604 USA
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The production and accumulation of trichothecene mycotoxins is responsible for much of the negative economic impact associated with Fusarium head blight. A variety of biochemical transformations to trichothecenes have been described, some of which result in a less toxic product. We expect that continued prospecting will reveal additional microbial transformations to trichothecenes, and eventually microbial enzymes having utility in plant protection or in restoring value to contaminated grain. We have developed methods for producing enrichment cultures in which complex microbial consortia (e.g., seeded from soil dilutions) are directed towards the transformation of deoxynivalenol (DON). While we can reliably produce enrichment cultures that transform DON, deriving from these communities a pure culture of an organism that transforms DON has remained elusive. Separately, we have performed hundreds of screens of individual isolates belonging to dozens of taxa for the ability to reduce the concentration of DON in culture media. Here we highlight two strains that have reliably transformed DON under varied culture conditions, including both broth and solid substrates. These strains both belong to the family Pseudonocardiaceae, within the Actinobacteria.

[P37] PROGRESS IN GENOTYPING AND PHENOTYPING WHEAT PLANTS WITH EDITING IN GENES ASSOCIATED WITH EITHER RESISTANCE OR SUSCEPTIBILITY TO FHB. Margaret Balcerzak[1], Vivijan Babic[2], Xiucheng Cui[1,3], Vishwanath Sollapura[1], Johann Schernthaner[1], Gopal Subramaniam[1], Raju Datla[2], and Thérèse Ouellet[1]. [1]Ottawa Research and Development Centre, Agriculture and AgriFood Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6; [2]Aquatic and Crop Resource Development, National Research Council Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9; and [3]Department of Biology, University of Ottawa, Ottawa, ON
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The clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9) has been used to inactivate two wheat genes identified in previous experiments. Expression of a non-specific lipid transfer protein (nsLTP) has been associated with resistance to Fusarium head blight (FHB) carried by the 5AS resistance QTL. Silencing of the Nuclear Factor X box-binding-Like 1 (NFXL1) gene in transient assay has been shown to reduce susceptibility to FHB of the wheat cultivar Roblin. Pairs of sgRNAs specific for those two genes were shown in an *in vitro* CRISPR/Cas9 assay using protoplasts to efficiently and specifically guide the sequence-specific cleavage of the DNA. Those sgRNAs have now been used to produce transgenic plants with gene editing of either nsLTP or NFXL1 in one to three of the wheat genomes. Progress on genotyping and phenotyping for FHB symptoms of the transgenic plants will be presented.

[P38] MOLECULAR MAPPING OF QTL FOR *FUSARIUM GRAMINEARUM* BIOMASS AND DEOXYNIVALENOL ACCUMULATION IN SPRING WHEAT GRAIN. Samia Barraies[1], Ron Knox[1], Richard Cuthbert[1], Maria Antonia Henriquez[2], Thérèse Ouellet[3], Margaret Balcerzak[3], Barbara Blackwell[3], Vijai Bhadauria[1], Brad Meyer[1], Yuefeng Ruan[1], and Jatinder Sangha[1]. [1]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road Box 1030, Swift Current, SK, Canada, S9H 3X2; [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden MB, Canada, R6M 1Y5; and [3]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa ON, Canada, K1A 0C6
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Fusarium graminearum a causal agent of Fusarium head blight (FHB) of wheat produces deoxynivalenol (DON), the predominant trichothecene mycotoxin in contaminated wheat grain that, when ingested, causes a wide range of acute and chronic effects in humans and animals. Understanding the genetics and identifying molecular markers associated with low FHB symptoms and DON levels is needed to select for resistance breeding in early generation lines. In this study grain samples from 178 doubled haploid (DH) lines derived from the elite cross Carberry/AC Cadillac were harvested from a Fusarium-inoculated nursery near Morden (MB). A qPCR-based analytical method was applied to quantify the biomass of *F. graminearum* in grain of each DH line. The DH lines were also evaluated for DON accumulation. We investigated the correlation between *Fusarium* biomass and DON levels, and identified molecular markers associated with low *Fusarium* infection and DON. A significant correlation was observed between the fungal biomass and the amount of DON produced ($r = 0.749$, $P<0.0001$, $n = 178$). Composite interval mapping detected QTL on chromosomes 3B, 4A, 5BS and 5BL for low DON and QTL on chromosomes 3B, 4B, 5BS, 5BL, and 7A for low *Fusarium* biomass. Resistance to the two traits co-located on chromosomes 3B, 5BS, and 5BL. The QTL on 4B accounted for the most *Fusarium* biomass variation at 9.5%. The QTL on 3B explained higher phenotypic variation for DON at 14.5% than for *Fusarium* biomass at 6.5%. This information will be valuable in marker-assisted breeding for lower DON accumulation in wheat grain.

[P39] GRAMILLIN A AND B ARE HOST-SPECIFIC PHYTOTOXINS PRODUCED BY *FUSARIUM* GRAMINEARUM. Barbara A. Blackwell[1], Adilah Bahadoor[2], Elizabeth K. Brauer[1], Whynn Bosnich[1], Danielle Schneiderman[1], Anne Johnston[1], Yves Aubin[3], Jeremy E. Melanson[2], and Linda J. Harris[1]. [1]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6; [2]Measurement Science and Standards, National Research Council Canada, Ottawa, ON, Canada; and [3]Centre for Biologics Evaluation, Biologics and Genetic Therapies Directorate, Health Canada, Ottawa, ON, Canada
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The *F. graminearum* genome contains an array of biosynthetic gene clusters that are also co-induced with the trichothecene genes, including the nonribosomal peptide synthetase 8 (NRPS8) gene cluster. Through targeted gene disruption, we demonstrated that NRPS8 (encoded by *GRA1*) is required for the biosynthesis of two novel cyclic lipopeptides, gramillins A and B. The full structural elucidation was performed on a purified but inseparable mixture of unlabeled gramillin A and B and ^{15}N-enriched gramillins using a combination of LC-HRMS, 1D and 2D NMR experiments. The gramillins possess a fused bicyclic structure of seven amino residues with ring closure of the main peptide macrocycle occurring via an anhydride bond and a disulfide bond between adjacent cysteines. The anhydride bond is stable under the acidic conditions observed during trichothecene and gramillin biosynthesis by *F. graminearum*. The gramillins are biosynthesized during maize silk infection, facilitating fungal virulence on maize. However, there is no significant reduction of wheat spike infection by *F. graminearum* unable to produce gramillin. Infiltration of purified gramillins induces cell death in maize, but not in wheat. *F. graminearum* deploys the gramillins as a virulence factor in maize, but not in wheat, thus displaying host-specific adaptation.

[P40] BARNYARD GRASS (*ECHINOCHLOA CRUSGALLI)* CONTROL WITH ARYLEX™ ACTIVE HERBICIDE AND SIMPLICITY™ HERBICIDE AS A FUSARIUM ALTERNATE HOST CONTROL STRATEGY. Rory Degenhardt[1], Jamshid Ashigh[1], and Katherine Ward[1]. [1]Corteva Agriscience, Agricultural Division of Dow-Dupont. 24th Floor, 215 - 2nd Street SW, Calgary, AB T2P 1M4
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Managing plants that can serve as an alternative host of Fusarium Head Blight pathogen (i.e., *Fusarium graminearum*) is an important strategy for the control of this pathogen in cereals. Barnyard Grass (*Echinochloa crusgalli)* is a competitive weed species in cereals in the western prairies that can serve as an alternate host for *Fusarium graminearum*. Small-plot research trials were conducted to evaluate the efficacy of the Group 2 graminicide Simplicity™ (pyroxsulam), and two herbicides containing the Group 4 Arylex™ active (halauxifen-methyl) on barnyard grass, when applied post-emergence in spring wheat in Western Canada. Results showed that post-emergence application of Pixxaro (5 g ae/ha Arylex + 77 g ae/ha fluroxypyr-meptyl + 350 g ae/ha MCPA ester), Paradigm (5 g ae/ha Arylex + 5 g ai/ha florasulam), or Simplicity at both the 11.25 and 15 g ai/ha rates, provided control of barnyard grass. The use of these herbicides will not only provide growers with robust tools for controlling barnyard grass using under-utilized modes of action for this weed, but may also improve management of Fusarium Head Blight in wheat by removing an alternate host for the pathogen.

