



2016

Research Report

Field Crop Development Centre
and Lacombe Research and Development Centre

Alberta



Agriculture and
Agri-Food Canada

Agriculture et
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From the Head of Research

In the last year we began a strategic planning exercise at FCDC, with the objective of prioritizing our objectives and ensuring proper resource allocation. This process helped us make decisions on where we should be headed in the short, medium and long term. Based on the information analyzed we decided on several changes that will modernize our program at different levels:

- Among the barley types that we work with, we decided to prioritize the two-row for feed, forage and malt. The effort in the six-row and hulless programs was adjusted to match the present and expected demand for the near and long-term future. The size of the overall barley program was increased with around 200 crosses made. The number of populations advanced by single-seed descent was increased to approximately 25 and different crossing techniques were experimented with during the indoor growing season.
- We continued growing F₃s and F₅s in the winter nursery at the University of California Experiment Station at El Centro, and also carried out seed increases.
- We continued introducing and crossing new germplasm from successful programs worldwide in order to expand our good genetic diversity.
- The plant pathology team continued screening, giving input and helping make decisions about the resistance present in our germplasm to the most important diseases, such as scald, stripe rust, net blotch, and Fusarium head blight.
- Our biotechnology lab is researching the newest technologies that are going to increase the efficiency of our breeding process, including genotyping by sequencing and genomic selection.

With these changes, we expect to continue to be competitive in agricultural research and release cultivars that are better than the ones available to farmers today.

The 2015 growing season emphasized how important it is for varieties to show wide adaptation, not just to variability within a field, but to changing conditions within a season, and differences between years. Cultivars had to develop well in dry conditions and then cope with excessive water at the end of the summer, while still maintaining the high productivity and quality needed. With the exception of hail damage on 25% of our experiments in Lacombe and almost the totality of our nursery in Olds, on average the final yields were higher than initially expected based on conditions earlier in the season. This shows the great resilience that improved barley has as a species.

We are looking forward to the new varieties that are going to contribute to the future of agriculture in Alberta.

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Purpose

Through genetic manipulation, we aim to develop high yielding enhanced barley cultivars adapted to Western Canada which also have superior agronomic types, the quality required by consumers in national and international markets, and the disease resistance necessary to protect the yield and quality achieved in a sustainable production system.

Target Area

The main target area for our breeding program is Western Canada, although some of our varieties have shown wide adaptation, including eastern Canada and different countries worldwide.

Barley Objectives

We create barley cultivars with:

1. Higher yield
2. Improved lodging resistance and enhanced agronomic type
3. Earliness to fit Western Canadian growing seasons
4. Superior quality for different final uses
5. Resistance to economically important diseases

To reach our objectives we must address the following areas of research:

I. Breeding / Variety Development

1. Breaking barriers of yield – recurrent selection in pre-breeding program
2. Supporting programs
 - a. Nitrogen use efficiency
 - b. Abiotic stress (drought tolerance and water logging tolerance)
3. Plant pathology: multiple disease resistance
 - a. Fusarium head blight (*Fusarium graminearum*)
 - b. Scald (*Rhynchosporium secalis*)
 - c. Net blotch (*Drechslera teres*)
 - d. Stripe rust (*Puccinia striiformis*)
 - e. Spot blotch (*Bipolaris sorokiniana*)
 - f. Surface-borne and loose smuts resistance (*Ustilago nigra*, *U. hordei*, and *U. nuda*)
 - g. Stem rust (*Puccinia graminis*) (including the new race UG99 – TTKSK)
 - h. Root rot (*Cochliobolus sativus*)
4. Improved end-use quality of barley
 - a. feed
 - i. grain quality
 - ii. forage quality
 - b. malt
 - c. food
5. Maintaining an active germplasm collection and long term storage in our gene bank for cultivar improvement.

II. Production Systems

1. Developing sustainable and integrated best management practices for malting, feed and food barley
 - a. seedling development
 - b. plant growth
 - c. nutrient use efficiency
 - d. soil health
 - e. sustainable rotations
 - f. manipulation of agronomic factors for improved yield and quality
 - g. fertility
 - h. seedbed utilization
 - i. weed management strategies
 - j. disease management strategies
2. Emerging agronomic and crop protection technologies
 - a. varietal response to manipulated agronomic factors
 - b. optimal agronomics for new barley markets (e.g. food barley)
 - c. Evaluating both hulled and hulless barley for the emerging craft malting industry in western Canada
 - d. Fungicide application timing and potential role of seed treatments
 - e. Annual forage utilization (e.g. triticale silage)
 - f. Disease mitigation strategies for close rotation barley or cereal silage/feed grain production

III. Technology Transfer and Market Development

1. Publicize the results of research in a “farmer friendly” format on the website and in print
2. Circulate the *Cereal Research Report* to industry
3. Update technical information on Ropin’ the Web
4. Develop new markets and improve existing ones for malt and feed barley
5. Continue awareness program with Alberta Barley
6. Develop Communication Plan as per recommendation of Management Committee
7. Develop videos to demonstrate FCDC research and goals
8. Submit article ideas to *GrainsWest* publication
9. Conduct tours as requested

Triticale Objectives

Spring Triticale

1. Higher yielding cultivars
2. Maintain good lodging resistance
3. Earlier maturity
4. High grain protein or starch content
5. Higher annual forage yields
6. Reduced awn cultivars for green feed production
7. High forage digestibility
8. Post-harvest sprouting resistant cultivars
9. High test weight

10. Disease resistance
11. Drought tolerance
12. Germplasm maintenance and improvement

Winter Triticale

1. Improved winter hardiness
2. High yielding cultivars
3. Snow mold resistant cultivars
4. Improved grain quality
5. High forage digestibility
6. Sprouting resistant cultivars
7. High test weight
8. Leaf disease resistance
9. Germplasm maintenance and improvement

Wheat Objectives

Winter Wheat

1. Improved winter hardiness
2. Higher yielding cultivars
3. Semi-dwarf cultivars
4. Good grain quality
5. Disease resistance
 - a. rusts
 - b. tan spot
 - c. take-all root rot (in Hermiston, USA)
 - d. powdery mildew
 - e. Fusarium head blight
 - f. snow mold
6. Earlier maturity
7. Sprouting resistance similar to spring wheat
8. Improved drought tolerance
9. Germplasm maintenance and improvement

Spring wheat

1. High yielding CPS varieties (higher grain yield than AAC Foray and Conquer) with early maturity, lodging resistant and good milling quality
2. High yielding general purpose varieties adapted to the western prairie of Canada
3. High level of durable resistance to stripe, leaf and stem rust diseases
4. Acceptable level of FHB tolerance in the new developed wheat lines (compared to SY985)
5. Develop specific wheat populations with unique traits (rusts resistance, FHB, grain quality, drought tolerance and strong straw) to enhance the wheat breeding programs in western Canada

Barley variety development

FCDC develops new two row, six-row and hulless barley varieties for producing feed, malt and food in Alberta and western Canada.

Two row

Two-rowed barley is the preferred hulled barley type grown on almost 95% of the barley acreage in Alberta. This type is the preferred malting and feed barley both domestically and internationally. An increase in production and utilization efficiency of two-rowed barley will have an important economic ripple effect throughout the agriculture industry.

FCDC develops two-row barley varieties with the following traits:

- strong straw
- high yield
- multiple disease resistance (scald, net blotch, smuts, FHB, stripe rust, spot blotch, root rot)
- drought tolerance
- pre-harvest sprouting resistance
- wide adaptation, nutrient efficiency
- quality characteristics desired by the market place

Successes

The two-row program has released ten varieties, including malting barley TR13609 in 2016. TR13609 is a promising new malting barley with potential for craft brewing. TR13609 has shown consistently low DON levels, accumulating up to 50% less DON than AC Metcalfe in 5 years of testing at Brandon. It has good kernel plumpness with a promising malting quality profile of low protein levels, high extract, low DP, and good modification with low wort beta-glucan. TR13609 will be marketed by SeCan.

TR13606 has interim registration. TR13606 has potential as a malting barley for the craft brewing market due to its higher extract and lower FAN. However, due to high beta-glucans and viscosity in micro-malt testing, we sought support for interim registration from the Prairie Recommending Committee for Oat and Barley so that we can have an opportunity to determine if varying the processing protocols in pilot malt testing will result in better modification.

In 2016, we have eight lines (six are malting) in the first year of Western Canadian Two-Row Barley Cooperative trials, and none in the second year of Coop testing. FCDC has one malt line, TR14617, in the second year of Western Canadian Malting Barley Collaborative testing run by the Brewing and Malting Barley Technical Institute to test for malt quality.

Six row

Six-row feed barley is a critically important crop in Alberta. Of the barley types, it has the best combination of yield, maturity, straw strength and barley leaf scald resistance. This is particularly important for the cooler, shorter growing season areas.

FCDC develops six-row barley varieties with the following characteristics:

- high grain and forage yield potential
- strong straw
- early maturity
- feed quality (grain and forage)
- disease resistance (scald, net blotch, smuts)

Successes

In 2016, 20 crosses are planned, ten of which are for germplasm development.

FCDC has seven lines in the 2016 Western Canadian Six-Row Barley Cooperative trials: six in the first year, and one that has been advanced to the second year. This line boasted the highest grain yield in the 2015 Coop tests, better lodging resistance than AC Ranger and Vivar, a good package of disease resistance, and plump seed that meets market requirements.

FCDC has nine lines of six-row barley in the 2016 Western Canadian Forage Barley Cooperative trials: eight in the first year, and one that has been advanced to the second year. This line has superior agronomic performance and high yield in both grain and forage.

FCDC has released 15 six-row feed varieties.

Hulless

FCDC's hulless barley program encompasses both six-row and two-row types. Hulless barley varieties can fit into the feed, forage and food industry.

We aim to develop hulless barley varieties for Alberta with the following characteristics:

- high digestible energy and protein
- drought and disease resistance
- food quality
- sprouting tolerance
- lodging resistance
- threshability
- malting, forage, or food quality
- forage yield

Successes

Twenty hulless crosses are planned for 2016 (ten of which are for germplasm), with four six-row crosses and 16 two-row crosses.

FCDC has 10 entries in the 2016 Western Canadian Hulless Barley Cooperative trials: eight in the first year and two that have advanced to the second year of testing. These lines show high yield potential, better lodging resistance than CDC McGwire, a good package of disease resistance, good threshing ability and plump seed.

FCDC also has two hulless barley entries in the first year of the 2016 Western Canadian Forage Barley Cooperative trials.

FCDC has registered seven hulless barley varieties, including three 2-row varieties and four 6-row.

Barley germplasm creation and evaluation

The success of any plant breeding program depends on the gene resources available. With the great ecological diversity of the grain producing areas of Alberta and western Canada it is essential that we maintain a broad genetic base in germplasm for the program.

New germplasm is introduced from breeding programs around the world and is grown in the field, evaluated for disease resistance, and described and screened for quality and other traits. To develop new germplasm, the best of the introduced lines are selected and crossed with superior varieties adapted to our region.

In 2015, germplasm was introduced from CIMMYT Mexico, ICARDA Morocco, Lebanon, and other breeding programs within Canada. International disease screening includes stripe and leaf rust in Washington; stripe rust, leaf rust and scald in Ecuador; scald, net blotch and leaf rust in Argentina and Uruguay; stem rust in Kenya, and stripe rust, scald and FHB in Mexico.

Currently, over 8100 lines are maintained in our germplasm bank, and over 45,000 pedigrees have passed through the Lacombe screening program.

Winter breeding nursery and seed increase

Growing winter nurseries in California and Oregon during FCDC's usual off season helps rapidly advance large numbers of populations at a relatively low cost.

Spring barley and spring triticale nurseries are grown in El Centro, California in cooperation with University of California – Davis. Spring cereals are planted in October and harvested in March.

Triticale and Wheat variety development

Spring triticale variety development

Spring triticale has shown great potential as a drought resistant feed crop under dryland conditions on the Canadian prairies. It has also proved to be an excellent silage alternative to barley and oats in the parkland zone.

FCDC aims to develop new spring triticale cultivars that have:

- improved agronomic performance, compared to Pronghorn
- early maturity
- improved sprouting resistance
- improved seed type, grain and dry matter yield
- reduced awn expression for feed and swath grazing uses

Progress

To date, FCDC has released 5 spring triticale varieties: Taza, Tyndal, Bunker, Pronghorn, and Wapiti.

In 2015, over 150 crosses were made, with 15% of these for targeted germplasm development.

In the winter of 2015, 60 segregating populations were grown in California. Specific heads were selected for medium height, early maturity and other yield traits and were advanced to the headrows. This shuttle breeding between Alberta and California allows us to speed up the breeding process.

Out of 1800 headrows grown in Lacombe, 128 lines were selected based on medium height, earliness, reduced awn, grain quality and forage potential. Fifteen lines were advanced to Western Triticale Cooperative B trials, and 12 lines were advanced to Coop C trials.

In 2016, the program will focus on grain and forage yield and quality with reduced awns. Early maturity, resistance to pre harvest sprouting and Fusarium head blight resistance are among the targets for new crosses in 2016.

Winter triticale and winter wheat variety development

Crop diversification, efficient land use and erosion control are a few of the many advantages of winter cereals. Winter cereals are also showing potential as for grazing when spring planted in both the brown and black soil zones. However, cultivars presently adapted to the Canadian prairies are late maturing and susceptible to lodging under high rainfall.

