AMERICAN OAT WORKERS CONFERENCE

AMERICAN
OAT
WORKERS

July 13-16, 2014
Ottawa, Ontario, Canada

http://aowc.ca

American Oat Workers Conference

Ottawa, Canada 2014

PLATINUM SPONSORS

QUAKER 1877

General Mills

GRAIN MILLERS

SILVER SPONSOR

Prairie Oat Growers Association

SPONSORS

PHYTOGENE RESOURCES

SeCan
Canada's Seed Partner

RICHARDSON

North American Millers' Association
NAMA

LGC

SPECIAL ACKNOWLEDGEMENT

Agriculture and Agri-Food Canada

Agriculture et Agroalimentaire Canada

AOW Conference Program
Ottawa, Canada

Sun. July 13 to Wed. July 16, 2014
http://aowc.ca

Sunday, July 13

4:00 – 8:00 pm: **Registration open** – 29th floor (Summit rotating restaurant)

7:00 – 9:00 pm: **Opening Mixer Reception** – 29th floor (Summit rotating restaurant)

Monday, July 14

7:30 – 8:30 am: **Breakfast** (catered buffet - in Summit rotating restaurant - upper floor)

8:30 am – 12:00 pm: Plenary Session (Cartier I)

8:30 am: **Opening Remarks** (Nick Tinker, Michèle Marcotte, Gilles Saindon, AAFC)

9:05 am: **The changing climate for oats: a European perspective (**Chris Green, Senova, UK)

9:45 am: **The changing climate for oats: an industry perspective** (Bruce Roskens/NAMA, Joe Lutz/General Mills, Gabe Gusmini/Pepsico)

10:30 am: **Health Break and Poster Viewing (Cartier II and III)**

10:50 am: **The changing climate for oats: an international perspective** (Steve Harrison, Louisiana State University, USA)

11:20 am: **Oat research horizons: genomics and information systems** (Jean-Luc Jannink, USDA-ARS, Ithaca, NY, USA)

12:00 pm: **Lunch** (catered buffet, in Summit rotating restaurant)

Monday, July 14

1:00 – 2:40 pm: Quality, nutrition, and processing (Cartier I)

Chair: Judith Frégeau-Reid

1:00 pm: **How oat processing affects the ability of β-glucan to reduce cholesterol and blood glucose** (Susan Tosh, AAFC, Guelph, ON, Canada)

1:20 pm: **A microscopic tour of β-glucan distribution and status in a range of oat food products** (Shea Miller, AAFC, Ottawa, ON, Canada)

1:40 pm: **Lipids in seeds of oat (*Avena* spp.), a potential oil crop** (Svetlana Leonova, Lund University, Lund, Sweden)

2:00 pm: **Pure Porridge Puzzle – People, Process, Purity and Price** (Beth Armour, Cream Hill Estates, Montreal, QC, Canada)

2:20 pm: **Oat-rice processing and quality evaluation** (Xinzhong Hu, Northwest A&F University, China)

2:40 pm: **Health Break and Poster viewing (Cartier II and III)**

3:20 – 5:50 pm: Agronomy and Physiology (Cartier I)

Chair: Jennifer Mitchell Fetch

3:20 pm: **High yield input systems and impact on yield and β-glucan levels** (Shawn Conley, University of Wisconsin, USA)

3:40 pm: **β-glucan, oil, and protein of oats as affected by variety, location, and N application** (Bao-Luo Ma, AAFC, Ottawa, ON, Canada)

4:00 pm: **The effect of nitrogen and fungicides on oat yield and quality?** (Bill May, AAFC, Indian Head, SK, Canada)

4:20 pm**: Modelling B-glucan content in oat using data from variety trials** (Stephen Shirtliffe, University of Saskatchewan, SK, Canada)

4:40 pm: **Phenotypic analysis of abiotic stress tolerance in Australian oat** (John Harris, South Australian Research and Development Institute, Australia)

6:30 pm: **Supper – on the "Groat Boat"** (details to be announced)

Tuesday, July 15

7:30 – 8:30 am: **Breakfast** (catered buffet, in Summit rotating restaurant)