[P41] VALIDATION OF UNIQUE METABOLIC FEATURES OF *CLONOSTACHYS ROSEA* STRAIN ACM941 CONTRIBUTING TO ITS BIO-CONTROL OF *FUSARIUM GRAMINEARUM*. Zerihun A. Demissie[1], Tom Witte[2], Simon Foote[1], Linda Harris[2], David Overy[2], and Michele C. Loewen[1]. [1]National Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario, K1A 0R6; and [2]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Clonostachys rosea strain ACM941 is patented as a biocontrol agent against the Fusarium Head Blight causative agent *Fusarium graminearum*. Although the molecular and biochemical basis are not yet fully resolved, previous studies have suggested that *C. rosea* secretes *Fusarium* growth inhibitors when grown in liquid medium. To gain insight into the genetic and metabolic factors contributing to this, we are

investigating ACM941's responses under a variety of different conditions that mimic natural environments. These include treatment with deoxynivalenol (DON) or Fusarium-spent media, plate confrontation and in comparison to other less potent strains of *C. rosea*. We are currently applying transcriptomic (RNAseq), metabolomic (HR-MS) profiling methods as well *in vivo* and *in vitro* functional characterization to identify and validate target genes, gene clusters, pathways and metabolites of interest. Notably, we have obtained new metabolomics data confirming accumulation of TMC151 metabolites in a *C. rosea vs. F. graminearum* plate confrontation assay, consistent with our prior identification of a potential biosynthetic gene cluster for this anti-fungal metabolite. An update on our production and testing of *C. rosea* lines with select genes from the putative TMC151 gene cluster knocked out will be presented.

[P42] PROGRESS IN THE TRANSFER OF FHB RESISTANCE FROM CHROMOSOME 7E OF *THINOPYRUM ELONGATUM* INTO CHROMOSOME 7D OF SPRING WHEAT. George Fedak[1], Danielle Wolfe[1], Dawn Chi[1], Therese Ouellet[1], Allen Xue[1], and Fangpu Han[2]. [1]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6; and [2]State Key Laboratory of Plant Cell and Chromosome Engineering, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, No.1 West Beicheng Rd Chaoyang District, Beijing 100101, China
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As has been reported in the past, the long arm of chromosome 7E from *Thinopyrum elongatum* has an exceptionally high level of FHB resistance, eg 9.6% infected florets compared to Chinese Spring the parental cultivar at 57.5% infected florets. The substitution line 7E (7D) was used as the source of resistance in the process of applying the *Ph* mutant to enhance recombination. Progeny of the *Ph* treatment were screened, beginning at the BC F_2 stage with 7E specific markers, mainly developed by the Ouellet lab. Segregates were also inoculated with FHB. The objective being to identify segregates with FHB resistance but carrying the minimal amount of chromatin from chromosome 7E. Screening at the early stages revealed introgressions in the long and short arms of chromosomes 7A, 7B and 7D. Selection was carried out for 5 generations and about 500 progeny to confine introgression to the long arm of chromosome 7D. The most recent lines, had introgression on the long arms of chromosome 7D in the area of barc 53 and barc 111 and other introgression in the telomeric area of 7D at markers barc76, cfd69. G1SH analysis confined the telomeric introgressions.

[P43] VARIATION IN PHENOLIC CONTENT AND COMPOSITION IN MAIZE VARIETIES WITH DIFFERING LEVELS OF RESISTANCE TO *FUSARIUM GRAMINEARUM.* Mehri Hadinezhad, Linda J. Harris, and S. Shea Miller. Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Kernel phenolic content of 5 inbred lines from AAFCs maize breeding program, and 6 recombinant inbred lines (RILs) with differing levels of resistance to *Fusarium graminearum*, as well as B73 (a public inbred), were measured at 11 and 15 days after self-crossing. Sequential extractions were performed to yield soluble free, soluble conjugated, and bound phenolic fractions. Total phenolic content of the fractions was measured with the Folin-Ciocalteu assay, and the phenolic acid profile of each fraction was determined by HPLC-DAD analysis. For all fractions, the concentration (µg/g dry tissue) decreased from day 11 to day 15, due to dilution with increased endosperm volume. The proportion of bound phenolics, however, increased in the same time period at the expense of the conjugated and free fractions. The highest proportion of phenolics were in the bound fraction (63-87%), followed by conjugated phenolics (6-28%), and the free fraction (6-14%). With respect to phenolic acid profile, *t*-ferulic acid was predominant in the bound fraction, caffeic acid was the major component in the conjugated fraction, and chlorogenic acid dominated the free fraction. A significant negative correlation ($r = 0.58$, $P < 0.05$) was observed between the concentration of bound phenolics and disease severity at 15 days after silking. In addition, a significant correlation was observed between free phenolics and smut susceptibility ($r = 0.73$, $P < 0.05$).

[P44] SCREENING OF DURUM WHEAT GERMPLASM WITH ENHANCED FUSARIUM HEAD BLIGHT RESISTANCE. Jemanesh K. Haile[1], Hermann Bürstmayr[2], and Curtis J. Pozniak[1]. [1]Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8; and [2]University of Natural Resources and Life Sciences Vienna, Institute of Biotechnology in Plant Production, Konrad Lorenz Str. 20, A-3430 Tulln, Austria
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In recent years, durum wheat production in Western Canada has been seriously threatened by epidemics of Fusarium head blight (FHB), caused mainly by *Fusarium graminearum*. Deployment of FHB-resistant cultivars has been considered the most effective and cost-efficient strategy to combat this disease. However, limited progress has been made in improving FHB resistance in durum wheat. Additionally, most current durum wheat cultivars are highly susceptible and there is narrow genetic variation for FHB resistance in elite germplasm. Therefore, extensive screening of new germplasm collections is important. Six crosses were made between Canadian breeding lines and a European breeding line DBC-480 that carries the FHB resistance gene *Fhb1* (DBC-480-1/DT881, DBC-480-10-2/DT881, DBC-480-fam-3/DT881, DBC-480-1/D04X.84.030, DBC-480-10-2/D04X.84.088 and DBC-480-fam-3/D04X.84.104). The progeny from the crosses and 10 susceptible and moderately susceptible checks were evaluated for type II resistance in the greenhouse during December 2017 to April 2018. We used a mixture of 3-ADON and 15-ADON chemotypes, which are dominant in Western Canada, for point inoculation. The inoculated spikes were scored for disease severity 21 days after inoculation according to a 0-100% scale for the visually infected spikelets. Differences in severity responses were observed among and within crosses; particularly, progeny from three crosses showed a 21 to 33% reduction in disease severity than the moderately susceptible durum check cultivars. About 35% of the plants from these crosses were advanced for further evaluation and could also be used as parents in future crosses to enhance FHB resistance breeding in durum wheat.

[P45] EXPLORING THE GENETIC DIVERSITY AND MYCOTOXIGENIC POTENTIAL OF CANADIAN *FUSARIUM POAE* ISOLATES. Linda J. Harris, Anne Johnston, Anne Hermans, Amanda Sproule, Frédéric Vachon, Tom Witte, Allen Xue, Jeremy Dettman, Nguyen Hai, and David Overy. Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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FHB-damaged grain is often co-contaminated with a number of *Fusarium* species, including *Fusarium graminearum* (main causal agent of FHB), *Fusarium avenaceum*, and *Fusarium poae*. These species are each capable of producing a diverse set of mycotoxins and other secondary metabolites. Recent Ontario surveys suggest that *F. poae* is the main fungus isolated from oats while *F. poae* and *F. graminearum* share the title of most commonly isolated from barley. European and Asian isolates of *F. poae* have been reported to produce type A and type B trichothecenes as well as beauvericin, cyclonerodiol, and enniatins, but little is known about the mycotoxigenic potential of Canadian isolates. We are interested in the genetic diversity and mycotoxin profile of the Canadian *F. poae* population. A set of 207 *F. poae* monosporic strains were obtained from oat, barley and wheat samples collected in several Canadian provinces (primarily ON but also QC and SK, 2006-2017 field seasons). Sequencing the *tef1α* gene confirmed the species identification and sequencing two trichothecene biosynthetic genes (*TRI1* and *TRI8*) allowed assignment of the isolates into 13 groups. Metabolomic profiling on YES agar demonstrated the chemotype diversity of an initial set of 160 strains and the production of certain trichothecenes and emerging mycotoxins was confirmed. Emerging mycotoxins diacetoxyscirpenol and beauvericin were consistently produced by all strains. A representative subset of 46 strains was chosen for intensified metabolomics profiling and genome sequencing (NextSeq).