FCDC aims to develop new winter triticale varieties with earlier maturity, improved lodging resistance, shorter stature, improved seed type and improved sprouting resistance.

FCDC also intends to release new winter wheat cultivars with earlier maturity, improved lodging resistance (semi-dwarf), and disease resistance in the black soil zone.

Progress

In general, crosses between winter triticale and spring triticale were promising. Several populations showed a very lush growth at juvenile stages, which makes them suitable for grazing and forage.

Significant progress was achieved in yellow rust resistance in winter wheat nurseries, due to the yellow rust infection that occurred in the material at Lacombe and Olds in 2015. Susceptible lines and populations were discarded while resistant lines and introductions were identified and will be evaluated for other significant traits.

Four winter wheat lines were advanced to the Western Winter Wheat Coop B level trials, and three lines were advanced from Coop B to C level. The lines showed a high level of yellow rust resistance, good winter hardiness and had a significantly higher grain yield than the general purpose checks.

In 2015, the FCDC initiated the first Winter Triticale Coop trials in western Canada. The trial included 9 winter triticale candidates.

To date, FCDC has released four winter triticale varieties: Metzger, Luoma, Bobcat, and Pika; the first winter wheat variety Pintail was released in 2011.

Spring wheat variety and germplasm development

The key objective is to develop new high yielding varieties of CPS and CNHR spring wheat to meet market quality needs. We focus mainly on grain yield, lodging resistance, early maturity, disease resistance and agronomic adaptability to the Parkland and Peace River regions.

Progress

Over 1200 new spring wheat introduction from CIMMYT and ICARDA were evaluated in Lacombe for stripe rust resistance, plant height, earliness and grain quality. 290 lines were selected for further evaluation under multiple locations in Alberta.

60 new crosses were made. The main target of the crossing program was grain yield, pyramiding stripe rust resistance genes and earliness. The F₁ progeny was grown in the growth room during winter time.

75 promising lines were evaluated in yield trials in western Canada. High yielding lines with multiple diseases resistance and good milling quality will be advanced to the B level Coop trial.

Germplasm development

Spring triticale

Although spring triticale has shown great potential in the brown soil zones for seed and in the black soil zones for forage, a number of deficiencies such as late maturity and sprouting susceptibility have limited progress.

The chances of developing vastly improved cultivars increases with the degree of genetic variability. FCDC evaluates unique germplasm and breeding lines from programs in Europe, USA, Mexico (CIMMYT) and other research institutes in Canada for adaptation potential.

This material is evaluated for maturity, height, lodging resistance, seed type and sprouting resistance prior to its use in the breeding program. In 2015, 77 new introductions from CIMMYT were evaluated in Lacombe. Selected lines will be evaluated in multi-location yield trials.

Winter triticale and winter wheat

Although both winter wheat and winter triticale are adapted to severe winter conditions, they have less cold tolerance than rye. Additionally, winter triticale does not have the earliness of winter wheat.

Introductions from Europe, USA, and Turkey are evaluated at FCDC. New germplasm lines in both species are created to transfer traits from adapted wheat and rye cultivars into triticale.

All new introductions and germplasm is evaluated for cold tolerance, maturity, seed type, quality, plant height and other characteristics prior to being used in the breeding program.

In 2015, 390 new winter wheat introductions were grown in Lacombe. The promising lines will be evaluated for winter in multiple locations across western Canada.

Winter breeding nursery and seed increase

Growing winter nurseries in California and Oregon during FCDC's usual off season helps rapidly advance large numbers of populations at a relatively low cost.

Spring barley and spring triticale nurseries are grown in El Centro, California in cooperation with University of California – Davis. Spring cereals are planted in October and harvested in March. There were 19 F6 populations and 40 F5 populations of spring triticale growing in 2015.

Winter wheat and winter triticale are grown in Hermiston, Oregon, in cooperation with Oregon State University. Winter cereals are planted in Oregon in October and harvested in March. In 2015, 128 winter wheat and triticale F2 increases, and 180 yield trial increases were grown.

Grain and forage quality evaluation with near-infrared reflectance spectroscopy (NIRS)

Every year FCDC needs to determine the nutritional quality of almost 20,000 grain samples. As grain quality can vary so greatly, a rapid and economic system to measure quality is needed. Since 1993, FCDC has been developing near-infrared reflectance spectroscopy (NIRS) technology for grain and forage quality assessment. This involves developing calibration models to predict the feed, malt and food quality of grains for the breeding programs at FCDC. NIRS is used in the genetic selection process to quickly assess new lines for superior quality and decide on further advancement.

This project relies on our industry partners to identify the end use quality traits that are important to focus on. In partnership with industry, this technology can be transferred to all stakeholders in the Canadian grain characterization system to assess value from producer to end-user.

NIRS development

Since the program was started in 1993 we have developed 59 calibrations for individual quality traits in barley, wheat, triticale and forage (Table 1). These calibration models are developed by comparing NIRS data to traditional wet chemistry results. Once the models have been tested and a certain degree of accuracy is assured, they are used in the FCDC breeding programs to not only evaluate new lines but also identify germplasm with specific quality traits.

These models are continuously being validated and updated with new samples and chemistry. We work with a wide range of industry partners to expand our quality database, which allows us to keep our models up to date, and to stay current with the industry quality requirements and targets. This past year we have sent 184 samples to Rahr Malting for malting evaluation, 48 samples to the Canadian Grain Commission for hulless barley evaluation and 800 samples to Alberta Innovates Technology Futures for toxin analysis. When the data is completed it will be used to update our current calibrations.

We have also been added to a project with Dr. Sheri Strydhorst (Alberta Agriculture and Forestry), looking at quality changes with agronomic treatments. We needed to develop equations that would match their analysis from the first year of the project, and these were completed in the fall of 2015. Barley and wheat calibrations developed will be used for the remaining years of the project. In 2015, we analysed 199 pea samples, 1344 wheat samples and 2238 barley samples for this project.

We are continually strengthening our ties to other industry groups to develop analysis tools to support the goals of the breeding programs.

Table 1. NIRS quality calibrations

Characteristic	Number
Barley	
Feed quality	12
Malt quality	13
Hulless malt quality	11
Silage	7
DON	2
Colour, pearling quality	3
Triticale and Winter Wheat	
Quality	11

Quality Evaluation

In 2015 the grain quality laboratory analyzed over 21,000 samples for specific quality traits. In addition to our own samples we also provide some quality analysis for other research groups within Alberta Agriculture and Forestry, Lacombe, Brandon and Saskatoon.

Malting quality in hulless barley

In 2014 we developed 18 new calibrations for the malting quality evaluation of hulless barley. Of these equations, 11 have the accuracy needed to be used in our system for screening. In 2015, we utilized these equations to evaluate 2050 hulless barley lines for potential malt quality. Prospective samples were advanced for further testing. We received wet chemistry data for another 48 hulless barley samples in 2015. These samples were used to validate the equations developed in 2014 and then added to make the database more robust. A further 48 samples were sent from the 2015 crop year as part of this project, and these will be included in the database as well.

Analyzing FHB infected grain

We have completed the first year of a project to enhance our detection of Deoxynivalenol (DON) and monitor the chemotypes and infection of DON in grains. In 2015 we ran 1534 DON infected samples through the lab. We selected 800 of these samples for further testing through HPLC, to determine the amount of DON, 3ADON and 15ADON. The wet chemistry for these samples was completed this spring and will be used to create new NIR calibration equations for the different DON chemotypes. There is a further 2 years in this project which will allow us to validate the new equations and add to our database. This project will allow us to further develop our ability to quickly and accurately test for DON content in Fusarium Head Blight affected kernels. The calibrations for the different chemotypes will be completed to use on the 2016 crop year samples.

Biotechnology tools in cereal breeding

Improved understanding of the molecular mechanisms behind disease resistance and crop quality may allow plant breeders to better design breeding and crop protection strategies. By comparing barley DNA and/or protein profiles, specific polymorphism can be identified and correlated to the trait of interest. These identified differences in DNA sequences can be adapted for use as a molecular marker. Molecular markers are validated and those that prove reliable will be adapted into the breeding program. Developing and using molecular markers to select important traits will improve gene deployment, allow gene pyramiding and ultimately produce better quality varieties. Various molecular techniques and methodologies are also adapted to study cereal pathogens in order to better predict their virulence and control disease.

The biotechnology laboratory has been focused on the development of molecular markers to aid the selection of new lines with improved disease resistance (scald, Fusarium head blight, net blotch,

stripe rust, smut and spot blotch) dormancy, malt quality enzymes, nitrogen use efficiency and in vitro fiber digestibility of forage.

Scald resistance

Scald (*Rhynchosporium commune*) of barley is a prevalent disease in central Alberta, and causes considerable yield and quality losses. Scald can rapidly change in pathotype composition and frequency, making it difficult to develop durable resistance in barley. Barley resistance genes are specific to the scald race. The cultivar ‘Seebe’ carries durable genetic resistance; however, it has been difficult to transfer this into new malting barley types.

In 2015, we identified by genotyping by sequencing method, 10 new single nucleotide polymorphism (SNP) markers that could be used by breeders to follow the transfer of scald resistance genes on barley chromosomes 2H, 3H, 4H, 5H and 6H from Seebe and Shyri cultivars. SNP markers have an advantage over older marker types, as SNP assays can be easily scaled-up on non gel based analysis systems, and thereby can increase sample through-put while reducing the cost for genotyping.

Over the past decade we have identified multiple quantitative trait loci (QTLs) linked to scald resistance, which allow us to predict scald resistance in breeding lines. Using these molecular markers we have been successful at breaking the negative linkage to malt quality while improving scald resistance. However, the effectiveness of our selection for scald resistance varies depending on barley genetics, environment, and the scald races present. Over 3,100 malt barley breeding lines were screened for scald resistance using these markers in the summers of 2011, 2012, 2013 and 2014, 2015 and will be continued in 2016.

Scald disease resistance is complicated by the ability of the scald pathogen to quickly adapt to single gene host resistance. Barley breeders must pyramid scald resistance genes in order to provide more durable resistance. We have been genotyping (fingerprinting) scald races present in central Alberta fields. By producing genetic fingerprints of the various scald races in central Alberta we hope to more precisely map the resistance genes in the barley plant specific for the races present in farmers’ fields.

Quality

In addition to the disease resistance work, we have also been developing markers to improve crop quality. The dormancy trait is strongly influenced by the environment and is controlled by multiple genes. In the past, we have genotyped recombinant inbred lines for dormancy/ preharvest sprouting tolerance and silage phenotypes. A population with a Samson barley background was analysed by SSR and DArT genotyping. The most dominant QTLs were located near the 5H (centromere), 2HS, 4HS and 7HL. We are currently validating these QTLs for selecting slight dormancy without affecting malt quality.

We have also studied the inheritance of feed quality (silage and green feed components) and like dormancy these traits are also controlled by multiple genes and affected by the environment. We genotyped 4 recombinant inbred line populations with a Falcon barley background by utilizing SSR,

DArT and genotyped by sequencing marker analysis. Although several QTLs have been identified, very few functional molecular markers have been identified for use in breeding programs. As an alternative approach, we plan to use these markers to develop to test a new statistical based methods by whole genome selection.

Pathology Laboratory

Disease resistance screening of barley, triticale, and winter wheat lines

Cereal leaf diseases reduce crop yield and quality on an annual basis. New varieties require improved disease resistance over check varieties in order to be registered.

Advanced lines are tested in screening nurseries. Both barley and triticale are evaluated in inoculated tests for leaf spot diseases at Lacombe, Edmonton, Saskatoon, and Brandon. Barley and triticale are also screened for stripe rust resistance in the nurseries located at Washington State University, and at ICARDA in Mexico. Severity of diseases caused by natural infections are evaluated at the breeding nurseries of Olds, Calmar, Trochu, Morrin, and Lacombe. Resistant lines that are identified by screening will be included in the germplasm creation project to accumulate disease resistance into adapted lines. Lab and field techniques are being modified and developed for improvement of screening efficiency.

Scald screening

Large-scale hill plot nurseries to screen for resistance to scald were conducted at both Lacombe and Edmonton. In 2015, the scald nursery at Lacombe had a total of 6512 hill plots representing material from the FCDC program as well as programs at Saskatoon, Brandon, and the western barley Coop tests.

A total of 2,724 FCDC lines were screened for scald at Lacombe and Edmonton. The screening results showed that one third each of the lines are considered to be resistant, intermediate, and susceptible, respectively, in the Edmonton nursery.

Spot form net blotch

In 2015, a spot-form net blotch nursery was set up at the Lacombe Research Centre with a total of 1566 hill plots representing material from the FCDC program as well as programs at Saskatoon, Brandon, and the western barley Coop tests. Approximately 649 FCDC breeding lines were evaluated for spot-form net blotch resistance on July 13 and August 10, 2015. Most entries likely had intermediate levels of resistance.

Table 2. FCDC breeding lines evaluated for spot form net blotch in Lacombe, 2015.