8:30 – 9:00 am: **The Oat Newsletter and the AOWC: where we've been and where we're going** (Charlene Wight, AAFC, Ottawa, ON, Canada; Mike McMullen, NDSU, USA)

9:00 – 10:20 am: Pathology (Cartier I)

Chair: Michael Bonman

9:00 am: **Effect of timing of inoculation and *Fusarium* species on the development of *Fusarium* head blight and deoxynivalenol contamination in oat** (Allen Xue, AAFC, Ottawa, ON, Canada)

9:20 am: **Effects of cropping factors and health promoting compounds in different oat cultivars on *Fusarium* species infection and mycotoxin contamination** (Susanne Vogelsgang, Agroscope, Zurich, Switzerland)

9:40 am: **Quantitative trait loci from two genotypes of oat (*Avena sativa* L.) conditioning resistance to *Puccinia coronata*** (Ebrahiem Babiker, USDA-ARS, Aberdeen, ID, USA)

10:00 am: **Development of SNP markers for breeding disease resistant oat varieties** (Gnanesh Nanjappa, AAFC, Winnipeg, MB, Canada)

10:20 am: **Health Break and Poster Viewing, Cartier II and III**

10:40 am – 12:00 pm: Breeding/Germplasm (Cartier I)

Chair: Aaron Beattie

10:40 am: **Structure of the oat genepool at Plant Gene Resources of Canada** (Axel Diederichson, AAFC, Saskatoon, SK, Canada)

11:00 am: **SNP and DArT diversity in European oat germplasm** (Alf Ceplitis, Lantmännen Agriculture, Svalöv, Sweden)

11:20 am: **Genetic structure of a Chilean oat core collection based on GBS SNPs** (Monica Mathias-Ramwell, INIA, Cajón-Vilcún, Chile)

11:40 am: **Management of oat germplasm in China** (Zongwen Zhang, CAAS, Beijing, China)

12:00 pm: **Lunch** (catered buffet - in Summit rotating restaurant)

Tuesday, July 15

1:00 – 2:20 pm: Breeding/Molecular Tools I (Cartier I)

Chair: Nick Tinker

1:00 pm: **The new state-of-the-art oat consensus map: where to next?** (Jessica Schlueter, University of North Carolina at Charlotte, NC, USA)

1:30 pm: **Genetic diversity among oat lines of the North American Collaborative Oat Research Enterprise (CORE)** (Kathy Klos, USDA-ARS, Aberdeen, ID, USA)

2:00 pm: **What can we learn from diploid oats: The IBERS Diploid Avena Genomics Resource (DAGR) and its application to hexaploid oat breeding** (Catherine Howarth, IBERS, Aberystwyth University, UK)

2:20 pm: **Health Break and Poster Viewing (Cartier II and III)**

2:40 – 4:00 pm: Breeding/Molecular Tools II

Chair: Steve Molnar

2:40 pm: **Development of protein rich tetraploid oat, current state and prospects** (Gideon Ladizinski, The Hebrew University of Jerusalem, Israel)

3:00 pm: **What does CSlF6 gene sequence tell us about genome relationships in polyploid *Avena*?** (Rick Jellen, Brigham Young University, Provo, UT)

3:20 pm: **Discrimination of new dwarf oat lines by allelism tests, SSR markers and plant height components** (Toshinobu Morikawa, Osaka Prefecture University)

3:40 pm: **Genetic variation in oat panicle structure and grain quality** (Irene Griffiths, IBERS, Aberystwyth University, Wales, UK

5:15 pm: **First bus to Museum** (Alternately, a 2km walk across bridge)

5:45 pm: **Second bus to Museum**

6:00 – 7:00 pm: **Cocktails in Canada Hall, Canadian Museum of History**

7:00 – 9:30 pm: **Banquet in Grand Hall, Canadian Museum of History**

9:30 – 10:00 pm: **Multiple bus trips back to hotel (or walk)**

Wednesday, July 16

7:30 – 8:30 am: **Breakfast** (catered buffet, in Summit rotating restaurant)

8:30 – 10:00 am: **AOW Business meeting** (all welcome) **Cartier I**

Chair: Nick Tinker Secretary: Mike Bonman

10:00 – 10:30 am: **Buses to ECORC, AAFC for field tour**

10:30 – 12:30 pm: **Field tour of Central Experimental Farm** (ECORC, refreshments in field)