[P46] TRANSCRIPTOMICS RESPONSE OF AAC TENACIOUS AFTER INOCULATION WITH *FUSARIUM GRAMINEARUM*. Maria Antonia Henriquez[1], Sean Walkowiak[2], Kirby Nilsen[2], and Curtis Pozniak[2]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100; and [2]Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8
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Fusarium head blight (FHB), is the most serious fungal disease affecting wheat and other small grain cereals in Canada. This disease is caused by a number of *Fusarium* species. In Canada, *Fusarium graminearum* is the main causal agent of FHB in grain. This fungus can cause severe yield and quality losses. Yield losses occur mainly by reduction in grain quality due to shriveled and/or discolored kernels, which are referred to as Fusarium-damaged kernels (FDK), and contamination of grain with the trichothecene mycotoxin deoxynivalenol (DON). The most effective method to decrease FHB of cereal crops is to develop resistant cultivars. In this project, we performed transcriptome analysis of the resistant cultivar AAC Tenacious and the susceptible cultivar Roblin. Confocal microscopy from spikelets and rachis of infected wheat spikes showed no visible FHB symptoms on the spikelet(s) above or below the inoculated floret in AAC Tenacious. However, *Fusarium graminearum* was present in the rachis above or below the point of inoculation. Data revealed that the rachis node could play an important structural and/or genetic role in the control of FHB in AAC Tenacious. RNA-seq data analysis from the rachis node and rachilla will be discussed. This study will contribute to the identification of intra- and inter-genomic variation of wheat expressed genes, genes associated with FHB resistance, and to the development of SNP markers associated with improved FHB resistance in wheat.

[P47] ANALYSIS OF FUSARIUM HEAD BLIGHT RESISTANCE IN A CANADIAN WINTER WHEAT DOUBLED HAPLOID POPULATION. Minkyung Kang-Choi[1,2], André Kalikililo[2], Mitra Serajazari[1], Nicholas Wilker[1], Allen Xue[2], Sylvie Cloutier[2], Alireza Navabi[1], and Gavin Humphreys[2]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON, Canada N1G 2W1; and [2]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Fusarium head blight (FHB) is one of the most devastating diseases of wheat, causing significant reduction in grain yield and end-use quality. The Canadian winter wheat varieties, 'AC Morley' and 'Emerson' have shown notable FHB resistance in the field, but the genetic nature of FHB resistance in these varieties is not well understood. FHB resistance is a quantitative trait that is controlled by multiple genes, and it is affected by genotype (G), environment (E), and their interaction. Studies have reported a relationship between morphological traits such as plant height and anther extrusion/retention, and FHB resistance. To study the genetic basis of resistance in 'AC Morley' and 'Emerson', a F_1-derived doubled haploid (DH) population was developed. The population was tested for FHB resistance both in the greenhouse using point inoculation and in inoculated field nurseries followed by mist irrigation along with checks. Indoor screening for FHB Type II resistance was performed in the summer 2017 at the Ottawa Research and Development Centre, and field evaluation for FHB visual rating index ((FHB incidence x FHB severity) /100) was conducted in 2017/18 cropping year at two locations, Ottawa and Elora, ON, Canada. In addition to FHB resistance-related data, morphological characteristics, such as plant height and anther extrusion, were also used in the analysis. Transgressive segregation for type II resistance and field resistance was detected in the 'AC Morley' and 'Emerson' DH population, and the lowest average disease index score rated was 5% from type II testing and less than 1% from field evaluation.

[P48] ADEPIDYN® A NEW FUNGICIDE FOR FUSARIUM HEAD BLIGHT DISEASE CONTROL IN WHEAT. Robert Klewchuk[1], Kurt Anaka[1] , Brady Code[1], Matt Underwood[1], and Eric Tedford[2]. [1]Syngenta Canada Inc., 140 Research Lane, Guelph, ON, Canada, N1G 4Z3; and [2]Syngenta Crop Protection, Greensboro, NC, USA, 27419
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Fusarium Head Blight (FHB) is a threat to cereal production in many parts of the world. Management of FHB has been primarily achieved through a limited number of De-Methylation Inhibitor (DMI) triazole

fungicides. The window of application for effective control can be limited dependent on growing conditions and some DMI technology can be limited by a narrow window of application at flowering. FHB foliar management has exclusively relied on DMI technology in Canada and can result in high selection pressure on the pathogen and reduced efficacy upon repeated use. Adepidyn® fungicide is a carboximide succinate dehydrogenase inhibitor (SDHI) from Syngenta and the only carboximide SDHI to demonstrate high activity against diseases caused by *Fusarium*. In field trials conducted across North America, Adepidyn® fungicide was effective against FHB when applied from mid ear emergence through flowering (BBCH 57 to BBCH 65), offering consistency across the application window. In field trials, the performance of Adepidyn® fungicide matched or exceeded the efficacy observed by DMI fungicides, enhanced the duration of control and helped to reduce mycotoxin levels. The potency of Adepidyn® fungicide, its wide-spectrum of activity, extended application flexibility, and long residual control provide for exceptional disease management in cereals.

[P49] EFFECT OF PLANT GROWTH REGULATORS ON FUSARIUM HEAD BLIGHT INFECTION OF SPRING WHEAT. Younyoung Lee, Zesong Ye, and Anita Brûlé-Babel. Department of Plant Science, University of Manitoba, 66 Dafoe Rd., Winnipeg, MB, Canada, R3T 2N2
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Plant growth regulators (PGRs) are being used to reduce plant height and lodging, and increase yield in intensively managed spring wheat cultivars. However, short plant stature has been associated with higher incidence of Fusarium head blight (FHB) in wheat. This may be because spikes of short plants are closer to the inoculum source, or plants may carry semi-dwarfing alleles that increase anther retention. The objective of this study was to determine the effect of the plant growth regulator Manipulator™ on FHB, plant height, anther retention, and yield of spring wheat genotypes that differ in height and FHB resistance. This experiment was conducted at two locations, Winnipeg and Carman, Manitoba, in 2018. The experimental design was a four replicate split plot with PGR (+/-) and inoculation treatment (+/-) as the main plot effect and cultivar (AAC Tenacious, AAC Cameron, AAC Brandon, Prosper and AAC Penhold) as the subplot effect. Cultivars were chosen to provide a range of classes, plant heights, and reactions to FHB. Plots were six 3m long rows (17 cm spacing). Manipulator was applied at the recommended rate and timing. Inoculations were conducted with a mix of four *Fusarium graminearum* isolates at 50% anthesis and three days later. Mist irrigation was used after each inoculation to maintain humidity for FHB infection. Data were collected on emergence, anther retention, FHB incidence and severity, plant height, lodging, spikes/m^2 yield, kernel weight, and test weight. Data will be analyzed and presented. This experiment will be repeated in 2019 and 2020.