	Average rating	Range
FCDC breeding lines	5.1	4.0 – 7.0
Check lines	5.1	3.0 – 7.0

0-9 scale where 0-3 is resistant to moderately resistant; 3-4 is intermediate; ≥ 5 is moderately susceptible to susceptible

Net form net blotch

A net-form net blotch nursery was conducted at the Lacombe Research Centre with a total of 1217 hill plots representing material from the FCDC program as well as programs at Saskatoon, Brandon, and the western barley Coop tests. Approximately 300 FCDC breeding lines were evaluated for net-form net blotch resistance on July 13 and August 10, 2015 (Table 3).

Table 3. FCDC breeding lines evaluated for net form net blotch in Lacombe, 2015.

	Average rating	Range
FCDC breeding lines	3.3	0 – 6.0
Check lines	3.0	0 – 7.0

0 – 9 scale where ≤ 3 is resistant to moderately resistant; ≥ 5 is moderately susceptible to susceptible

Screening Cereal Diseases in Germplasm, Yield, Coop and Regional Trials

For the 2015 season, we screened resistance for various diseases in different nurseries. The major results included screening 2,350 plots for the barley leaf spot complex, 1,191 plots for stripe rust and 140 plots for spot-form of net blotch resistance. Lines and germplasm resistant to the above diseases were identified. Stripe rust of wheat and leaf spot of barley were found to be relatively severe in a few breeding trials. The wide range of disease severity suggests that selection for disease resistance should be achievable as a result of the sufficient differentiation in disease reactions among the materials evaluated.

Surveying cereal diseases in Central Alberta

To provide sustainable management of leaf diseases, an ongoing and clear indication of the changing disease situation in western Canada is needed. Changes in pathogen virulence and prevalence will have a large impact on the management strategies used by farmers and the direction breeding programs take with regard to the developing and using disease resistance.

A small survey to document diseases of barley was conducted in 20 fields in Central Alberta in late July (Table 4). Growing conditions in Central Alberta were poor in May and June with much lower than normal levels of precipitation, but with near average temperatures. In July and August conditions were near average for both precipitation and temperature. Disease development throughout the surveyed region was lower than found in previous years.

During October 2014 to early October 2015, 37 winter wheat fields and 24 spring wheat fields were surveyed primarily to document stripe rust situations (Table 5).

Table 4. Disease incidence and severity in 20 commercial barley fields in Central Alberta, 2015.

Disease (severity rating scale)*	Fields affected (%)	Overall average severity	Range in average severity per field
Scald (PLAD)	40	1.4	0 – 11
Netted net blotch (PLAD)	30	<1	0 – 1
Other leaf spots** (PLAD)	100	3.5	1 – 16
Total Leaf Area Diseased (PLAD)	100	5	1 – 17
Common root rot (0-4)	100	2	1 – 3

*PLAD - Percentage leaf area diseased

** Other leaf spots diagnosed as spotted net blotch (*P. teres* f. *maculata*) or spot blotch (*Cochliobolus sativus*)

Table 5. Foliar disease incidence and severity in 24 spring and 37 winter wheat fields surveyed in central Alberta in 2014 and 2015.

Disease	Light*	Intermediate*	Severe*	Fields affected
Leaf spot ¹ complex in spring wheat	12	6	0	18
Stripe rust ² in spring wheat	6	0	2	8
Stripe rust ² in winter wheat	18	4	6	28

¹ *P. tritici-repentis*, *Stagonospora* and *Septoria* spp. ²*Puccinia striiformis* f.sp. *tritici*

* Leaf spot complex scale of 0-9: light = 0.1 to 3.9, intermediate = 4 to 5.9, severe = 6 to 9.

Stripe rust scale: light = 1 - 10%, intermediate = 11 - 29%, severe = 30% or higher.

Stripe rust management

Stripe rust caused by *Puccinia striiformis* has been increasing in prevalence in central Alberta. In 2011, wheat yield reductions reached 45% at Lacombe. To prevent or reduce losses by this disease, research is needed to understand the epidemiology of stripe rust in Alberta and to formulate integrated management strategies using durable resistance and appropriate cultural practices.

Identification of stripe rust pathogens

Barley and wheat stripe rust are primarily caused by two different pathogens, Psh (barley pathogen) and Pst (wheat pathogen). Identifying and monitoring the stripe rust pathogen allows us to implement effective management practices including genetic resistance for the breeding program. Recent field tests in central Alberta demonstrated that under natural infection conditions, stripe rust caused yield losses ranging from 10 – 60% in susceptible barley cultivars/lines, while losses were negligible or much lighter for resistant cultivars.

The objective of this test was to identify stripe rust pathogens based on virulence on a set of barley and wheat cultivars and lines known as differentials. These differentials with specific resistance gene(s) help distinguish races of the stripe rust pathogen based on infection type/pattern. As a result, stripe rust pathogens or strains will be identified based on the reactions on individual differential.

The present study showed that although the classification of the majority of pathogen samples corresponded to the sampling hosts (i.e. either wheat or barley), a few samples that had been collected from barley hosts were found to belong to Pst strains, suggesting that barley, not wheat, harbored stripe rust strains that were capable of attacking both barley and wheat. The results also showed that current Psh strains had substantial increases in virulence on barley compared with Psh strains collected previously in central Alberta. Further study is needed to determine if the increase in virulence by these newer Psh strains is of epidemiological significance.

Management of stripe rust using foliar applied fungicide combined with cultivar resistance

Demonstrating yield losses in Central Alberta will allow cereal producers to use available control methods for effective stripe rust management.

Seven cultivars of spring wheat and three lines/cultivars of barley varying in disease reactions were used. Tilt was foliar-sprayed at disease onset (~5% severity) in the main plots with the fungicide treatment, while no Tilt was applied for the plots without the treatment. At the end of season, plots were harvested and yield components were determined. The responses for yield components in relation to cultivars varying in their levels of disease resistance were also determined.

Stripe rust was found to be the major disease in the plots as a result of natural infection. Tilt was applied at the heading stage of wheat in 2012 and 2013. The fungicide was applied at the flowering stage and heading stage due to early onset and rapid stripe rust development in 2014. Yield losses to stripe rust ranged from 10-60% in susceptible barley and 20-89% in susceptible wheat, while the losses in resistant and intermediate barley and wheat cultivars were negligible or much less than susceptible cultivars.

In conclusion, the use of resistant cultivars is sufficient to reduce yield losses when stripe rust risk is low to moderate. Fungicide application is needed for added protection for resistant cultivars when disease risk is high. Furthermore, it is important to identify common diseases that occur in the field and region, given that multiple diseases may be present. This will allow the producer to use the cultivars that are specifically resistant to individual diseases for effective disease management.

Project Funding

The following agencies contribute to the Barley Research Cluster: Agriculture and Agri-Food Canada, Alberta Barley, Atlantic Grains Council, Brewing and Malting Barley Research Institute, Rahr Malting, and Western Grains Research Foundation.

The following agencies contribute to the Beef Science Cluster: Agriculture and Agri-Food Canada, Alberta Beef Producers, Alberta Cattle Feeders Association, Alberta Livestock and Meat Agency, Beef Canada Research Council, Beef Farmers of Ontario, Manitoba Beef Producers, and Quebec Beef Producers.

Cluster funding varies between projects as funds are directed from the contributing agencies based on project activities.

Breeding barley and triticale for yield, disease resistance and feed quality

2014 - 2018

Funded by Alberta Beef Producers, Alberta Crop Industry Development Fund, and the Beef Science Cluster

This project enhances the variety and germplasm development of the public breeding programs in western Canada and around the world for barley and triticale.

This project supports a collaboration in which the public plant breeding programs of barley and triticale in western Canada (Field Crop Development Centre, Crop Development Centre, and Agriculture and Agri-Food Canada) and the international centres (International Centre for Agricultural Research in the Dry Areas [ICARDA] and International Maize and Wheat Improvement Centre [CIMMYT]) work together for the benefit of all programs, toward the development of superior varieties.

Goals

Using conventional plant breeding methods and new technologies, new varieties for western Canada and germplasm for the breeding programs involved will be developed. This project will develop:

- superior yielding varieties of barley and triticale with improved feeding quality as grain and cereal silage
- superior water use and nitrogen use efficiency in barley and triticale
- multiple disease and multiple gene resistance by pyramiding disease resistance genes
- germplasm to secure future breeding potential of new varieties beyond the 5 year scope of this project

Successes

We are selecting lines with quality factors, aimed at the cattle industry, of high percent plump grain, high test weight, and higher fibre digestibility in forage. For the monogastric feed industry, quality factors include digestible energy content and protein digestibility. We have also stepped up efforts to incorporate Fusarium head blight resistance and stripe rust resistance.

We continue to receive new germplasm from the international Centers and selected breeding programs around the world and evaluate and incorporate this in the crossing blocks. Crosses for forage and feed are being increased in the barley, triticale and wheat programs.

This project, building on a previous project (2009-2013), has to date released nine barley varieties, a winter triticale, and a spring triticale.

Developing nitrogen efficient barley

2013 - 2016

Funded by Alberta Innovates Bio-Solutions, Alberta Crop Industry Development Fund, Alberta Barley

Developing and using varieties that use nitrogen efficiently is important for two reasons. Nitrogen fertilizer accounts for one of the major costs associated with the production of high yielding crops. In addition to an impact on the producer's bottom line, excessive N amounts can be detrimental to the environment.

Developing nitrogen efficient cultivars

In our previous study, begun in 2007, we identified N efficient lines from FCDC germplasm as well as from international sources. This project was aimed at deploying these germplasm lines in the breeding program to develop varieties with improved NUE. In addition, the present project continues evaluation for commercial potential of the N efficient lines from the previous project.

Crossing and developing lines with even more NUE

Not all lines that use N more efficiently do so in the same way. In some lines N is taken up from the soil very efficiently, in others it is used within the plant and turned into grain more efficiently. One of the activities of the current project was to intercross the previously identified germplasm to pyramid these different types of NUE genes, thereby developing cultivars with further enhanced NUE.

In the last three years, we have made a number of crosses for NUE (Table 6). Stable lines have already been developed from the two sets of crosses conducted in 2013 and 2014. These lines will be evaluated and selected for NUE and other desirable traits starting from the 2016 growing season.

After several more seasons of evaluation, we hope to identify breeding lines that are not only superior in N efficiency but also show disease resistance and required grain and forage quality. The populations from the new 2015 crosses are being advanced using the accelerated single seed descent method. Once the generation is advanced and stable lines have been developed, these will also be subjected to selection.

Evaluating lines for commercialization

We have continued to evaluate NUE lines developed through the previous project to identify the best ones for commercial release. In 2015, a number of advanced breeding lines included in the 1st through 4th year of yield testing (Yield 1 to Yield 4) were evaluated under field conditions (Table 6). Each test set was a replicated trial and the research methodology was the same as for the standard breeding trials. The test lines were characterized for NUE, desirable agronomic traits, reaction to diseases and feed grain and forage quality.

The best lines were selected based on grain yield and NUE characteristics, and advanced to the next stage. Two of the lines selected from the Yield 4 test were included into the Western Canadian Co-operative trial. These materials will be tested for two years in the Coop and may be recommended for release as a variety, if they continue to perform well.

Table 6. Summary of the 2015 barley nitrogen use efficiency tests.

Test Stage	Number of lines (populations)		Note
	Tested	Advanced	
Crossing block	12	12	Crosses were successfully completed.
Segregating populations	21	21	These were grown to advance generations. Some are already at an advanced stage and will be subjected to selection as of 2016.
Head rows	400	56	These were newly developed stable lines. The best looking 56 lines were selected.
NUE tests (Yield 1, Yield 2)	145	44	These were lines either in the first or second year of yield testing. The lines were primarily evaluated and selected for NUE and other desirable agronomic traits.
Multi-location yield trials (Yield 3, Yield 4)	9	4	These were lines included in the advanced Yield 3 and Yield 4 tests and were evaluated at 6 and 11 locations, respectively. Two of the three lines tested in Yield 4 were advanced to the 1 st year Coop. Two of the six lines in Yield 3 were advanced to Yield 4.

Developing molecular markers for NUE

Developing molecular markers involves phenotyping (evaluating physical characteristics of the population under both low and high fertility conditions) and genotyping (molecular characterization

of this population). By comparing the phenotypic and genotypic data, we may identify genetic markers that are associated with NUE.

Two populations, T09154 (developed from I09502 x Vivar cross) and T09156 (from I09505 x Vivar cross), are being used for the marker development work. Vivar was consistently superior in tests of N efficiency among the cultivars commonly grown in Alberta. The other two parents, I09502 and I09505, are new introductions and also showed a good N efficiency. These crossing parents were of different genetic backgrounds and seem to carry different genes for NUE than Vivar. The efficiency of I09502 and I09505 stems from their superior ability to take up more N from the soil, while Vivar excels at utilizing the N taken up for grain formation.

Phenotyping and genotyping of the first population, T09154, have been completed. The second population T09156 was also genotyped, but the phenotyping was incomplete due to hail damages in 2015. This report is based on data from the one population.

Results showed a total of six markers significantly associated with NUE and related traits. These markers were distributed across different chromosomes, and each controlling 20 to 36% of the phenotypic variations in NUE and related traits. Nitrogen use efficiency is a complex trait involving many processes and many underlying genes, and the observation of many markers associated with this trait is not surprising.

These newly identified markers will be used in selection in the coming years and validated. The availability of markers for NUE will not only help us make better progress in the genetic improvement of NUE but also enhances the overall efficiency of the breeding process.