12:30 pm: **Catered Working Lunch at ECORC, AAFC**

1:00 – 3:00 pm: **Breeders: speed-dating and discussion Chair: Weikai Yan**

1:00 pm: **Breeding Oats for Western Washington** (Louisa Winkler, Washington State Univ., USA)

1:10 pm: **Oat breeding in Argentina** (Liliana Wehrhahne, Chacra Experimental Barrow, Argentina)

1:20 pm: **Oat breeding in Chile** (Monica Mathias-Ramwell, INIA, Cajón-Vilcún, Chile)

1:30 pm: **Oat Breeding at IBERS, UK** (Sandy Cowan, IBERS, Aberystwyth University, UK)

1:40 pm: **Oat Breeding Efforts in Turkey** (Ziya Dumlupinar, Kahramanmaras Sutcu Imam University, Turkey)

1:50 pm: **Forage oat breeding in Morocco** (Naima Shaimi, National Institut for Agricultural Research (INRA), Morocco)

2:00 pm: **Oat Breeding in Brazil** (Itamar Nava or Luiz Federizzi, UFRGS, Porto Alegre, RS, Brazil)

2:10 pm: **Oat breeding at Oat Advantage** (Jim Dyck, Oat Advantage, Saskatoon, SK, Canada)

2:20 pm: **Oat breeding at PhytoGene Resources** (Art McElroy, Phytogene Resources Inc., Orléans, ON, Canada)

2:30 pm: **Oat Breeding at AAFC, Winnipeg** (Jennifer Mitchell Fetch, AAFC Morden, MB, Canada)

2:40 pm: **Oat Breeding at the University of Saskatchewan** (Aaron Beattie, CDC, University of Saskatchewan, SK, Canada)

2:50 pm: **Oat Breeding at Lantmännen** (Alf Ceplitis, Lantmännen Agriculture, Svalöv, Sweden)

3:00 pm: **The Australian National Oat Breeding Program** (Pamela Zwer, South Australian Research & Development Institute)

3:00 – 4:00 pm: **Continued breeder discussion opportunities**

4:00 pm: Bus to hotel

American Oat Workers Officers

Chairman	Nick Tinker/Weikai Yan
Chair-elect	Vacant
Past Chairman	Steve Harrison
Secretary	Michael Bonman
Newsletter editor	Jean-Luc Jannink
Northeast USA	Mark Sorrells
Western USA	Kathy Klos (nom)
Southern USA	Amir Ibrahim
USDA-ARS	Jose Costa (nom)
Eastern Canada	Art McElroy
Western Canada	Curt McCartney
AAFC	Vacant
Mexico	Julio Huerta (nom)
South America	Luiz Federizzi
Industry	Bruce Roskens
Member-at-large	Dennis Galbraith
Member-at-large	Dave Marshall
Member-at-large	Steve Shirtliffe

Awards and Recognition Committee

Jennifer Mitchell Fetch

Steve Molnar

Joe Lutz

Program Committee

Shea Miller

Charlene Wight

Nick Tinker

Fundraising

Jennifer Mitchell Fetch

Steve Molnar

Treasurer

Judith Frégeau-Reid

American Oat Workers Conference 2014

Abstracts of Session Talks

Session 1: Plenary Session, Monday, July 14

The changing climate for oats: a European perspective*

Christopher Green

Senova Limited, 49 North Road, Great Abington, Cambridge CB21 6AS www.senova.uk.com
Correspondence: chris.green@senova.uk.com

The global challenges of growth in population, decline in arable land, finite resources and water availability, coupled with an ageing population, wealth disparity and increasing urbanisation are being recognised at all international and national levels. This has placed agriculture high on the political agenda and with it the role of increasing agricultural productivity in a more efficient and sustainable manner is recognised as the key priority.

Public breeding programmes have increasingly been recognised as a near market activity and the consequence has been a sustained reduction in funding and a transfer of this and associated activities to the commercial sector. In Europe there has been a realignment of public funds to support more strategic research, which is aimed at underpinning near market breeding. Such commercial engagement in breeding has fundamentally changed the landscape.