[P50] FUSARIUM HEAD BLIGHT RESISTANCE QTL IN AN ELITE DOUBLED HAPLOID WINTER WHEAT CROSS 32C*17/PEREGRINE. Yang Lin[1], Anita Brûlé-Babel[1], Curt McCartney[2], Michele C. Loewen[3], and Gavin Humphreys[4]. [1]Department of Plant Science, Faculty of Agricultural and Food Sciences, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2; [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, Canada, R6M 1Y5; [3]National Research Council of Canada, 100 Sussex Drive, Ottawa, ON, Canada, K1A 0R6; and [4]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, ON, Canada, K1A 0C6
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Resistance to Fusarium head blight (FHB) is complex and involves multiple genes with relatively small effects. The breeding line 32C*17 did not carry the widely known *Fhb* genes (*Fhb1*, *Fhb2*, and *Fhb5*) but still showed strong FHB resistance under severe disease pressure in both Canada and Germany. A doubled haploid population was generated from the cross between 32C*17 and the cultivar Peregrine with intermediate FHB resistance. Disease incidence (Inc), severity, Fusarium damaged kernels and deoxynivalenol (DON) were collected from six site-years of field tests and one year of greenhouse testing. Genotyping was done with the 90K wheat Illumina Infinium iSelect SNP array platform. A linkage map with the total length of 1827.56cM was generated and covered approximately 80% of the wheat genome. Transgressive segregation was observed for all FHB traits measured. Several FHB QTLs were detected, but were not consistently shown through all site years. The 32C*17 alleles reduced Inc and DON for QTL identified on chromosomes 6D and 4D. The distance between the 4D QTL and the *Rht-D1* locus was 10-

12 cM in the linkage map and approximately 450,358,490 bp in the physical map, thus this 4D FHB resistance was not directly affected by the *Rht-D1* locus. Peregrine showed intermediate field severity (32.6%) and high greenhouse severity (75.3%), but it still contributed a Type II resistance QTL on the chromosome 3A in both field and greenhouse tests. This study revealed FHB resistance of 32C*17 was mainly contributed by the result of Type I resistance.

[P51] IDENTIFICATION OF PUTATIVE PATTERN RECOGNITION RECEPTORS INVOLVED IN PERCEPTION OF *FUSARIUM GRAMINEARUM*. N.K. Manes[1,2], E.K. Brauer[2], and R. Subramaniam[1,2]. [1]Dept. of Biology, Carleton University, 1125 Colonel By Dr, Ottawa, ON K1S 5B6; and [2]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Resistance to Fusarium head blight (FHB) is quantitative. Many years of research in the model plant *Arabidopsis thaliana* has affirmed that components of innate immunity are a major contributor of quantitative resistance. In view of this knowledge, we used the non-host *A. thaliana* to identify components of plant immunity involved in FHB resistance. Plants perceive the presence of microbes via its transmembrane localised pattern recognition receptors (PRRs). PRRs recognize evolutionary conserved regions of a protein present on the pathogens, referred to as pathogen associated molecular patterns or PAMPs. Widely characterized PRRs have been studied in context of bacterial pathogens, but very little is known about that recognize fungi. Here in this study, we used GFP-labelled *Fusarium graminearum* to screen 236 T-DNA lines of PRRs from *A. thaliana*. The screen identified PRRs that are both resistant and susceptible to *F. graminearum* infection. Details of the screen will be presented. Furthermore, the screen underscores of the utility of non-host *A. thaliana* to identify components of FHB resistance.

[P52] RESISTANCE TO FUSARIUM HEAD BLIGHT IS INCREASED BY THE WHEAT LEAF RUST RESISTANCE GENES *LR34* AND *LR67*. Brent D. McCallum, Colin W. Hiebert, and Maria Antonia Henriquez**.** Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, R6M 1Y5, Canada
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The wheat leaf rust resistance gene *Lr34* provides resistance to stripe rust, stem rust, powdery mildew and other diseases. Similarly *Lr67* acts as a multi-pest resistance gene. Both genes interact with other resistance genes in an additive manner. We developed two doubled haploid populations in the Thatcher near-isogenic background, to test the effects of *Lr34* and *Lr67* on Fusarium Head Blight (FHB). The progeny from the crosses Thatcher-*Lr34*/Thatcher-*Lr13* and Thatcher-*Lr67*/Thatcher-*Lr13*, with 84 and 88 progeny lines respectively, were tested in *Fusarium graminearum* inoculated and irrigated field nurseries 2016 and 2017. Visual FHB Index (VRI) was determined in the field and DON content was measured on harvested samples. *Lr34* significantly ($P < 0.05$) reduced VRI and DON, *Lr67* significantly reduced DON, while *Lr13* did not reduce VRI in either cross but did have a significant effect of reducing DON in the cross with *Lr34*. This could have important implications for developing FHB resistance since *Lr34* is already incorporated into a high proportion of Canadian wheat cultivars.

[P53] IDENTIFICATION OF CANDIDATE *FUSARIUM GRAMINEARUM* EFFECTORS DURING INFECTION OF *ARABIDOPSIS THALIANA* USING BIOTIN IDENTIFICATION (BIOID). Mary G. Miltenburg[1,2], Chris Rampitsch[3], Madiha Khan[4], Darrell Desveaux[4], and Rajagopal Subramaniam[1,2,4]. [1]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, K1A 0C6; [2]Dept. of Biology, Carleton University, 1125 Colonel By Drive, Ottawa, ON, K1S 5B6; [3]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100 #100, Morden, MB R6M 1Y5; and [4]Dept. of Cell and Systems Biology, University of Toronto, 25 Harbord Street, Toronto, ON, M5S 3G5
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Fusarium graminearum is a fungal pathogen that causes Fusarium head blight (FHB) in wheat, barley, and other cereal crops. Infection results in the buildup of mycotoxin, making the grain unfit for livestock

feed and human consumption. To further develop ways of combatting FHB it is necessary to improve our understanding of plant-pathogen interactions. This includes identifying proteins which are secreted from pathogens to overcome plant defenses and cause disease, which are known as effectors or virulence proteins. A technique known as proximity-dependant biotin identification (BioID) was used to identify potential effector proteins secreted by *F. graminearum* during the infection of *Arabidopsis* seedlings. BioID is a technique that can be used to identify populations of proximal proteins and novel protein-protein interactions. It uses a promiscuous biotin ligase (BirA) which biotinylates proximal proteins that can then be isolated by affinity purification and mass spectrometry. The ability of BirA to biotinylate proteins in *Arabidopsis* seedlings grown in liquid media supplemented with exogenous biotin was first confirmed. Protein was extracted from *Arabidopsis* seedlings at different time points during infection, and affinity purification was performed to isolate biotin-labelled proteins which were analyzed via mass spectrometry. Analysis of the mass spectrometry results revealed a number of putative effector proteins, which were filtered based on known secreted *F. graminearum* proteins. Currently, assays for characterization of these candidate effectors are being developed which will examine their role in virulence, as well as their localization within a host.

[P54] FITNESS OF THREE *FUSARIUM* PATHOGENS ON OAT GENOTYPES WITH DIFFERENT LEVELS OF RESISTANCE TO FUSARIUM HEAD BLIGHT. Mitali, B., Beyene, B., and Wang, X. Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, Manitoba, Canada, R6M 1Y5
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Fusarium head blight (FHB) has become the most important disease affecting Canadian oat industry, which results in not only yield loss but also contaminates oat grains with mycotoxins that are harmful to human and livestock. Deoxynivalenol, produced mostly by *Fusarium graminearum*, is usually the main trichothecene found in oat grains. However recent surveys in western Canada have indicated that multiple *Fusarium* species, including *F. poae*, *F. graminearum* and *F. sporotrichiolodies,* could be found in commercial oat fields. The complexity of *Fusarium* species affecting oat has raised the concern that whether additional mycotoxins could be detected in oat grains and the effectiveness of resistance deployed in current varieties to different *Fusarium* species. It is also unclear that whether the competition among *Fusarium* species during the infection will have any impact on the production of mycotoxins. In this study, we evaluate the response of ten oat genotypes to three *Fusarium* pathogens, including *F. poae*, *F. graminearum* and *F. sporotrichiolodies.* oat plants are inoculated with isolates from different *Fusarium* species, separately or in combinations. *Fusarium* DNA in infected plants is quantified using qPCR and mycotoxins produced by these *Fusarium* isolates in contaminated grains are evaluated. Our preliminary study indicates that *F. poae* might have a synergistic effect on the virulence of *F. graminearum* and its production of mycotoxins during the infection process suggesting that *F. poae* might play an important role in FHB disease complex affecting oat and post a serious threat to Canadian oat industry.