Collaborating with Alberta Innovates Technology Futures

A second aspect of the molecular work is being carried out in collaboration with Alberta Innovates Technology Futures, Vegreville. This group is undertaking the discovery of novel genes involved in NUE in plants by using deep super serial analysis of gene expression (SuperSAGE).

This technology produces a comprehensive profile of which genes are actively working in the plant at the time of sampling. By analyzing samples taken during anthesis, at the beginning of grain filling and in the middle of grain filling, we hope to find the genes that are active at these stages and responsible for better within plant nitrogen utilization.

The study was carried out using two genotypes contrasting for NUE (Vivar and I09502) and grown under low and high fertility conditions. The data revealed a number of differences between the genes that are active in Vivar vs. I09502, and also a number of differences if the plants were grown in low vs. high fertility conditions. We are working on the data to narrow down this list of differentially expressed genes to some key genes. From this we will be developing molecular markers that eventually can be used to quickly identify if a line carries these NUE genes.

Enhancing selection for malt quality in two-row and hulless barley

2013-2018

Funded by the Barley Cluster

FCDC is working on developing selection tools to benefit two-row hulled and hulless barley malting quality in barley breeding programs to better meet the needs of the malting industry.

Malting quality NIRS calibrations

FCDC is working to determine near infra-red reflectance spectroscopy (NIRS) calibrations for malting traits in hulless barley and to enhance the NIRS malting calibrations for hulled two-row barley. FCDC is working with the Grain Research Laboratory (GRL), the Canadian Malting Barley Technical Centre, and two malting plants in Alberta.

Malting marker validation and marker assisted selection

We are focusing on identifying and validating markers associated with enzymes that are important in the breakdown of cell walls, the conversion of starch to sugar, the breakdown of lipids and the transport of proteins.

Leaf samples are screened for the above using selected molecular markers. Those lines advanced to the next generation will be analyzed for malting quality using NIRS. The best lines of these will be advanced further. The feedback loop of selection based on MAS and NIRS malting quality will be used to adjust and refine the markers that are useful for the selected malting populations.

Measuring malting traits in the program

We will continue to make crosses, advance bulks and make selections as documented in the Two-row Breeding Program. Wet chemistry on advanced lines will be used to confirm the lines with the best malting quality.

Results

FCDC continued studies to improve our selection efficiencies for malting quality in two-rowed hulled and hulless barley. We have been able to develop robust calibrations for malting quality in hulless barley that we hope to validate with data from the 2015 crop growing season. We are advancing promising two-rowed malting lines within the FCDC breeding program using molecular marker work.

The NIRS calibrations were used to screen samples from the 2015 breeding program for potential hulled and hulless malting lines. In 2015, approximately 1000 lines with malting potential were

grown in the Yield trials, and 4000 lines with malting potential were grown in headrows. Lines that showed agronomic and malting potential were advanced for further testing.

Six advanced lines were entered into the first year of Coop testing in 2016 as malting types based on quality and agronomic merit. These lines were assessed for malting quality both by NIRS and micro-malting done by Rahr Malting.

From the 2014 germplasm headrows, nineteen hulless lines from eight populations with potential for malting quality were advanced to Yield trials in 2015. Of these lines, ten have been selected for the 2016 BMY2 and one has been re-entered into the 2016 BMY1. Malting quality was assessed using NIRS calibrations developed for hulless malting barley.

From the 2014 germplasm bulks, 2,535 lines (2171 hulled and 364 hulless) from thirty-two populations with the potential for malting quality were grown out as headrows in 2015. However, due to hail damage and seed supply issues, selections could only be made from 19 of these populations, from which 20 hulless lines were selected for the 2016 BMY1 nursery. From the remaining populations, lines were advanced to a special 2016 BGH2 nursery.

New models and protocols for analysis of field-scale agronomic trials

2012-2016

Funded by Alberta Crop Industry Development Fund (ACIDF)

Small-plot (e.g. 2 x 5 m) trials are a fundamental tool for breeding and agronomy research. Plant breeders and agronomists have followed a protocol for this which includes: identify a homogeneous site near a research station, arrange treatments or treatment combinations in small plots according to a complete or incomplete block design, collect data from individual plots within and between blocks and finally analyze the data according to the statistical methods (e.g., analysis of variance, ANOVA, or regression analysis) for different experimental designs. However, this design-based approach to field crop research has increasingly been supplemented by a new model-based approach that takes advantage of the availability of geo-referenced data such as GPS-based yield monitor data from field-scale trials or from farm fields.

Statistical analysis of field-scale trials needs to consider an additional complication of spatial correlation that the neighboring data points are more likely correlated than the data points far apart. This spatial correlation is not generally considered in traditional small-plot breeding or agronomy trials because different types of complete and incomplete block designs would accommodate the assumption of plot-to-plot homogeneity within blocks or replications. This project develops a new approach to the spatial analysis of yield monitor data and other precision farming data. It goes

beyond the usual procedures and protocols for processing and analyzing precision farming data in the past.

Currently, recommended inputs or farm-level decisions such as variable rate applications are often based on ‘eyeballing’ yield/soil maps from raw data at one farm in one year. In contrast, with our new approach, these recommendations or decisions will be based on the maps or information derived from predicted data at multiple farms/locations over multiple years under tested, statistically sound spatial models. Thus the recommendations or decisions based on our new approach will be less *ad hoc* and thereby should exhibit a higher level of reliability, consistency and predictability.

Results

We have developed new model-based procedures/protocols and implemented them in a software package called PFR (Precision Farming Rake) in R and Microsoft Excel environments. The PFR package includes geostatistical tools and the mixed-model methods for identifying, testing and validating different spatial covariance structures with given information (yield/soil data) in particular farm fields. The PFR is still in the final stage of development.

We have investigated and implemented computationally feasible interpolation methods for error correction and data alignment to enable the analysis of massive, highly imbalanced data sets in precision farming.

We have developed new statistical methods for true assessment of the stability of spatial structures across different years and different data layers.

We have applied the new methods/software packages to the analysis of the field-scale or precision farming data from ACIDF-funded projects (“Barley 180” and “Wheat 150”).

Effects of increasing nitrogen rates on malting barley quality and yield

2013 – 2018

Funded by the Barley Cluster

This project will determine the effects of increasing nitrogen rates on new Canadian and US malting barley varieties compared to the most commonly grown variety. This project will also compare the nitrogen response of Australian malting barley varieties to Canadian varieties, and will identify synergies between malting and feed barley to maintain the integrity and value of the barley as a feed crop (should it be rejected for malting).

Effect of increasing nitrogen rates on new Canadian and US malting varieties

This study will provide valuable information on which of the newer varieties respond best to nitrogen both in terms of nitrogen use efficiency and effect on end-quality of malting and feed barley. Possible outcomes include the identification of malting varieties that are relatively efficient at utilizing nitrogen and that are less affected by nitrogen in terms of protein, β -glucan and other quality parameters that improve overall modification.

One trial was conducted at seven locations (Beaverlodge, Lacombe and Lethbridge, AB; Scott, Melfort and Indian Head, SK; Brandon, MB) in western Canada. Varieties grown were AC Metcalfe (control), AAC Synergy, CDC Kindersley, Voyager and Cerveza. Nitrogen at four rates (0, 25, 50 and 100 kg/ha) was applied to each variety.

Results - Malt and wort quality – 2014 growing season

Analysis and preliminary interpretation of data for the quality variables (Canadian Grain Commission) from 2014 have been completed. Two locations (Beaverlodge and Lacombe) were chosen for malting and quality analysis. Results were similar to those obtained in 2013.

Generally, increasing nitrogen rates had a negative effect on cell wall modification as demonstrated by decreasing malt friability and fine extract. AAC Synergy and ABI Voyager exhibited the highest water uptake during steeping while Cerveza exhibited the lowest. Malt friability was highest for AAC Synergy and lowest for Cerveza which also had the highest levels of β -glucan. Although malt friability decreased as nitrogen rates increased, the decrease in friability was not as dramatic for AAC Synergy as for the other varieties, especially Cerveza.

There were some significant variety by nitrogen rate interactions indicating that the response to increasing nitrogen rates differed among varieties. With increasing N fertilization, the malt proteins increased at slower rates in AAC Synergy and Voyager than in Cerveza. The decrease in malt friability with increasing nitrogen was less in AAC Synergy and ABI Voyager than in Cerveza. The amount of fine extract for AAC Synergy, ABI Voyager, and CDC Kindersley was significantly higher and relatively independent of increasing nitrogen rates compared to Cerveza. AAC Synergy and CDC Kindersley produced wort with relatively low levels of β -glucans that were relatively independent of the increasing N fertilization rates. These results again suggest that varieties may differ with respect to their ability to resist the negative effects of increasing rates of nitrogen on certain malting quality parameters of barley.

Results - Yield and yield component parameters – 2015 growing season

The first (multi-location) experiment was conducted as planned at all locations in 2015. The second experiment was conducted at Lacombe. A severe hailstorm at Lacombe on July 21 rendered data from that site very unreliable therefore it is not reported. Unfortunately, this means that no data are available for the second experiment. All agronomic data were collected from the other locations.

Data processing and analysis have been completed for most agronomic variables. The results were generally similar to those obtained in 2014. All of the new varieties (Cerveza, CDC Kindersley, AAC Synergy and ABI Voyager) produced higher yields than AC Metcalfe, and both AAC Synergy and ABI Voyager tended to have lower protein than the other varieties. AAC Synergy and Cerveza produced less tillers than the other varieties. Kernel weight and plumpness were highest with AAC Synergy and ABI Voyager.

Unlike the 2014 results, lodging did not differ among varieties, and differences in maturity were less pronounced. As expected, yield, protein concentration, tillering and lodging increased with increasing nitrogen rate while kernel plumpness decreased.

Conclusions

AAC Synergy again displayed excellent agronomic and malting characteristics, and may take over from AC Metcalfe as the most widely grown malting barley variety in western Canada.

Improving malting barley production in Eastern Canada

2014 - 2018

Funded by the Barley Cluster

Currently only two malting barley cultivars, Cerveza and Newdale, are recommended for Eastern Canada. While malting plants and microbreweries are willing to purchase local barley if it meets standards, studies on the cultural practices on malting quality in eastern Canada are lacking.

Identifying improved malting barley cultivars

FCDC and the Crop Development Centre (CDC) in Saskatoon are sending advanced malting lines every year for evaluation by the Eastern Cereal and Oilseed Research Centre (ECORC) at Charlottetown. Data is collected on grain yield, test weight, seed weight, plant height, lodging resistance, heading date, and disease reactions and submitted back to FCDC and CDC breeders. Together, superior lines will be selected for screening across Eastern Canada and possibly be entered into the pre-registration trials for Eastern Canada. Improved lines will be released as new cultivars. In much the same way, several European and other international malting varieties will be introduced for testing at Charlottetown, with the Canadian Grain Commission analyzing these introductions for malting quality.

Developing improved cultural practices for malting barley production in Eastern Canada

Researchers in Western Canada have completed comprehensive studies on the effects of seeding rate, nitrogen rate and cultivar on barley malting quality. Our methodology will be very similar to

one conducted in Western Canada. We plan to use two seeding rates (200 and 400 seed/m²), 5 nitrogen rates (0, 30, 60, 90, and 120 kg/ha⁻¹) and two cultivars (Cerveza and Newdale) and plant the 20 treatment combinations with 4 replications at each of six locations across Eastern Canada for 4 years.

Data will be collected on barley density, grain yield, test weight, seed weight, plant height, lodging resistance, heading date, percent plump seed, protein content, and deoxynivalenol (DON) content (if Fusarium head blight is present). Based on quality (grain protein and germination), certain tests will be malted, and analyzed (malt extract (fine grind), Kolbach index, wort β -glucan, diastatic power and α -amylase). The agronomic and quality data will be analyzed and scientific manuscript will be prepared.

Plant growth regulator use on malting barley

2013-2018

Funded by the Barley Cluster

This study will clearly identify the risks and benefits (in terms of barley yield and quality, and economics) associated with applying plant growth regulators (PGRs) to malting barley in western Canada. It will also identify the most effective PGR to optimize yield and quality of barley grown under western Canadian conditions.

Results

Malt and wort quality parameters (Canadian Grain Commission) – 2014 growing season

Analysis and preliminary interpretation of data for the quality variables (Canadian Grain Commission) from 2014 have been completed. Unfortunately, only one location, Lacombe, was malted due to pre-harvest sprouting at the other locations.

Results were generally similar to those obtained in 2013. PGR application had little or no effect on germination energy or index. Seed treated with ethephon tended to take up more water (as indicated by increased steep-out moisture levels). Ethephon application also resulted in lower levels of wort β -glucan, higher levels of free-amino acid nitrogen (FAN) and malt soluble proteins, and improved friability. Thus ethephon-treated plants produced kernels with overall better modification. These effects were likely secondary and caused by the smaller kernel size of ethephon treated plants. Chlormequat and trinexapac also increased malt friability, but not to the same extent as ethephon.

There were no PGR by seeding rate interactions for most of the variables measured and the few cases where interactions did occur, differences were of minor significance. As expected, increasing the seeding rate from 200 to 300 seeds/m² sometimes increased yield and improved endosperm modification.