Oat production in Europe is in decline. Today crop production is favoured in the Scandinavian countries, Poland and Germany whilst the large area in Spain is mostly devoted to producing a fodder crop. With Sweden and Finland producing well in excess of their domestic requirement, they are reliant on exports to sustain profitability. The area in Poland will probably continue its downward spiral as growers turn to more profitable crops. The German oat crop will also be under pressure where corn for biogas will continue to encroach upon minor crop plantings. The French market will remain static, where most of the oat crop is black oats for the equine market.

In the UK, consumption has increased dramatically and the amount used for human food consumption (500,000 tonnes) represents some 70% of our total annual production, with the balance used on farm or in the equine sector. However, 2012 provided to be our wettest autumn on record and close to a million hectares did not get planted with winter crop. A shortage of available spring seed in the UK coupled with good availability of spring oat seed in Europe, resulted in a dramatic seed importation and a massive increased planting. With almost a million tonnes coming to harvest compared to the UK's more normal 700,000 tonnes, the price collapsed. So, once again oats are on the production roller coaster.

Oats are unique. They could arguably provide one of the best food stocks for humanitarian aid. They richly add to our biodiversity. In an era where sustainability and carbon footprints are important issues oats have a role to play. In driving home this policy and in order to stimulate crop diversity, the new European Agricultural reforms have at their core a three crop policy where growers must establish three different crops if they are to receive area payments. But as we know production is not the problem. It is securing and sustaining new markets either in the volume animal feed sector or in dedicated added value chains that will govern the crop's destiny.

* The full report from this presentation is available in the Oat Newsletter, 2014, Vol. 1

The changing climate for oats: an international perspective

Stephen Harrison[1] and Md Ali Babar[2]

[1]School of Plant, Environmental, & Soil Sciences, Louisiana State University Agricultural Center, 104 MB Sturgis Hall, Baton Rouge, LA – USA 70803; [2]Agronomy Dept, Institute of Food and Agricultural Sciences, University of Florida, 3105 McCarty Hall, Gainesville, FL-USA, 32611

Correspondence: SHarrison@agcenter.lsu.edu

The oat research community reminds me a lot of the Louisiana coastline. It has shrunken considerably over the past 30 years despite our best efforts to maintain its vitality and functionality. There are fewer oat pathologists, breeders, geneticists, and agronomists and these scientists are faced with the task of accomplishing more with diminishing resources. International collaboration is probably the greatest strength of the oat community, and is fueled by a desire to make maximum gains with minimal resources. We often think of oats as a commodity that is turned into human food by the large milling and food industry sectors, and this is certainly vital to the future of oats as a crop. However, oats are quite diverse in end-use around the globe and have tremendous potential in food and non-food applications. The future success of oats on a global basis will depend on collaborative efforts such as the Quaker International Oat Nursery and also on innovative partnerships to identify and expand markets and uses of oats. The success of these partnerships will depend in part, on our ability to re-evaluate concepts of Intellectual Property and forge new agreements that balance a need to capture additional program resources with the benefits of shared knowledge, technology, and germplasm.

How an international oat information system will accelerate oat improvement

Jean-Luc Jannink[1], Dave Matthews, Vic Blake, Clay Birkett, James Clohessy,
Gerard Lazo, Yung-Fen Huang, Nick Tinker
[1]USDA-ARS and Cornell University, Ithaca, NY
Correspondence: jeanluc.work@gmail.com

Effective data management accelerates individual breeding programs. Given high throughput genotyping and, in the future, phenotyping, breeders spend more time assembling and formatting datasets than analyzing them. Used at the individual breeding program level, an effective oat breeders' database makes these tasks trivial. Accurate evaluation of oat breeding lines that accounts for interaction with environment requires multi-environment trials. Evaluation in many environments requires collaboration. In this context, an international oat information system facilitates the pooling and sharing of data. The system becomes a collaboration tool that brings additional data within each breeder's range. Current research to accelerate breeding is focusing on prediction using high-density marker data. This data does not substitute phenotypic data, but leverages it. In fact, genomic prediction needs large numbers of observations on as many lines as possible. While prediction can be effective within single programs, evidence to date suggests that intelligent pooling of larger datasets across programs will make prediction more accurate. Challenges face such across-program predictions but addressing them will be scientifically rewarding and beneficial to oat improvement.