[P55] IDENTIFICATION OF QUANTITATIVE TRAIT LOCI (QTL) ASSOCIATED WITH FUSARIUM HEAD BLIGHT RESISTANCE IN A DOUBLED HAPLOID D8006W/SUPERIOR WINTER WHEAT POPULATION. Anjan Neupane[1], Ljiljana Tamburic-Ilincic[2], Anita Brûlé-Babel[1], and Curt McCartney[3]
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Fusarium head blight (FHB) caused by *Fusarium graminearum* is a major disease of wheat in North America. FHB infection reduces grain yield, affects end-use quality, and accumulates mycotoxins such as deoxynivalenol (DON) in the grain. The objective of this research was to identify QTL associated with FHB resistance. A doubled haploid soft white winter wheat population consisting of 107 lines from the cross D8006W/Superior was used. Evaluation for FHB reaction was performed using spray inoculation of a macroconidia mixture of four *F. graminearum* isolates representing two chemotypes in replicated field disease nurseries in three locations in Canada in 2016 and 2017 and one location in 2018. Disease

incidence and severity were recorded 21 days post inoculation and FHB index was calculated. Percentage Fusarium damaged kernels and DON content were measured from collected grain samples. Both parental lines showed moderate reaction across all environments for FHB traits. However, the population showed transgressive segregation for FHB reaction with a wide continuous distribution. Genotyping of the population was performed using the 90K Illumina Infinium iSelect single nucleotide polymorphism array and 5194 high quality SNP were selected for analysis. Linkage mapping and QTL analysis was conducted. Several consistent FHB resistance QTL were detected on chromosomes 1A, 2D, 4B, 5A and 7A across multiple environments. Significant FHB resistance QTL identified from this project will be used in winter wheat breeding programs using marker assisted selection.

[P56] INTROGRESSION OF A 7EL DNA FRAGMENT FROM THINOPYRUM ELONGATUM CARRYING FHB RESISTANCE INTO CHINESE SPRING WHEAT BACKGROUND RESULTS IN VARIABLE EXPRESSION OF 7EL GENES. Thérèse Ouellet[1], Aparna Haldar[1,2], Farideh Tekieh[1,2], Emma Hsueh[3], David Konkin[3], and George Fedak[1]. [1]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6; [2]Department of Biology, University of Ottawa, Ottawa, ON, Canada, K1N 6N5; and [3]Aquatic and Crop Resource Development, National Research Council Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9. Correspondence to: therese.ouellet@canada.ca

Thinopyrum elongatum, a close wild relative of wheat, carries genetic resistance to Fusarium head blight (FHB) on the long arm of its chromosome 7E (7EL). A Chinese Spring (CS) ph1b line was crossed with a CS-7E(7D) substitution line to facilitate introgression of 7E fragments from *Thinopyrum* DNA into the 7D chromosome of wheat. Previously designed genomic markers specific for 7EL and for 7D were used to characterize the introgressed material. Progeny from BC_1F_5 and BC_1F_7 families with introgression of about 22 and 41 Mbp, respectively, have been genotyped and phenotyped to confirm the 7EL region of introgression and their response to FHB. In addition, gene expression analysis was performed for selected 7EL genes present in those fragments, to examine the impact of introgression on their expression. To our surprise, expression of 7EL genes present in the introgressed fragments was highly variable in the introgressed progeny examined when compared to their expression pattern in the addition line CS-7EL. Results of the genotyping, phenotyping and gene expression analysis will be presented.

[P57] GENOMIC SELECTION IN DURUM WHEAT: PREDICTION ACCURACIES OF FHB RESISTANCE IN A DIVERSITY PANEL AND ITS APPLICATION IN BIPARENTAL BREEDING POPULATIONS. Raja Ragupathy[1], Yuefeng Ruan[1], Samia Berraies[1], Heather Campbell[1], Brad Meyer[1], Richard D. Cuthbert[1], Maria Antonia Henriquez[2], Santosh Kumar[3], Andrew Burt[3], Wentao Zhang[4], Pierre Fobert[4], and Ron E. Knox[1]. [1]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), Swift Current, SK, S9H 3X2; [2]Morden Research and Development Centre, AAFC, Morden, MB, R6M 1Y5; [3]Brandon Research and Development Centre, AAFC, Brandon, MB, R7A 5Y3; and [4]Aquatic and Crop Resources Development Centre, National Research Council of Canada, Saskatoon, SK, S7N 0W9
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Fusarium head blight (FHB) is a major disease in durum wheat and resistance to FHB involves multiple loci. Hence, prediction of breeding values using genome-wide markers is a promising strategy for selection among non-phenotyped individuals and accelerate genetic gain. In the present study, different statistical models namely, ridge regression-best linear unbiased predictor (rrBLUP), Bayes B and reproducing kernel Hilbert spaces (RKHS) regression are being evaluated. A durum diversity panel consisting of 200 individuals, and two doubled haploid populations from the crosses DT707/DT696 and Strongfield/Blackbird were genotyped using the 90K Infinium iSelect SNP array. The accessions were evaluated for FHB incidence, severity and index in replicated field nurseries at two locations (Brandon and Morden) in 2015, 2016 and 2017. Phenotypic data analysis was carried out to estimate least square (LS) means. From the genotyping assay, a total of 6,899 SNPs were found to be present among the 195 accessions of the durum panel. Using 80% of the 195 lines as the training set, and the remaining 39 lines as the validation set, predictions were carried out in rrBLUP with 100 independent iterations. The mean prediction accuracy for FHB index was found to be 0.57 and 0.52 for Brandon and Morden, respectively. Similarly, the within year genomic prediction accuracy was found to be 0.48, 0.34 and 0.39 for 2015, 2016

and 2017, respectively. Development of two-step genomic selection models using Bayes B and RKHS algorithms and their implementation in breeding populations as test sets is ongoing, and the results will be presented.

[P58] TRANSCRIPTOME ANALYSIS OF AAC TENACIOUS RESISTANCE RESPONSE TO FUSARIUM HEAD BLIGHT USING HIGH THROUGHPUT RNA SEQUENCING. Hamed Soren Seifi[1], Mitra Serajazari[1], Mina Kaviani, Nicholas Wilker[1] and Harpinder Singh Randhawa[2], and Alireza Navabi[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; and [2]Lethbridge Research and Development Centre, Lethbridge, AB, T1J 4B1, Canada
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High yield and quality of wheat (*Triticum aestivum* L.) is seriously threatened by assorted types of biotic and abiotic stress factors, among which Fusarium head blight (FHB; caused by the fungus *Fusarium graminearum*) has historically been most damaging. The mycotoxin produced by this fungus is harmful for human health and livestock feed and productivity. The objectives of this research were to identify molecular defense mechanisms in the AAC Tenacious (Tenacious) variety, which exhibits very high levels of resistance against FHB, both in terms of incidence and severity. In our study, Tenacious was compared with the highly susceptible variety Wilkin following *F. graminearum* and mock inoculations. A total of 202 genes were identified to be differentially upregulated in the resistant interaction compared to the susceptible one. Further gene ontology analysis revealed prominent representations of several pathways involved in plant immune response including lignin biosynthesis, detoxificaton and defense signaling. Moreover, epi-fluorescence microscopy showed strong deposition of phenolic compounds in the infected areas of lemma and palea of the resistant Tenacious, while kernels remained totally intact, suggesting a prominent role for these parts of the florets in suppressing FHB in Tenacious head. Further experiments are under way to fully unravel effective resistance mechanisms against FHB in Tenacious both at the cellular and transcriptional levels.