Yield and yield component parameters – 2015 growing season

The experiment was conducted as planned at all locations in 2015. Data processing and analysis are complete and data for most locations have been analyzed. As occurred in 2014, results were variable among sites for some of the parameters measured. Ethephon, but not chlormequat or trinexapac, reduced plant height at both Lacombe and Lethbridge, while all three PGRs reduced height at Brandon and Scott.

Significant lodging occurred only at Brandon where the extent of lodging was reduced by trinexapac. In spite of lack of lodging at Lacombe, ethephon and trinexapac increased yield by 7 and 13%, respectively. However, at Scott, both ethephon and chlormequat application resulted in yield reductions of 14 and 10%, respectively. This variability is disconcerting, and is reminiscent of the results obtained in 2014, where ethephon increased yield at Lacombe, but resulted in reduced yield at Brandon and Indian Head.

Variable effects on other agronomic parameters were also evident. Ethephon increased tillering at Lacombe and Brandon but had no effect on tillering at Lethbridge or Scott. Excessive tillering can impact malting quality by delaying maturity and reducing kernel uniformity. Ethephon reduced kernel weight at Lethbridge and Scott and both kernel weight and plumpness at Brandon while trinexapac reduced kernel plumpness at Lethbridge. This may be negative since plump seed is used by the maltsters to select barley for malting grade. Also of concern was that ethephon delayed maturity considerably at Lethbridge.

Pre harvest glyphosate effects on malting barley germination, yield and quality

2013 – 2018

Funded by the Barley Cluster

This study will clearly identify the risks, if any, of applying pre-harvest glyphosate as a dry-down on malting barley in western Canada. Timing of application may be critical to avoid negative effects of the herbicide on seed germination and quality of the malt.

If no significant negative effects are documented by the end of the study, growers could have an important tool to mitigate the impact of secondary growth prior to harvest and speed up maturity, improve seed uniformity and overall quality. We believe that this would result in an increase in the amount of barley that would be deemed acceptable for malting. Alternatively, if the risks in terms of impaired plant development, seed germination, yield or quality are deemed significant, malting barley growers would be advised not to adopt this practice.

This study was conducted in five locations in western Canada (Beaverlodge, Lacombe and Lethbridge, AB; Scott and Indian Head, SK). The effects of timing of glyphosate application (soft dough, hard dough and maturity) at two rates (900 and 1125 g a.e./ha, or recommended and 25% higher than recommended) on an early (AC Metcalfe) and late maturing (CDC Meredith) malting barley variety were determined. The higher glyphosate rate will be used to determine possible negative effects in the event of growers inadvertently exceeding the recommended glyphosate rate.

Results

Germination characteristics, glyphosate residues, and malt and wort quality parameters (Canadian Grain Commission)– 2014 growing season

Analysis and preliminary interpretation of data on glyphosate residues and quality parameters (Canadian Grain Commission) from 2014 have been completed. Detectable levels of glyphosate were found at both application rates and the three application times. Trends were similar to 2013.

Glyphosate residues generally increased with increasing rates of application and decreased when glyphosate was applied at later stages of maturity. The average glyphosate levels exceeded the maximum allowable residue limit (MRL) of 10 mg/kg only when glyphosate was applied at the higher rate and at the soft dough stage; however, levels higher than MRL were found at some locations even at lower application rates and/or at later stages of seed maturity. Generally higher levels of glyphosate residue were found in AC Metcalfe compared to CDC Meredith. Seed samples exhibited germination energy >95%. It can be concluded, therefore, that glyphosate residues were too low to have any significant effect on the germination energy of barley.

The highest glyphosate levels were observed in barley grown in Scott, but even at this location the highest residue level was below 40 mg/kg and no negative effects on germination energy were observed. Protein and moisture contents in barley were within acceptable ranges at all growing locations.

Malt quality analyses were performed on barley from Beaverlodge and Scott. The glyphosate residue appeared to negatively affect the growth of roots during the malting process; the percentage of roots decreased with increasing level of glyphosate residue and the levels of α -amylase in malt decreased with increasing levels of glyphosate residue. Similar results were observed in 2013. Other malt parameters were generally not affected by glyphosate treatments.

Yield and yield component parameters – 2015 growing season

The experiment was conducted at all locations in 2015. All data were collected. Data processing and analysis has been completed. As in previous years, results were very variable among locations.

The few effects that occurred on yield were negative. At Beaverlodge and Lacombe, glyphosate applications had no effect on yield, kernel weight or plumpness. At Lethbridge, glyphosate did not affect AC Metcalfe, but CDC Meredith yield reductions occurred at all stages with the high

glyphosate rate. This had not been found previously, and suggests that pre-harvest glyphosate application may be riskier than previously thought. At Scott, results were more similar to previous years with reductions in yield occurring mainly when glyphosate was applied at the soft dough stage. In general, where glyphosate resulted in yield reductions, kernel weight and plumpness were also reduced.

Preliminary conclusions

The results over the past three years suggest minor benefits associated with very infrequent barley yield increases following pre-harvest glyphosate application. These minor benefits may not outweigh risks associated with reduced yield and kernel plumpness following early application, as well as unacceptable glyphosate levels in the seed, and possible effects on root growth during the malting process. The experiment will be conducted for a final year in 2016. Data from all sites and years will be considered before final recommendations are made.

Effect of seeding and nitrogen rate on β -glucan in hulless barley

2013 - 2018

Funded by the Barley Cluster

Barley for food presently accounts for only 0.2% of barley production in western Canada. However, with the recent Health Canada approval of the claim linking the consumption of barley β -glucan with low blood cholesterol, demand and market development may expand.

Hulless varieties are ideal for milling and contain relatively high levels of β -glucan, and several varieties have been developed for the food market. It is important, however, that these varieties undergo extensive agronomic evaluation to optimize quality and yield. This study will provide important information on combinations of seeding rate and nitrogen rate to optimize β -glucan levels in hulless barley varieties, and thus enhance the health value and market feasibility of the barley.

Trials are run at 5 locations in western Canada (Beaverlodge, Lacombe and Lethbridge, AB; Melfort and Indian Head, SK; and Brandon, MB). The effects of nitrogen rate (60 and 120 kg/ha), and seeding rate on CDC Hilrose and CDC Rattan hulless barley were determined.

Results

Food quality parameters (Canadian Grain Commission) – 2014 growing season

Analysis and preliminary interpretation of data for the quality variables (Canadian Grain Commission) from 2014 have been completed. Generally, similar trends were observed in 2014 as in 2013.

The increasing nitrogen rates significantly increased the content of protein, but decreased the content of starch in the grain. Increasing nitrogen rates also increased the content of β -glucan but had no significant effect on soluble dietary fibre. Generally, increasing the seeding rate resulted in a decrease in the levels of β -glucans and soluble fibre, but an increase in the levels of arabinoxylans and insoluble dietary fibre. The results also indicated significant effects of genotypes, environments, and seeding rates on the composition, molecular structure and molecular weight of barley dietary fibre constituents.

Yield and yield component parameters – 2015 growing season

The experiment was conducted as planned at all locations in 2015. A severe hail storm at Lacombe resulted in unusable data. Otherwise, all agronomic data were collected and analyzed. Results were generally similar to those obtained in 2013 and 2014.

Plant emergence was slightly higher with the variety Rattan compared to Hilrose, and as a result, tillering was higher. Yield did not differ between the varieties but Rattan had higher protein. Hilrose was taller than Rattan, but surprisingly lodging was slightly higher with Rattan. Seeding rate or nitrogen rate did not affect lodging. As expected, days to kernel maturity increased at the high nitrogen rate, and decreased with increasing seeding rate, and Hilrose took two days longer to mature. Kernel plumpness was higher with Rattan.

Innovative swath grazing and increasing forage research

2013 - 2018

Funded by the Beef Science Cluster

Each year 50% of the Alberta calf crop is backgrounded and 80% of Saskatchewan cow-calf producers retain ownership over winter post-weaning. If 30% of the 0.8 million Alberta calves backgrounded annually reduced costs from \$1.50 hd-day⁻¹ to \$0.70 hd-day⁻¹ for 150 days by swath grazing, savings would be \$28.8 million. Improved varieties and management could result in more savings.

This study aims to reduce the cost of calf production by reducing the cost of overwintering beef cows as a result of improving carrying capacity of swath grazed pastures. In addition, a forage scientist will be trained to increase scientific capacity.

Weathering losses under swath grazing conditions (2013 - 2016)

By comparing "in-swath" weathering losses among popular and new cereal lines used for swath grazing, we hope to improve recommendations to reduce weathering loss. The most popular (based on Grey Wooded Forage Association survey) and best (from FCDC breeding program) varieties of barley, triticale and oat, and one corn variety will be swathed mid-September. One corn, winter triticale, and fall rye were not swathed. Yield and forage quality will be determined in September and measured monthly until April (8 months).

Yields of crops grown were as expected. Generally, corn > spring triticale > oat > barley > winter triticale > fall rye, although they were not always significantly different. Forage quality as indicated by in vitro true digestibility and cell wall digestibility ranked winter triticale > fall rye > corn > barley = Bunker triticale > Taza triticale = oat. Winter triticale and fall rye are spring planted and are therefore vegetative. With the rare exception of winter triticale, most species declined in quality throughout winter. However, the species that had the highest quality in the fall had the highest quality in the spring. Taking into consideration that cow requirements increase throughout winter feeding, towards calving, and forage quality decreases at least slightly, corn was the only species that had the capacity to maintain cow weight and condition from September through until March. In 2014-15 we can estimate that cows winter-grazing spring triticale and barley would have lost weight during February and March. It appears that the loss in forage quality during winter is inevitable, but the amount of loss is somewhat unpredictable. We observe that loss occurs when precipitation occurs during fall after cutting and due to snow thaw or melt during the winter. When there is a snow cover and temperatures are below freezing and stable, forage quality doesn't change much.

The potential carrying capacity is influenced more by yield than by quality. This is why corn and spring triticale have the highest carrying capacity and winter cereals the lowest. Spring triticale and oat have a lower daily feeding cost than corn because they cost less per ha to grow. Depending on the year potential feeding cost per day for corn was close to the same feeding cost as barley, but was usually higher than oat and spring triticale.

Using strip mixtures to improving swath grazing quality (2013 – 2015)

The aim of this part of the project was to determine the feasibility of strip-mixtures of spring and winter triticale to improve swath nutritive value. Treatments include Bunker spring triticale, strips of Bunker and Pika winter triticale (3:1), and a control.

Yield for both swath grazed treatments was lower in 2014 (61%) than in 2013 mostly due to a later planting date and lower July and August rainfall. Carrying capacity is a function of grazing days, stocking rate, utilization and forage quality. In 2013-14 cows were removed from swath grazing after approximately 90 days compared to about 120 days in 2014-15. We allowed cows to remain on

swaths longer in 2014-15 because of lower snow depth and because of a February thaw. This resulted in significantly more days for swath grazing. However, we estimate that cows consumed less forage daily, because winter triticale and the lower parts of the spring triticale swath were frozen to the ground and or crusted over.

Swath grazed cows lost weight at a greater rate in 2014-15 than in 2013-14, because they were left on the swath-grazed treatment longer and closer to pregnancy. The body condition score of the swath-grazed cows in 2014-15 was less than desirable coming off pasture.

Forage quality of spring and winter triticale going into the winter in both years was as expected. The initial forage quality of the swath grazed treatments in 2013 and 2014 were comparable. Over winter spring triticale lost digestibility and increased in fiber more than winter triticale. The weighted value for IVTD, which takes into account the amount of winter and spring triticale, indicated the higher nutritive value of the strips of winter and spring triticale planted together. However, access of winter triticale to cows was an issue. It appeared that when snow was the only barrier, utilization of the winter triticale was not a problem, however icing-over prevented cows from accessing it. When snow was the only barrier it appeared that utilization was superior for the winter/spring triticale treatment over the triticale swath-alone.

Selecting new varieties for swath grazing (2015-2018)

By testing and comparing new barley and triticale lines specifically selected for high fiber digestibility to currently popular forage type varieties, we hope to identify new varieties for swath grazing. Canmore barley (released 2013) and 94L triticale (unreleased FCDC breeding line) will be compared to popular forage varieties CDC Maverick barley and Bunker triticale. These trials planted in the spring of 2015 showed that the triticale had good carrying capacity due to their high yields and desire by the cattle to eat them effectively. Canmore barley also did very well. The poorest performer was CDC Maverick, which despite having high yields was less effectively eaten by the cattle, so cattle came off with the poorest body condition scores.

Increasing capacity of forage research (2013-14 to 2017-18)

Currently there is a lack of crop-based production "systems" scientists with background to work on topics that will have an economic impact on the beef industry. Dr. Raquel Doce, a NSERC Post-Doctoral fellow, has been employed with funding supplied by the beef cluster. Dr. Doce has been involved in the work described above and other projects. Unfortunately due to family matters, she has returned to Spain.

Monocultures and intercropping in continuous cereal production for silage

2008-2016

Funded by the Barley Cluster

Silage producers, whether they are meeting on-farm needs or local market needs, will often look at continuous cereal production, which leads to productivity issues related to diseases and perhaps weeds. Mixtures and intercropping research (especially mixtures in Lacombe) have been looked at, but typically only for a single year at a time, as trial locations change each year. It is unique to look at the impact of mixtures and intercropping on the same plot area for several years in a row.