[P59] CRYPTIC ACTIVATION OF SECONDARY METABOLIC CLUSTERS BY CONSTITUTIVE EXPRESSION OF TRANSCRIPTION FACTOR IN FUSARIUM GRAMINEARUM. Kristina Shostak[1], Amanda Sproule[1], John Vierula[2], David Overy[1], and Gopal Subramaniam[1]. [1]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, K1A 0C6; and [2]Carleton University, 1125 Colonel By Drive, Ottawa, K1S 5B6
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Fusarium graminearum, causative agent of FHB, results in major economic losses worldwide. To develop effective disease management strategies, a comprehensive understanding of the organism's pathogenicity is required. To date, the full role of transcription factor Tri6 in pathogenicity has not been established. As such, its main role is thought to be regulation of deoxynivalenol (DON) production. Several lines of evidence indicate that Tri6 is a global regulator affecting different pathways involved in virulence. Our goal is to establish its role in production of novel secondary metabolites with a role in infection cycle in wheat (*Triticum aestivum*). *F. graminearum* is predicted to possess 67 secondary metabolic clusters encoding small secondary metabolites which could contribute to pathogenicity under specific conditions. Our hypothesis is that Tri6 regulates some of these clusters during the pathogenic cycle. In order to identify regulated clusters, cryptic cluster activation method was pursued. *F. graminearum* strain constitutively expressing *Tri6* was grown in nutrient-rich media at different time-points. The gene and metabolite expression levels were measured and compared with a Δ*Tri6* deletion strain grown under same conditions. Genes from several previously uncharacterized secondary metabolic clusters were differentially expressed in response to constitutive expression of *Tri6*. Metabolomic analysis revealed two novel compounds regulated by Tri6. Isolation and characterization of these molecules as well as identification of their originating biosynthetic cluster is ongoing.

[P60] THE PREVALENCE AND DIVERSITY OF FUSARIUM SPECIES CAUSING FUSARIUM HEAD BLIGHT ON OAT IN MANITOBA. Mourita Tabassum[1], Mitali Banik[2], Meconnen Beyene[2], Fouad Daayf[1], and Xiben Wang[2]. [1]University of Manitoba, Winnipeg, MB, Canada R3T 2N2; and [2]Morden Research and Development Center, Agriculture and Agri-Food Canada, Route 100 Morden, MB, Canada, R6M 1Y5
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Fusarium head blight (FHB), a devastating fungal disease causes by Fusarium spp., can lead to dramatic yield losses and mycotoxin contamination in commercial cereal production. Trichothecenes type-A (T-2 and HT-2) and type-B (DON and NIV) are the most common mycotoxins produced by Fusarium species and recognized as the most acute poisoning mycotoxins. Recent surveys conducted in western Canada have indicated that FHB was common in commercial oat fields. So, this study emphasis on the prevalence and diversity of Fusarium species found in commercial oat fields in Manitoba. 168 samples were collected from 2016 to 2018 and examined for the presence of the following pathogens: Fusarium graminearum, Fusarium poae, Fusarium avenaceum, and Fusarium sporotrichioides through morphological and molecular (conventional and real-time PCR) analysis. Our results suggest that F. poae is the most common Fusarium species found in Oat, followed by F. graminearum and F. sporotrichiodies. In addition, a phylogenetic approach is used to investigate the relationship among F. poae (160 isolates) using (translation elongation factor1-α, Tri1, and Tri8). Furthermore, the level of mycotoxins in grain samples will be analyzed using LC-MS/MS and the correlation between Fusarium DNA and mycotoxin levels will be investigated.

[P61] IDENTIFICATION OF QUANTITATIVE TRAIT LOCI (QTL) ASSOCIATED WITH FUSARIUM HEAD BLIGHT AND SEPTORIA RESISTANCE IN A WINTER WHEAT POPULATION. Ljiljana Tamburic-Ilincic[1] and Silvia Barcellos Rosa[1, 2]. [1]University of Guelph, Ridgetown Campus, 120 Main St E, Ridgetown, ON, Canada, N0P 2C0; and [2]CÉROM, Saint-Mathieu-de-Beloeil, QC, Canada, J3G 0E2
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Fusarium head blight (FHB) and Septoria tritici blotch (STB) are important wheat diseases in North America. The objective of this study was to map loci associated with FHB traits, STB and plant height in a Maxine/ FTHP Redeemer winter wheat population. Evaluation of FHB and STB resistance was performed using spray inoculation of a mixture of *F. graminearum* and *Septoria tritici blotch* isolates, respectively and under natural infections in replicated trials across three environments in Ontario, Canada. FHB disease incidence and severity were recorded and FHB index was calculated. For both diseases, the population showed a continuous distribution pattern and transgressive segregation of progeny. DArT markers were used to generate a genetic map and quantitative trait loci (QTL) analysis were performed by evaluating 105 doubled-haploid lines. FHB resistance QTL were identified on chromosome 2A, 4A, 6A, 3B, 4B, 2D and 3D, while QTL for STB were identified on chromosome 4B and 7A. Plant height QTL were identified on chromosome 4A, 6A, 4B and 2D. QTL identified in this study will be used in winter wheat breeding programs using marker assisted selection (MAS). Key words: Fusarium head blight, Septoria tritici blotch, winter wheat, quantitative trait loci, marker assisted selection

[P62] DETERMINATION OF SOLUBILIZATION RATE, OPTIMAL GRINDING AND EXTRACTION OF DEOXYNIVALENOL FROM WHEAT. M. E. Taylor[1] and R. W. Newkirk[1]. [1]Department of Animal and Poultry Science, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Dr, Saskatoon SK S7N 5A8
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Deoxynivalenol (DON), a secondary metabolite produced by Fusarium graminearum is a major concern worldwide in wheat due to loss of grain quality and toxic effects of DON. Three separate experiments were performed. Infection structures of F. graminearum exist both inside and outside the grain, producing DON, allowed it to be washed off. Intact wheat was soaked and mixed on a magnetic mixer for 1, 5 10, 15, and 20 minutes. The results indicate that 21-55% of DON was transferred into the liquid fraction with increased soaking time ($P < 0.01$). There are three major types of grinders used within both scientific and industry communities, the Retsch, Udy mill, and BUNN grinders. Wheat samples were ground using a Retsch grinder, Udy mill, or BUNN grinder and DON analysis was performed. The comparison of grinders indicated that there was no significant difference between the three grinders. Extraction of DON is

typically accomplished by grinding samples then mixing them in a solution and running the DON test. Ultrasonication is commonly used to lyse cells for extraction of DNA or organelles. In the last experiment, six ground wheat samples were vortex mixed or ultrasonicated in an ultrasonic bath for 2, 3, 6, and 9 minutes. Time did not significantly affect DON extraction by vortex mixing or ultrasonication. The ultrasonic bath significantly increased DON extraction ($P<0.05$) by 11% compared to vortex mixing. These experiments show that soaking grain reduces DON, different grinders have no effect, and ultrasonication increases DON extraction.

[P63] GENETIC ANALYSIS OF RESISTANCE TO FUSARIUM HEAD BLIGHT IN SPRING WHEAT CULTIVARS AC BARRIE, REEDER AND CUTLER. Dinushika Thambugala[1], Anita Brûlé-Babel[2], Barbara Blackwell[3], George Fedak[3], Adam Foster[4], Jeannie Gilbert[1], Maria Antonia Henriquez[1], Richard Martin[4], Brent McCallum[1], Dean Spaner[5], Muhammad Iqbal[5], Curtis Pozniak[6], Amidou N'Diaye[6], and Curt McCartney[1]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, R6M 1Y5, Canada; [2]Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada; [3]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, K1A 0C6, Canada; [4]Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, Charlottetown, PEI, C1A 4N6, Canada; [5]Faculty of Agricultural, Life & Environmental Sciences, University of Alberta, Edmonton, AB, T6G 2P, Canada; and [6]Crop Development Centre, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada
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Fusarium head blight (FHB) is the most destructive disease in wheat worldwide, leading to severe yield and quality losses. To dissect FHB resistance in moderately resistant Canadian spring wheat cultivar AC Barrie, a recombinant inbred line (RIL) population from the cross Cutler/AC Barrie and a doubled haploid (DH) population from the cross AC Barrie/Reeder were phenotyped in replicated field trials in eight environments between 2013 and 2016, and genotyped with Illumina Infinium 90K wheat SNP beadchip. The linkage map of the Cutler/AC Barrie RIL population consisted of 26 linkage groups, 10,178 SNPs, and spanned 2438 cM. The AC Barrie/Reeder linkage map contained 28 linkage groups, 10,877 SNPs markers constituted a total genetic length of 2845 cM. QTL analyses identified fourteen QTL controlling FHB resistance in the AC Barrie/Cutler RIL population on chromosomes 1B, 2A, 2B, 2D, 3B, 4D, 5A, 5B and 6B, with AC Barrie contributing the resistant allele at most of these loci. Major QTL for FHB resistance from AC Barrie were mapped on chromosomes 3B and 6B at the expected locations of *Fhb1* and *Fhb2*. Ten QTL controlling FHB resistance were identified from AC Barrie/Reeder DH population on chromosomes 1B, 2B, 2D, 3B, 4B, 5A, 5B, 7A, 7D and AC Barrie alleles contributed six of these QTL. Reeder alleles contributed two major FHB resistance QTL on chromosomes 3B and 5A at the expected locations of *Fhb1* and *Fhb5*. This study provides insight into the genetic basis of FHB resistance in spring wheat cultivars AC Barrie, Reeder and Cutler.

[P64] DIFFERENTIAL GENE RESPONSE TO *FUSARIUM GRAMINEARUM* IN 'NORMAN' BARLEY. James Tucker[12], Ana Badea[1], Sujit Maiti[2], Bill Legge[1], and Dilantha Fernando[2]. [1]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Rd., Brandon, MB, Canada, R7C 1A1; and [2]Department of Plant Science, 205 Agriculture Building, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2
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Barley (*Hordeum vulgare* L.) is an ancient grain with a long history of production in Canada. Since the mid-90's, barley acres have declined in part due to epidemics of Fusarium head blight caused by *Fusarium graminearum* which renders grains unsuitable for use due to associated mycotoxins. Developing resistant cultivars has been a long-term breeding goal for Agriculture and Agri-Food Canada's Brandon Research and Development Centre, however progress has been limited by the absence of useful resistance sources. An alternative breeding strategy was employed where *in vitro* selection was applied with doubled haploid tissue culture. 'Norman' is a moderately resistant variety that was developed from 'CDC Kendall' via anther-culture on growth media containing deoxynivalenol. Plants of each variety were grown under replication in a growth chamber, and separately inoculated with mixtures of chemotypes (15ADON, 3ADON, NIV) vs. Mock. Highest disease severity was observed in the 3ADON treatment. Spikes were sampled at 72 and 96 hours post infection and flash-frozen and total RNA was

extracted. Sequencing (mRNA) was conducted using an Illumina HiSeq 4000 PE 100 bp, where on average 64 x 10^6 reads (X2 PE) were observed per sample. Reads were aligned to the 2016 barley reference genome using HISAT2. The number of significant differentially expressed genes between varieties increased over time for 15ADON and 3ADON, but not for NIV treatment. Gene functions of differentially expressed genes in this study were exemplified by protein binding, sugar hydrolysis, oxidization, membrane composition, ion and DNA binding; specific genes will be presented.

[P65] THE IMPACT OF SEED TREATMENT, FOLIAR FUNGICIDE TIMING, AND PLANT GROWTH REGULATOR ON DEOXYNIVALENOL CONTENT OF BARLEY. T.K. Turkington[1], K. Xi[2], H. Klein-Gebbinck[3], K.N., Harker[1], J.T., O'Donovan[1], B.D. Tidemann[1], G. Semach[3], B., Beres[4], G., Peng[5], W.E., May[6], R.M., Mohr[7], A. Foster[8], R.A., Martin[8], and B.A. Blackwell[9]. [1]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), Lacombe AB T4L 1W1; [2]Field Crop Development Centre, Alberta Agriculture and Forestry, Lacombe, AB T4L 1W1; [3]Beaverlodge Research Farm, AAFC, Beaverlodge, AB T0H 0C0; [4]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB T1J 4B1; [5]Saskatoon Research and Development Centre, AAFC, Saskatoon, SK S7N 0X2; [6]Indian Head Research Farm, AAFC, Indian Head, SK S0G 2K0; [7]Brandon Research and Development Centre, AAFC, Brandon, MB R7A 5Y3; [8]Charlottetown Research and Development Centre, AAFC, Charlottetown, PEI C1A 4N6; and [9]Ottawa Research and Development Centre, AAFC, Ottawa, ONT K1A 0C6
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A preliminary assessment of the impact of seed treatment, fungicide timing (flag leaf versus head emergence), and plant growth regulator (PGR) on deoxynivalenol (DON) content of malting barley was conducted in 2016 at Melfort and Indian Head, Saskatchewan and Brandon, Manitoba. These sites were in areas where *Fusarium graminearum* was well-established, while 2016 was a year where weather conditions favoured Fusarium head blight development and DON levels were >1 ppm for the check treatments. Insure™ (triticonazole + pyraclostrobin + metalaxyl) seed treatment was used at two times the recommended rate, while Twinline™ (metconazole + pyraclostrobin) and Prosaro™ (tebuconazole + prothioconazole) fungicides were applied at recommended rates at flag leaf and head emergence, respectively. The PGR Ethrel™ (Ethephon) was applied between flag leaf emergence and just prior to head emergence. Significant treatment effects only occurred at Melfort and Indian Head. At both sites Prosaro™ application at head emergence reduced DON from 1.9 to 1.6 ppm, and 2.2 to 0.9 ppm, respectively. At Melfort there was also a significant main effect due to flag leaf fungicide where DON levels were slightly higher when fungicide was applied. At Indian Head, some interactions with fungicide at head emergence were significant, whereby DON levels were always lowest (<1 ppm) and similar when fungicide was applied at head emergence regardless of the other treatments. Other interactions occurred at Melfort and Indian Head, but differences were smaller, with DON levels remaining above 1 ppm and ranging from 1.5-2.2 ppm, and 1.4-1.7 ppm, respectively.

[P66] *FUSARIUM* SPECIES IN RYE IN MANITOBA FROM 2016 TO 2018. Duoduo Wang[1], Anita Brûlé-Babel[1], Maria Antonia Henriquez[2], James Larsen[3], and Teresa De Kievit[4]. [1]Department of Plant Science, Faculty of Agricultural and Food Sciences, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2; [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, Canada, R6M 1Y5; [3]Harrow Research and Development Centre, Agriculture and Agri-Food Canada, Harrow, On, Canada, N0R 1G0; and [4]Department of Microbiology, Faculty of Science, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2
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Very little is known about which *Fusarium* species infect rye and cause Fusarium head blight in rye in Canada. The objective of this study was to conduct a survey of *Fusarium* species infecting fall rye in Manitoba. Spike samples were collected in Manitoba from 18 naturally infected fall rye fields in 2016, five fields in 2017, and two fields in 2018. Kernels from infected spikes were cultured on Spezieller Nährstoffarmer Agar (SNA) plates. More than two hundred single spore isolates were obtained from 650 kernels cultured from the 2016 field samples. Based on morphological features evaluated under the microscope, six species were identified: *F. graminearum*, *F. avenaceum*, *F. culmorum*, *F. equiseti*, *F. poae* and *F. sporotrichioides*. In 2017, only one *Fusarium* species, *F. graminearum,* was isolated from 50 kernel samples. In 2018, two species, *F. graminearum* and *F. poae*, were isolated from 280 kernel

samples. The preliminary results showed that *F. graminearum* (71%) was the most common *Fusarium* species infecting fall rye in Manitoba, followed by *F. sporotrichioides* (14%) and *F. poae* (12%). The species identification of the single spore isolates is being confirmed by DNA sequencing. A greenhouse experiment will be conducted to examine the reaction of selected fall rye genotypes to different *Fusarium* species, including *F. graminearum*, *F. sporotrichioides*, *F. poae*, and *F. avenaceum*.