Mini silo experiments were conducted by Dr. Tim McAllister at AAFC Lethbridge.

Barley variety, mixtures, and intercropping

This study aims to compare and contrast the effects of monocultures, mixtures, intercropping and rotational diversity on crop health, disease levels, productivity and quality in a cereal silage production system. Treatments included continuous barley, continuous barley mix (3 varieties), continuous intercrop of barley, oat and spring triticale, and continuous intercrop of barley, oat, and spring seeded winter triticale. These treatments used either the same variety every year or rotated varieties (on a three year rotation).

At Lacombe in 2014, silage yields on a wet basis were significantly lowest for the barley only rotational treatments, while the highest yields occurred for the continuous intercrop. On a dry weight basis silage yields at Lethbridge tended to be highest in the barley mixture and intercropping treatments with spring triticale where the varieties changed each year.

Overall results indicate that the addition of diversity in terms of different crop types and perhaps barley genetics can help to reduce the level of leaf disease and improve silage productivity. The increased lactic acid production and reduced pH suggest that ensiling an intercrop of barley, oat and triticale enhanced fermentation during ensilage and could be a potential method to improve silage quality. This work demonstrates that high-quality silage can be generated for intercrop cereal silage and that this approach could be a valuable asset in terms of avoiding monoculture production systems and the buildup of plant diseases that are associated with this practice.

Impact of foliar disease development on silage quality and feed

This study aims to assess the impact of disease accumulation and disease avoidance management strategies such as rotation and fungicide application on the ensiling properties and feed value of barley silage in experiments using small ruminants. The experiment will be conducted over a four-year period at Lacombe and Lethbridge, AB, beginning in 2013. Treatment combinations include the following: rotation (barley on barley, barley on canola, barley on oat, barley on triticale), variety

(Chigwell – resistant, Sundre – net blotch susceptible), and fungicide (Twinline (BASF), at recommended rates and applied at flag leaf emergence) treatments (two year rotation sequence).

In 2013, only the effects of barley variety and fungicide (yes or no) were evaluated. At Lacombe, variety, fungicide and the interaction of variety and fungicide had significant effects on penultimate leaf disease severity. Sundre had significantly higher disease severity compared with Chigwell, while fungicide application significantly reduced disease severity. Differences between varieties were mainly due to increased levels of net-form net blotch on Sundre, although Chigwell had moderate to high levels of spot-form net blotch. Reductions in disease severity due to fungicides tended to be greater for Sundre versus Chigwell. At Lacombe in 2013, silage yields on a wet or dry weight basis were similar for both varieties, and regardless of whether fungicide was used or not. Unfortunately, at Lethbridge severe hail caused severe damage to the trial and no data was collected. In 2014, results indicated that silage yields (wet or dry) tended to be lowest with barley planted on barley residue of the same variety and where no fungicide was applied. Fungicide application tended to increase silage yields, but typically only when barley was planted on barley residue of the same variety. Planting barley on residue of a non-host crop with or without fungicide tended to give the highest yields; however, at Lacombe barley planted on triticale tended to have somewhat lower yields.

Quality assessments – Studies 1 and 2

Describing the main microbial populations involved in silage processing and their changes along the course of ensiling is of great interest to better understand and improve silage conservation. Fresh forages of barley, oat, triticale and a mix of these 3 crops were ensiled in mini silos. Fermentation characteristics and nutritive value of silages were determined after 90 days of fermentation and aerobic stability was determined over a 14 days period. A detailed analysis of the microbial communities found in silage was carried out through rDNA sequencing and changes in microbial core genome population were observed over time. Silages characteristics after fermentation were associated with well-processed silages. The microbial core genome diversity observed within silage decreased over time. Taxonomic bacterial communities profiles showed a high dominance of Lactobacillales order after fermentation, followed by an increase of the proportion of Bacillales order during aerobic exposure. Diversity of the fungal core genome decreased over ensiling process and number of crops' specific OTUs was increasing during aerobic exposure. OTUs assigned to filamentous fungi were observed in core genome at ensiling and after aerobic exposure whereas yeasts belonging mainly to Saccharomycetales order were largely dominating the fungal population after 90 and 104 days. Bacterial and fungal orders typically associated with silage spoilage were identified in core genome after aerobic exposure.

DNA on a chip selection: from genetic data to practical application in the FCDC breeding program

2014-2016

Funded by *Growing Forward 2*

In order for traditional breeding programs to routinely use new technologies such as marker assisted selection (MAS), their application must be low cost, quick and accurate. DNA microchips offer a fast, accurate and inexpensive way to genotype, while providing loads of timely data for breeders. At present, cereal lines are usually selected using phenotypic and NIRS quality data, although a limited amount of MAS has been used for specific traits. As a new approach we are developing a customised low density single nucleotide polymorphism (SNP) panel for trait selection within FCDC breeding lines. This SNP panel will be added to a previously developed next generation genotyping assay, allowing rapid, accurate and inexpensive genotyping.

We are focused on identifying SNPs linked to disease resistance (scald, stripe rust, Fusarium head blight, smut and net blotch), malt quality enzymes, and *in vitro* fiber digestibility. After reviewing previous research, we have identified markers for several of these traits, including scald resistance markers, malt quality markers, and several SNPs for stripe rust and net blotch.

Results

In 2015, we utilized the next generation sequencing platform, Ion Torrent, for genotyping by sequencing (GBS) and genome resequencing. By utilizing the Ion Torrent software and the program TASSEL we are able to identify SNPs. We filter out informative and polymorphic SNP markers by aligning GBS sequences with reference barley genome (Morex), comparing GBS sequences from multiple FCDC lines, and then comparing our SNPs with the original PCR-based markers. To date we have analyzed genetic populations by GBS that were previously phenotyped for *in-vitro* fibre digestibility, scald, stripe rust, seed dormancy and nitrogen use efficiency. We have identified several SNPs potentially linked to scald, *in-vitro* fibre digestibility, stripe rust and nitrogen use efficiency. We hope to complete our final data analysis in 2016.

Our goal is to use these SNP markers to build a personalized genotyping panel for FCDC. Dependent on further funding we plan to either add the selected SNP markers to the commercially available 400+ SNP panel from Eureka Genomics (California) or develop a targeted sequencing process for specific trait disease resistance and quality linked SNP that could be performed in house.

Feed and malting barley: linking enzymes to disease resistance

2014-2017

Funded by Alberta Barley

Fusarium head blight incited by *Fusarium graminearum* has caused considerable quality and yield losses in wheat and barley in the eastern prairie region of western Canada. In Alberta, FHB has not been extensively present in the field, but resistant/tolerant cultivars adapted for Alberta need to be developed to prevent potential FHB epidemics in the future.

Typically FCDC starts screening for FHB reactions in early Yield trials in the field. With laboratory screening techniques, we will be able to preliminarily screen earlier breeding generations for disease tolerance or resistance. Only those lines with the best resistance would then be sent away for more expensive field evaluation.

In addition, *in vitro* laboratory screening will provide us an opportunity to better understand the mechanisms behind disease resistance. FHB tolerance is a result of many disease resistance genes working together, and by identifying the different types of resistance we will be equipped to pyramid multiple resistance genes into one line and thereby improve overall FHB tolerance.

Measuring the plant's defense system

Currently we are working to design an *in vitro* protocol to test the role of enzymes in FHB resistance. One group of genes, referred to as defense response genes, have been linked to broad spectrum FHB resistance. These genes encode proteins such as enzymes β -1,3-glucanase and chitinase, which are thought to both degrade the fungal cell wall, thereby slowing fungal growth, and at the same time signal the plant to switch on its defense system.

After comparing different substrates, we found that assessing the enzyme activity of β -glucanase was the best way to determine FHB resistance. Based on our preliminary results, β -glucanase was found at higher levels in resistant barley cultivars than in susceptible ones when challenged by FHB. This assay has been somewhat standardized after performing multiple experiments under different conditions.

During 2015 we have developed a new test that measures peroxidase activity. Peroxidase activity typically increases upon pathogen recognition in plant tissue after inoculation. This test appears to be more effective when attempting to measure resistance levels in barley to the net blotch pathogen. Analysis of secreted protein present in intracellular wash fluid, the location where plant and pathogens initially meet, revealed changes in protein profiles before and after pathogen inoculation. We plan to better characterize these proteins secreted during pathogen interaction in 2016.

A time saving tool

This procedure is a practical and time-saving tool. In this enzyme assay, there is no need to grow the plants under controlled conditions, as long as a small quantity of seed is available for testing. A second advantage is that grain is more amenable to effective sterilization and thus, less likely to become contaminated. The tool has potential to help streamline the screening system if by no other method than identifying lines which lack any genetic resistance to *F. graminearum* and allowing their removal from further testing in more expensive FHB nurseries.

These results are based on the preliminary studies and more research is needed to determine the experimental conditions or the measured parameters that potentially caused inconsistent or variable results observed in this investigation.

Association mapping for agronomic traits in two-row barley

2014-2018

Funded by the Barley Cluster

Association analysis is a genome-wide genetic mapping tool that has been adopted by plant breeders to identify genomic regions linked to traits of interest. This project will use both an existing association mapping population as well as create a new, updated population in an effort to identify molecular markers that are linked to important agronomic traits such as yield, maturity, and straw strength.

Existing association mapping population

The currently existing association mapping population contains 91 lines of two-row barley. This population was genotyped and identified 6,265 polymorphic SNP markers. This genotypic data will be combined with historical agronomic data collected as part of the Two-Row Coop between 1995 and 2005, as well as with agronomic data collected from trials grown at FCDC (Lacombe), CDC (Saskatoon), and AAFC (Brandon). In 2014 the Brandon and Saskatoon locations were damaged by flooding and so only data from Lacombe was able to be used. We propose to grow for an additional year (2016) to compensate for these lost field sites in 2014. After these recent trials are completed the data will be analyzed.

New association mapping population

Given that the current association mapping population includes Two-Row Coop lines only up to 2005, a new association mapping population will be created using Two-Row Coop lines that have been evaluated since 2005. Association mapping will be conducted, as above, and significant

marker-trait associations will be compared between the two different populations to explore how the germplasm has changed over time. Due to the poor field season in 2014, we delayed collecting seed for the new population. That work will start this summer and a seed increase will occur over the winter of 2015/16 to be ready for the summer of 2017.

A new platform for linking, integrating and mining phenomic and genomic data for Canadian barley

2014-2016

Funded by *Growing Forward 2*

With the increasing availability of abundant and cheap DNA markers and next-generation genomic resources, barley breeders at FCDC and elsewhere are increasingly interested in the use of such marker information for genomic prediction and selection to accelerate the breeding cycle. Over the past four decades, FCDC has accumulated a huge amount of phenotyping data on yield, agronomic performance, grain quality and disease responses. However, we have little or no marker or genomic information for the corresponding genotypes and breeding lines. In most cases, this is due to limited access to information; marker information and genomics resources are stored in different databases and maintained by different user groups, with no mechanism for data sharing and integration.

This project aims to develop a Barley Breeding Platform (BBP) that links, integrates, and mines phenotypic and genomic data accumulated by barley breeders and other scientists at FCDC. BBP represents FCDC's important first step towards exploring the use of a new breeding strategy known as genomic selection or simply 'selection without phenotyping' that has the potential to substantially shorten the breeding cycle and reduce associated costs. The development of BBP will benefit FCDC and other Canadian barley breeding programs by making the variety development process more effective and faster. It also has a potential to serve as a one-stop information warehouse that hosts phenotypic and genomic data for barley breeders, students, extension agronomists and producers in Alberta and across western Canada.

Results

The current version of BBP has three modules: (i) Database; (ii) Statistical genomics; (iii) Bioinformatics. In view of the fact that alpha lattice design is now a standard experimental design for most breeding trials where there are often a large number of entries, a function of alpha designs and field layout plans for an arbitrary number of entries is now being added to the BBP package.

The BBP database module is built using the community edition of MySQL (www.mysql.com/). The BBP database employs the Role-Based Access Control policies (i.e., each user's access level to the database depends on his/her role in a given project) to ensure appropriate data sharing and security.

The Statistical genomics module uses a cross-environment computing strategy to ‘glue’ several well-known R and free terminal software packages for large-scale genome-wide prediction and QTL detection based on Bayesian Shrinkage and regularized (penalized) statistical models.

The Bioinformatics module allows users to extract latest gene annotation data from the Ensembl Database (<http://uswest.ensembl.org/index.html>) by providing standard Gene Ontology terminology. While BBP is developed with specific users (plant breeders and geneticists) in mind, the new concept presented here should be equally applicable for application developments in other research disciplines.

A multiple trait genomic selection system (MTGSS) for next-generation plant breeding

2016-2018

Funded by *Growing Forward 2*

Over the past 40 years, FCDC has developed new cereal cultivars at the lowest possible cost, while trying to simultaneously improve multiple traits demanded by producers, processors and end users. The FCDC cereal breeding programs remain based largely on phenotypic selection, requiring field trials at multiple locations replicated over years. A new breeding strategy known as genomic selection (GS) is to use the genome-wide DNA marker information for selecting superior breeding lines prior to or even without phenotyping, and thus the GS strategy may help shorten the breeding cycle and reduce associated costs. However, GS is a data-rich, analysis-intensive procedure, particularly when multiple traits are jointly considered. Thus, its correct and effective use for breeding programs is beyond breeders' usual dossier.

A Multiple Trait Genomic Selection System (MTGSS) will be developed to leverage the computing resources of publicly accessible user-developed GS software packages (particularly those written in R) for single-trait analysis, but will incorporate multi-trait GS analysis running within the Microsoft Excel environment. The new, unique feature of MTGSS will be its cross-environment connectivity, thereby combining the computing power and wrapping capability available in the R environment and the user-friendliness for data loading, data reporting and visual display in the Excel environment through coding with Visual Basic for Applications (VBA). Thus, the user will only need to see the interfaces built in Excel, but with R or other software running in the background in response to calls through VBA scripts in the Excel environment. FCDC breeders and scientists can easily access and use the MTGSS for their breeding and research activities.

Scald variation in relation to barley resistance

2014 - 2018

Funded by the Barley Cluster

Scald of barley is prevalent in central Alberta and has caused considerable yield and quality losses. Rapid changes in scald races have rendered some cultivar resistance ineffective. Many cultivars were found to have an increase in susceptibility as a result of extreme variability in virulence of *Rhynchosporium secalis*. A previous study showed that resistance remained in a few cultivars such as Seebe, Kasota, Mahigan and CDC Dolly. Resistance in cultivars was found to be location dependent, indicating an uneven development of *R. secalis* races in Alberta.

The objective of this long term study is to monitor race variation in relation to cultivar resistance across western Canada and to provide insights into the probable mechanisms that have rendered resistance ineffective. This information is essential to help prolong cultivar resistance.

Barley cultivars and differentials are grown in hill plots across Alberta to evaluate scald reactions. The hill plots in all locations were naturally infected, except for the Edmonton site which was inoculated twice using a mix of two scald pathotypes.

Results

Broad sense heritability of resistance to scald of barley was estimated based on the ratio of genotypic variance over the total variance from the race variation (RV) tests, yield trials and germplasm tests across central Alberta. Heritability ranging from 0.57-0.91 was obtained in all the tests with the RV being slightly higher in heritability than in other two types of field trials, suggesting that major genes in the lines and cultivars played a role in the estimate of high heritability in the RV tests. The moderate to high heritability in all the tests suggests that the current assessment method was adequate to estimate genetic resistance in large scale field tests.

There were significant genotype by environment interactions in the majority of 2010 to 2014 RV tests. This is indicative of pathogen variation under different environmental conditions. While a cluster consisting of several differentials with major resistance genes was consistently observed, some of the resistant cultivars such as Seebe, Manny and Sundre were distributed differently among trials. This suggests that environment and pathogen played a role in causing variability of barley scald resistance.

Effect of plant growth regulators on barley productivity and quality

2013-2018

Funded by the Barley Cluster

Over the past decade Prairie producers have moved to a canola/cereal rotation for economic considerations, or to continuous barley, for on-farm feed. As a consequence the risk of plant diseases has increased, and to combat this producers have increasingly relied on host resistance and fungicide application. Producers and crop consultants require more information related to expected yield losses from foliar diseases in varieties with a range of disease resistance levels. Yield losses for those varieties with resistance or intermediate resistance may not justify the use of foliar fungicides as the yield responses to fungicide application may be limited.

The first component of this study will determine the interactive effects of seed treatment and plant growth regulator (PGR) application, with flag leaf emergence or head emergence fungicide application on malting barley quality, yield, microbial load, and mycotoxin level. PGR application may help to optimize yield and quality of malting barley by mitigating the effects of lodging. Limiting the amount of lodging may help to reduce microbial load and toxin contamination of harvested grain, especially in conjunction with head applications of fungicide. The trial will also provide information as to the impact of head application of fungicide and the potential resulting residues on malt and brewing quality.

The second component of the study will investigate the interaction of seed treatment, fungicide application and level of disease resistance on disease development in barley.

Impact of seed treatments, plant growth regulators, and fungicide timing

This part of the study aims to determine the impact of seed treatments, plant growth regulators, and fungicide timings on crop health, disease levels, productivity and quality in barley.

AC Metcalfe was seeded at Lacombe, Beaverlodge, and Lethbridge, AB, at Scott, Melfort, and Indian Head, SK, at Brandon, MB, and at Charlottetown, PEI. A combination of seed treatment (Insure, BASF, at 2x the recommended rate), PGR application (Ethrel [ethephon], Bayer CropScience), flag leaf stage fungicide application (Twinline, BASF), and anthesis/head emergence stage fungicide application (Prosaro, Bayer CropScience)

Preliminary results show that the most significant factors impacting leaf disease severity later in the growing season, i.e. late milk/early dough, were either of the two fungicide applications. In terms of crop productivity, yields tended to be highest at most sites when a fungicide was applied, either at the flag leaf stage or head emergence stage. However, seed treatment had no effect at 4 of the 6 sites and resulted in small reductions in yield at Lethbridge and Melfort. At most sites in 2014,

lodging was limited and PGR either had no effect on yields or resulted in small yield reductions (e.g. Brandon).

Grain samples have been sent to the Canadian Grain Commission for malting quality analysis and to assess the impact of treatments on microbial characteristics of the grain. Assessments are ongoing.

Interaction of scald resistance with seed treatments and fungicides

Barley varieties were seeded at Lacombe, Melfort, and Charlottetown. A combination of seed treatment (Insure, BASF, at 2x the recommended rate), level of variety resistance (susceptible, intermediate, resistant), and flag leaf stage fungicide application (Twinline, BASF, at the recommended rate) was set up. The scald study used susceptible, intermediate and resistant varieties Xena, Busby, and Gadsby, respectively, while the net form net blotch study used Sundre, Chigwell, and Vivar.

Preliminary conclusions show that seed treatments did result in small reductions in disease, but these reductions were smaller compared to the effects of variety and flag leaf stage fungicide applications. At Lacombe, seed treatments resulted in a small increase in yield, especially for Xena and Busby. There was also somewhat of a synergistic effect of seed treatment and flag leaf stage fungicide application. However, at both sites the main factor influencing disease and yield increases was the application of fungicide at the flag leaf stage.

Net blotch virulence, resistance and sensitivity to fungicides

2009-2016

Funded by the Barley Cluster

Knowledge of the relative frequency and distribution of net form net blotch (NNB) and spot form net blotch (SNB) is limited; moreover we have limited up-to-date knowledge of the virulence and genetic structure present in these pathogen populations. The last comprehensive assessment of the *Pyrenophora teres* population was done in the 1980's and documented extensive variability in western Canada, including its presence on several resistant sources.

This project intend to conduct a prairie-wide assessment of the current status of the pathogens that cause netted and spotted net blotch of barley to determine: their variability in pathogenicity, virulence, and molecular characteristics (e.g. form, asexual versus sexual reproduction, mating type, recombination); their ability to overcome currently-used sources of resistance; and variation in the sensitivity to the fungicides registered to manage net blotch.

Pathogenic diversity in *Pyrenophora teres* f. *teres* (net form net blotch of barley) populations from the Canadian Prairies

Thirty-nine representative isolates of *Pyrenophora teres* Drechs. f. *teres* Smedeg. (Ptt) from the Canadian Prairies were evaluated for virulence on nine barley differentials. Isolates were grouped based on the relative number of resistant (r) and susceptible (s) differential reactions. These groups ranged from 9r/0s, to 1r/8s. Cluster analysis revealed 16 pathotype groups among the 39 isolates. Two pathotype groups, which comprised 44% of the isolates, were found to be predominant in the collection, while 10 isolates (26%) had distinct virulence profiles. Comparison of the results from an earlier study in the 1980s suggests the virulence profile of *P. teres* f. *teres* on the Prairies has changed in the last three decades. Seven new pathotypes also were identified for the first time in the Ptt population from the Canadian Prairies.

Pathogenic diversity in *Pyrenophora teres* f. *maculata* (spot form net blotch of barley) populations from the Canadian Prairies

Cluster analysis using microsatellite DNA markers was performed on a collection of 82 *Pyrenophora teres* Drechs. f. *maculata* Smedeg. isolates. Twenty-seven of these isolates were selected as representatives of different clades to assess pathogenic variation among them. Cluster analysis revealed 13 pathotype groups among the 27 representative isolates. Two pathotype groups, which comprised 52% of the isolates, were found to be predominant in the collection. Variation in virulence ranged from that of a Manitoba isolate which was virulent on 10 of the 11 differentials with an average disease rating of 6.1 (out of 9), to an avirulent isolate from Alberta with an average rating of 2.2. Among the genotypes tested, 'Herta' was the most susceptible with an average disease rating of almost 5.9. In contrast, the differential CI 9214 was resistant to all isolates, except two, with average rating scores of 2.8. Thus, the differential line CI 9214 and breeding material derived from it can be considered as potential sources of spot form net blotch resistance for Canadian Prairie barley breeding programs.

Ability of *Pyrenophora teres* pathotypes to overcome net blotch resistance in Canadian barley genotypes

Barley cultivars and lines resistant to net (NFNB) and spot (SFNB) forms of net blotch were evaluated against representative pathotypes of *Pyrenophora teres* Drechs. f. *teres* Smedeg. (Ptt) and *P. teres* Drechs. f. *maculata* Smedeg. (Ptm) at the seedling stage. The NFNB resistance in the cultivars Vivar and CDC Helgason was overcome by two and four of the Ptt isolates, respectively. AAC Synergy exhibited resistance against all Ptt pathotypes examined; however, two isolates caused disease severities of almost 5, suggesting some adaptation to the resistance in this cultivar. Resistance to SFNB in CDC Meredith was overcome by all pathotypes tested, while AAC Synergy, Cerveza and Major were resistant to all of the pathotypes. The identification of pathotypes virulent on cultivars classified as 'resistant' indicates the importance of not relying exclusively on resistance as the sole approach to disease management.

Sensitivity of Canadian prairies *Pyrenophora teres* f. *tere* and *P. teres* f. *maculata* isolates to propiconazole and pyraclostrobin

An evaluation of fungicide sensitivity to propiconazole and pyraclostrobin were conducted to identify any differences amongst the Ptt and Ptm isolates collected from the Canadian prairies and to investigate the occurrence of fungicide-tolerant strains in Ptt and Ptm populations collected from this region. Screening of Ptt and Ptm populations against different concentrations of each fungicide are currently being conducted. Initial analysis of data suggests the occurrence of fungicide tolerance for both tested fungicides in the Canadian prairies *P.teres* populations.

Determining yield losses in relation to cultivar resistance of winter wheat to stripe rust

2015-2018

Funded by *Growing Forward 2*

Epidemics of wheat stripe rust have frequently occurred and stripe rust on barley and triticale has been regularly observed in Alberta. The recent tests showed that this disease has caused 15 to 60% yield loss in spring wheat and 15 to 20% yield loss in barley in central Alberta. Early infection generally occurs and, thus, yield losses are likely greater in winter wheat.

However, yield loss information is not available about winter wheat associated with stripe rust reactions under central Alberta conditions. The objective of this project is to determine the efficacy of seed treatment and foliar fungicide in relation to winter wheat resistance or susceptibility in management of stripe rust.

Treatments

Field tests are conducted at Lacombe and Olds. A seed treatment (Raxil Pro) and/or foliar fungicide applied in June will be used on four cultivars, AC Radiant (MS), AC Bellatrix (S), Buteo (S) and Emerson (R). Disease assessment will be made at approximately two-week intervals during the growing season. The impact on grain yield, test weight and thousand kernel weight due to fungicide treatment and cultivar resistance/susceptibility will be determined.

Results

Plots at the Olds test were hailed out in the summer of 2015. Consequently, harvesting and data analysis was carried out for the Lacombe site.

A foliar spray or dual treatment (spray+seed treatment) significantly reduced yield losses by around 30% for susceptible AC Bellatrix. A foliar application and dual treatment also significantly reduced yield losses compared with seed treatment alone for AC Bellatrix. No significant differences in yield

were observed for other varieties including Emerson or AC Radiant. The first year results suggest that under central Alberta conditions a fungicide application such as foliar spray is needed to reduce yield losses by stripe rust when a susceptible winter wheat cultivar is grown. However, a foliar application may not be needed when a resistant cultivar is grown.

Winter wheat plots were seeded in Lacombe and Olds on September 11 and 12, 2015 to repeat the tests for the 2015/2016 season. Seedling emergence was found to be quite poor at the Lacombe site and the experimental plots were then ploughed in mid-May. As a result, we will be conducting the Olds test only for the 2015/2016 winter wheat growing season.

Rapid detection and monitoring of FHB mycotoxins in Alberta barley

2015-2018

Funded by *Growing Forward 2*

Mycotoxins pose a health hazard in food and feed when cereal grain is infected by *Fusarium graminearum*, the causal agent of Fusarium head blight (FHB). Near infrared reflectance spectroscopy (NIRS) will offer a quicker, more cost effective method of determining toxin content that could also be used throughout the industry. Not only will this help the food, feed, and malting industries, it will enable FCDC to screen barley lines for low toxin development, resulting in the release of new varieties with improved resistance to FHB.