[P67] EVALUATION OF FUSARIUM HEAD BLIGHT IN FALL RYE. Duoduo Wang[1], Anita Brûlé-Babel[1], James Larsen[2], Maria Antonia Henriquez[3], and Teresa De Kievit[4]. [1]Department of Plant Science, Faculty of Agricultural and Food Sciences, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2; [2]Harrow Research and Development Centre, Agriculture and Agri-Food Canada, Harrow, On, Canada, N0R 1G0; [3]Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, Canada, R6M 1Y5; and [4]Department of Microbiology, Faculty of Science, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2
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Fusarium head blight (FHB) is a common disease that reduces yield and end-use quality in cereals. Little is known about FHB in fall rye in Canada. New hybrid rye cultivars have been introduced into western Canada and information about FHB in rye is required to determine how to manage this disease. In this project, the reactions to *Fusarium graminearum* were evaluated on 70 fall rye genotypes, including lines from Canada, Germany, Poland, Russia and other countries. Seven winter wheat cultivars were used as checks in the trials. The project was conducted in three site years: 2017 Carman, 2018 Winnipeg, and 2018 Carman and will be continued in 2019. All plants were inoculated with a macroconidial suspension of *F. graminearum*, which was a mixture of two isolates of the15-acetyldeoxynivalenol (15ADON) chemotype and two isolates of the 3-acetyldeoxyivalenol (3ADON) chemotype. The concentration of the inoculum was 5 x 10^5 per ml, which was ten times higher than that usually used in wheat. Each plot was inoculated three times: at 30%, 50%, and 70% anthesis, followed by mist irrigation. Data were collected for disease incidence and disease severity in the field, and Fusarium damaged kernels and deoxynivalenol levels in the grain. Results from the field showed that there were differences among genotypes for disease incidence and severity. The most susceptible rye genotypes were not as susceptible as the susceptible wheat checks. In general rye genotypes had lower disease severity than disease incidence, indicating that there may be resistance to disease spread in rye.

[P68] NEW SOURCES OF RESISTANCE TO FUSARIUM HEAD BLIGHT IN SPRING WHEAT. Lipu Wang[1], Wentao Zhang[2], Axel Diederichsen[3], Andrew Sharpe[2], and Randy Kutcher[1]. [1]Cereal & Flax Pathology Lab, Department of Plant Sciences / Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; [2]National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9, Canada; and [3]Agriculture and AgriFood Canada, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada
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Fusarium head blight (FHB or scab) caused by Fusarium spp. is a destructive disease of wheat. Host resistance, coupled with other integrated pest management practices, is considered the best approach to control FHB. In an effort to identify novel sources of FHB resistance, we evaluated wheat germplasm in a Fusarium disease nursery in 2016 and 2017. Four thousand accessions from the Plant Gene Resource of Canada (PGRC), which has a world-wide collection of Triticum aestivum, were evaluated in a field FHB nursery for two seasons; 400 lines with highest resistance were selected for genome-wide association study (GWAS) to confirm the new resistance genes. In addition, 412 lines were evaluated from a synthetic hexaploid wheat association mapping (SHW AM) panel, which were created by crossing durum wheat (AABB) and Aegilops tauschii (DD) at the International Wheat Research Centre in Mexico (CIMMYT). The SHW AM panel was genotyped with wheat 90K Infinium SNP chips. A high density haplotype map was developed with markers identified by anchoring into the bread wheat consensus map. With the field data from 2016 and 2017, several novel FHB alleles/or QTLs were identified by GWAS in SHW AM panel.

[P69] AGGRESSIVENESS OF *FUSARIUM POAE* ISOLATES CAUSING HEAD BLIGHT IN OAT. Allen G. Xue, Yuanhong Chen, Barbara Blackwell, Linda J. Harris, and David P. Overy. Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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The aggressiveness of 15 *Fusarium poae* isolates in causing Fusarium head blight (FHB) in oat was studied under controlled conditions. Two oat genotypes varying in resistance to FHB were artificially inoculated with the 15 isolates 7-10 d after heading. FHB was rated for incidence (% infected spikes) and severity (% infected spikelets in the affected spikes) on 10-20 spikes in each of three pots per isolate and genotype combination, at 4, 7, 11, and 14 d after inoculation, and for Fusarium damaged kernels (FDK) and percentage of seed-borne infection from the *Fusarium* (SIF) after harvest. Severity of FHB over time was summarized as area under the disease progress curve (AUDPC). All isolates caused FHB symptoms on both oat genotypes, but were significantly less aggressive than the *F. graminearum* isolate used as a positive control. There were significant differences ($P < 0.05$) in AUDPC, FDK and SIF among the isolates. There was also significant isolate and cultivar interaction observed for FDK, suggesting that screening for resistance to FHB caused by *F. poae* requires the use of aggressive isolates or a mixture of several isolates.

[P70] IMPROVEMENT OH FHB RESISTANCE IN WHEAT: RESISTANT COMPONENTS, PHENOLOGY AND HEIGHT. Wentao Zhang[1], Kerry Boyle[1], Anita Brûlé-Babel[2], George Fedak[3], Peng Gao[1], Zeinab Robleh Djama[3], Brittany Polley[1], Bianyun Yu[1], Richard Cuthbert[5], Harpinder Randhawa[6], Robert Graf[6], and Pierre R. Fobert[1,4]. [1]Aquatic and Crop Resources Development, National Research Council of Canada, Saskatoon, SK, S7N 0W9; [2]Department of Plant Science, Agriculture Building, University of Manitoba Winnipeg, MB, R3T 2N2; [3]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, K1A 0C6; [4]Aquatic and Crop Resources Development, National Research Council of Canada, Ottawa, ON, K1A 0R6; [5]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, SwiftCurrent, SK S9H 3X2; and [6]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, T1J 4B1
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Fusarium head blight (FHB) is a devastating fungal disease of small-grain cereals that results in severe yield and quality losses. The most effective solution to address FHB is to develop resistant cultivars. FHB resistance controlled by a few resistant components including incidence, field severity, index, DON accumulation, FDK and spreading (greenhouse). Resistance conferred by each of these components is partial. The combination of different resistant components is necessary to achieve the desired FHB resistance to protect wheat from yield losses. Here, with analysis of a multi-parental mapping population targeted for FHB resistance, we will provide a detailed findings of the genetic architecture underlying these resistant components and their effects to improve of the resistance in wheat. In addition, phenology related genes including flower time, vernalisation and photoperiod as well as plant height genes also play important roles in FHB resistance. Thus, we will also provide some findings about the interactions of these genes with different resistant components. Finally, *FHB1* is the gene that confers major FHB resistance. However, the magnitude of its effect affects by genetic background. And additionally, in spite of recently published cloned the major *FHB1* gene, there is still arguable that this is the sole gene of *FHB1* underlying *FHB1* region. Therefore, we will also provide some findings about the effect of *FHB1* loci under Canadian wheat background and its effect contributed to these FHB resistant components.

[P71] PROTEOMICS ANALYSES OF FOUR CHEMOTYPES OF *FUSARIUM GRAMINEARUM* LEADS IN THE UNDERSTANDING OF MECHANISMS IN HOST PATHOGEN INTERACTION. Zhongwei Zou, Yaping Wang, Changqin Chen, and W.G. Dilantha Fernando. Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2
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Fusarium head blight (FHB) in wheat is caused by the fungal pathogen *Fusarium graminearum*, which results in reduced quality and quantity of grain. Protein samples from four different chemotypes including 3ADON, 15ADON, NIV, and NX2, were extracted from pellet and culture medium with three biological replications and subjected to iTRAQ (isobaric tags for relative and absolute quantification) analysis. A

total of 188 and 228 proteins were identified from pellet and culture medium, of which 80 and 117 proteins were significant and differentially expressed. In pellet proteins, 42 *F. graminearum* proteins were up regulated and the other 38 proteins were down regulated in the comparison of four chemotypes. In addition, 52 and 66 differentially expressed proteins were up regulated and down regulated respectively in culture medium. Based on sequence similarity to protein database, GO analysis indicates that the identified proteins were divided into 8/7 subcategories of 'cellular component', 8/5 subcategories of 'biological process', and 2/3 subcategories of 'molecular function', respectively, in pellet and culture medium. Numerous differentially expressed proteins between different chemotypes were furtherly analyzed. However, in culture medium, most of the identified proteins including the differentially expressed proteins are uncharacterized. These data will provide insights into understanding the mechanisms of wheat-fusarium interactions.

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