Methodology

Two- and six-row barley will be inoculated with known chemotypes in the greenhouse/chambers in Lacombe to produce samples for mycotoxin analysis. Disease severity ratings based on Fusarium damaged kernel (FDK) in the inoculated seed will be obtained. The relationship between FDK and chemotype toxin level in inoculated seed may be determined. Barley grain samples from the FHB nursery in Brandon, MB will be collected in 2015 - 2017 for chemotype identification using molecular markers and mycotoxin analyses.

Samples will be used to isolate the specific NIRS absorption wavelengths of DON, 3-ADON and 15-ADON by looking at the differences in the spectrum at the different concentrations. The identified wavelengths will then be used to develop several NIRS equations for each toxin using different combinations of wavelengths, math treatments and spectral corrections. Field-infected grain samples from the Brandon nursery will then be scanned and analyzed with the developed equations to identify any overlaps in the wavelengths between the toxins as well as to determine which wavelengths are most precise for the each toxin.

The associations in toxin content in infected barley lines from multiple season samples will be summarized and tabulated based on different analytic methods. We will present this data for adaptation of FHB evaluation in barley candidate line reactions in the Prairie Grain Development Committee. After NIRS equations have been validated, NIRS application may be used to demonstrate to the agricultural industry.

Results

There are several spectral regions that show variation between the samples. After eliminating the lower visible region (to eliminate the effect of color) and the areas of water absorption, 3 areas were visually identified as possible target areas; 1100 – 1200, 1670 – 1720 and 2100 to 2350nm. With results from the HPLC and the ELISA tests as well as the purified samples of the different chemotypes, we will now narrow down the regions of spectrum that are unique for each chemotype. These specific regions will allow us to develop calibrations for each chemotype without the cross reactivity that is commonly seen in ELISA tests.

Seven hundred barley samples from the Brandon FHB nursery were analyzed using HPLC in the chemistry lab of Alberta Innovates Technology Futures. The results from HPLC analysis will be used for the NIR calibration. Based on 206 of the 700 samples, there was no correlation between the amount of barley DNA and the toxins, while there were moderate levels of correlations ($P < 0.01$) between the amount of fungal DNA and the levels of toxins determined by all three methods of toxin analysis. Furthermore, there were consistently slightly higher levels of correlations between the amount of 3ADON than 15ADON in relation to the fungal and toxin-related DNA, indicating that the chemotypes produced specific 3ADON and/or 15ADON with the former being slightly more specific than the latter. It remains to be determined if the association of chemotype with mycotoxin production can be helpful for NIRS calibration. We may continue to evaluate the Beacon kit in order to separate and quantify the three components of mycotoxins.

Field Crop Development Centre Variety Descriptions

The following varieties are registered for sale as seed in western Canada as of the spring of 2016. More information on these varieties can be found at agriculture.alberta.ca (search FCDC). Seed distributors can be found in Alberta's Seed Guide at seed.ab.ca.

Barley Varieties

General Purpose Barley

Amisk was released in 2013. This 6-row semi-dwarf has plump seeds, with 16% more than AC Ranger and 14% more than Vivar. Amisk also has more plump seed than the two row checks AC Metcalfe and Xena, by 5% and 7%, respectively. The higher percent plump kernels facilitate even processing for cattle feed resulting in increased feed efficiency. Amisk has a better than average combination of disease resistance: resistant to stem rust and Septoria, moderately resistant to spot-form of net blotch, intermediate resistance to net-form of net blotch, scald, spot blotch, and common root rot. Amisk has strong straw with good lodging resistance, better than Vivar and AC Ranger. Forage yields are similar to Vivar. Quality traits equal to or exceed that of Vivar. Grain yields are similar to checks Vivar and AC Ranger. The heading, maturity days, 1000 kernel weight and test weight of Amisk are similar to checks. Amisk is distributed by SeCan (secan.com).

Busby was registered in 2008. This two-row hulled barley has similar silage yields to Seebe, with 10% higher grain yields, 4 days earlier maturity, similar height and higher test weights and percent plumps. Its test weight, kernel weight, and percent plump are similar to Xena, while its digestible energy content

(for swine) and starch content are higher. This variety has similar disease reactions as Seebe with the same excellent resistance to scald, stripe rust, and the surface-borne smuts, but susceptibility to common root rot and loose smut. It has better resistance to the spot form of net blotch than Seebe. Busby is distributed by Mastin Seeds Ltd. (mastinseeds.com).

Chigwell was registered in 2008. This 6-row, smooth-awned, hulled barley has good yield potential for grain and silage, similar to Vivar. It has good lodging resistance, excellent percent plump, and higher digestible energy (swine) and starch content than Vivar and AC Lacombe. It is resistant to the surface-borne smuts. It is moderately resistant to scald, spot blotch and net blotch (spot and net forms). It is susceptible to common root rot. Chigwell is distributed by SeCan (secan.com).

Gadsby was registered 2010. While taller than Xena, this 2-row barley has similar straw strength. It has a rough awn and is well-adapted to the Brown, Black, and Grey Soil zones of western Canada. It yields 10+% higher than Seebe for both grain and biomass. It heads and matures 2 days later than Xena but 2 days earlier than Seebe. This variety has

plumper, heavier kernels than Xena, with lower fibre and higher digestible energy content. It has resistance to the covered and loose smuts and scald, and moderate resistance to the spot form of net blotch. It has a moderately resistant / moderately susceptible reaction to common root rot, Fusarium head blight and stem rust. It is susceptible to the net form of net blotch and spot blotch. Gadsby is available from SeCan (secan.com)

Ponoka was registered in 2003. This 2-row has resistance to loose smut, covered smut and false loose smut. Intermediate resistance to scald, spot form net blotch, and common root rot. Field resistance to net (net form) and spot blotch is similar to or better than the checks. Silage yields are higher than AC Lacombe (the most common silage variety in Alberta), with higher grain yields than CDC Dolly. Yield of Ponoka is approximately 8% higher yielding overall, with yield 10% higher in the Black and 12% higher in Black/Grey soil zones than CDC Dolly. Matures 3 days later than CDC Dolly with lodging similar to CDC Dolly and Harrington. Kernel weight is lighter than CDC Dolly but heavier than Harrington. High plump. FHB reaction is fair, with DON levels similar to the checks. Ponoka is available from SeCan (secan.com)

Muskwa was registered in 2011. It is a 6-row, smooth-awned, hulled, general purpose barley. It's a semi-dwarf barley with strong straw, smut resistance and intermediate maturity traits equal to or better than Vivar. Muskwa has stable grain yield and is well-adapted to western Canada. It has a better than average combination of disease resistance package of spot blotch, scald and stem rust. It has good lodging resistance and

quality traits similar to Vivar. Muskwa is distributed by SeedNet (seednet.ca).

Seebe was registered in 1992. This 2-row barley is adapted to the high scald areas of Alberta, with scald resistance superior to all registered two-row varieties and equal to the best six-row varieties. In high scald areas it is higher yielding than Bridge. Maturity is 3-4 days later than Bridge in areas of high scald where the scald has hastened the maturity of more susceptible lines. Outstanding forage yields. Seebe is available from SeCan (secan.com)

Sundre was registered in 2005. It is a 6-row, smooth-awned feed barley with high grain and silage yields in central Alberta, and with good kernel weight and seed plumpness. In FCDC silage trials, Sundre out yielded the high yielding six-rowed varieties Vivar and AC Lacombe. These characteristics make it a desirable multi-purpose variety for the livestock industry. Sundre has multiple gene resistance to scald, as shown in multi-station, multi-year trials. It has resistance to covered smut and false loose smut. Sundre barley is distributed by Mastin Seeds Ltd. (mastinseeds.com).

Trochu was registered in 2000. This smooth-awned 6-row feed barley has high percent plump, test weight and kernel weight. It is higher yielding than AC Lacombe. The high percent plump kernels facilitate even processing for cattle feed resulting in increased feed efficiency. Lodging resistance is similar to AC Lacombe. It is resistant to the surface-borne smuts and common root rot. It is susceptible to loose smut. Trochu is distributed by SeCan (secan.com).

Vivar was registered in 2000. This 6-row semi-dwarf is higher yielding than all check varieties (AC Lacombe, CDC Earl) with high test weight, percent plump and kernel weight. Its maturity is equal to AC Lacombe (medium). It has good lodging resistance. Vivar has rough awns. It has intermediate reaction in the field to scald, net blotch and loose smut. It is resistant to the surface-borne smuts and common root rot. Vivar has an excellent ability to respond positively under high yielding conditions. Vivar is distributed by SeCan (secan.com).

Malting Barley

Bentley was registered in 2008. Bentley is available from Canterra Seeds and contracts are available under Canada Malting. This two-row hulled barley combines malting quality with excellent yield potential for grain and silage across western Canada. Its silage yields in the Coop trials were 108% of Virden. This line has good plumpness, kernel weight, and protein. It has reasonable extract, protein modification, and friability. It has good lodging resistance and is of similar maturity to AC Metcalfe. This variety has excellent resistance to the spot form of net blotch, and moderate resistance to spot blotch and the surface-borne smuts. Bentley is distributed by Canterra (canterra.com)

TR13606 received interim registration in 2016. TR13606 has potential as a malting barley for the craft brewing market due to its higher extract and lower FAN. Due to high beta-glucans and viscosity in micro-malt testing, TR13606 has interim registration to determine if varying the processing protocols

Food Barley

Canmore was registered in 2013. Canmore is a food grade barley with excellent yields, up to 115% of malt check AC Metcalfe. Similar grain yields to the feed check Xena and malt check CDC Copeland. Good pearling traits, hardness, alcohol yield and quality traits for shochu production. Canmore showed significantly higher or equal total starch content over AC Metcalfe and CDC Copeland. Canmore has higher percent plumps with similar test weight than all checks, and higher kernel weight than malting checks. Canmore is distributed by Canterra (canterra.com).

in pilot malt testing will result in better modification. TR13606 is a two-rowed barley that does especially well in the black soil zone yielding 15% higher than AC Metcalfe. TR13606 has good kernel traits similar to AC Metcalfe. TR13609 has a good combination of disease resistance including resistance to the surface-borne and loose smuts.

TR13609 is a new release in 2016. TR13609 is a promising new malting barley with potential for craft brewing. TR13609 has shown consistently low DON levels, accumulating up to 50% less DON than AC Metcalfe in 5 years of testing at Brandon. It has good kernel plumpness with a promising malting quality profile of low protein levels, high extract, low DP, and good modification with low wort beta-glucan. TR13609 is a two-rowed, rough-awned barley, well-adapted to all soil zones of western Canada with average yields 12% higher than AC Metcalfe and 6% higher than Copeland. TR13609 will be available from SeCan (secan.com)

Triticale Varieties

Spring Triticale

Bunker was registered in 2005. It is a reduced-awn triticale with resistance to FHB similar to the most resistant check variety (Pronghorn). Bunker is early maturing, similar to the check cultivars AC Ultima and Pronghorn, and has good leaf and stem rust resistance and improved test weight (bushel weight). Bunker also has higher silage yields (non-Coop data) than either AC Ultima or Pronghorn. Bunker is available from FP Genetics (fpgenetics.ca).

Taza was registered in 2010. It is an awnletted (reduced awn expression) standard height spring triticale line intended for use as a feed grain conserved forage, swath grazing crop and potentially for industrial use. Taza is adapted to the Canadian Prairie Provinces. It yields similar to Pronghorn but is equal to or higher than AC Ultima and AC Certa. This line has good lodging resistance, good test weight, and high kernel weight. Taza is moderately susceptible to moderately resistant to FHB; it is resistant to leaf rust and stem rust. Taza is available from Solick Seeds (solickseeds.ca).

Tyndal was registered in 2005. It is a reduced-awn triticale which has grain yields similar to the highest yielding triticale check cultivar AC Ultima. It also has good leaf and stem rust resistance, test weight, and lodging resistance. It is early maturing with high forage yields. Tyndal has acceptable levels of disease resistance, including FHB minimum requirements. Tyndal is distributed by SeCan (secan.com).

Winter Triticale

Bobcat was registered in 1999. It is about 20 cm shorter, 10% higher yielding, and has similar winter survival to Pika in the parkland areas. It is easy threshing and has short awnlettes, which may improve greenfeed production. However, it is lower yielding than Pika in the brown soils. Bobcat is available from Corns Brothers Farm Ltd. (cornsbrothers.ca).

Luoma was registered in 2008. Luoma is an awnletted winter triticale with high yield (10%), high kernel weight (3mg), high test weight (1kg), and good winter survival (15%) compared to the awnletted check Bobcat. It has resistance to leaf and stem rust. Luoma is available from Corns Brothers Farm Ltd. (cornsbrothers.ca).

Metzger was registered in 2009. Metzger is an awnletted winter triticale with high yield (10%), high kernel weight (3mg), high test weight (1kg), and good winter survival compared to the awnletted check Bobcat. It has resistance to leaf and stem rust. Metzger is available from Haney Farms (haneyfarms.com).

Wheat Varieties

Canada Western Special Purpose*

Pintail was registered in 2011. Pintail is an awnless general purpose winter wheat. It is higher yielding than CDC Falcon and has similar yields to Ptarmigan. Pintail has high levels of winter survival. Pintail also has good resistance to stripe rust and good lodging resistance. Pintail is distributed by Mastin Seeds Ltd. (mastinseeds.com).

* *As of August 1, 2016.*

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