American Oat Workers Conference 2014

Monday, July 14

Session 2: Quality, nutrition and processing

How oat processing affects the ability of oat beta-glucan to reduce cholesterol and blood glucose

Susan M. Tosh

Agriculture and Agri-Food Canada, Guelph Food Research Centre, 93 Stone Rd W, Guelph, ON, N1G 5C9, Canada

Correspondence: susan.tosh@agr.gc.ca

The health benefits of oats have now been well established. The ability of oats to lower serum total and LDL-cholesterol in persons with mildly elevated cholesterol has been recognized by the American, Canadian, European and Malaysian governments. Oats have also been shown to ameliorate blood glucose levels after meals. Now the challenge is to develop and produce commercial products which provide health benefits to consumers. The major soluble dietary fibre in oats, mixed linkage β-glucan, has been shown to be the bioactive component of oats responsible for these effects. Oat β-glucan is a high molecular weight polysaccharide that forms viscous solutions at low concentrations which slows mixing of the meal bolus, resulting in delayed absorption of glucose and increased excretion of cholesterol and its metabolites. To maintain the effectiveness of the food products made with oats, it is necessary to maintain the high molecular weight and solubility of the β-glucan which are responsible for producing the high viscosity. Enzyme activity, oxidizing agents and high shear can cause depolymerization of β-glucan and reduce the magnitude of the health benefits. These factors need to be controlled during processing of oat products, such as bread, other baked goods, breakfast cereals and beverages, to achieve maximum viscosity development during digestion. Understanding how the soluble fibre in oats regulates blood glucose, insulin and cholesterol in humans can help food processors design and manufacture foods which optimize the efficacy of oat β-glucan for the benefit of consumers.

A microscopic tour of β-glucan distribution and status in a range of oat food products

S. Shea Miller[1], S.M. Tosh[2], T. Gamel[2], E-S. M. Abdel-Aal[2]

[1]AAFC-ECORC, Ottawa, Canada; [2]AAFC- Guelph Food Research Centre, Guelph, Canada

Correspondence: shea.miller@agr.gc.ca

Mixed linkage (1-3),(1-4)-β-D-glucan (β-glucan) from oats is a soluble fibre that has been demonstrated to have beneficial effects on carbohydrate and lipid metabolism in humans. However, different processing methods will affect the microstructure of oat ingredients in the final product, and the bio accessibility and status of the β-glucan in the product as well. β-Glucan can be incorporated into the diet in a wide variety of food products. Whole groats can be boiled and eaten as a rice substitute. In perhaps the most familiar application, oats are milled and rolled to produce oatmeal used to make porridge or baked goods, or further fractionated to produce oat bran. Oat bran can be consumed as a cereal, or as an ingredient in oat-based products. Bakery products are also a convenient vehicle for delivery of β-glucan in the diet, and a wide range of products containing oats and oat fractions are now available. However, the status of β-glucan in a product (e.g., amount solubilized, molecular weight) will impact its physiological efficacy. In this presentation we will illustrate the role of microscopy in helping to elucidate β-glucan distribution and status in a range of traditional and novel oat foods. Rolled oats and oat bran retain most of the characteristics of the whole oat, while in products such as breads, muffins, extruded cereals, and pasta, the microstructure and β-glucan state are altered to varying degrees. The relative amounts of β-glucan solubilisation and depolymerisation will influence the magnitude of benefit(s) obtained by consuming these products.

Lipids in Seeds of Oat (*Avena* spp.), a Potential Oil Crop

Svetlana Leonova[1], Åsa Grimberg[2], Sten Stymne[2], Anders S. Carlsson[2]

[1]Lund University, Center of Chemistry and Chemical Engineering, Lund 221 00 Sweden;
[2]Swedish University of Agricultural Sciences (SLU), Växtskydsvägen 1, Alnarp 23053 Sweden

Correspondence: svetlana.leonova@tbiokem.lth.se

New oil crops with high yield and oil content are urgently needed. Oat is the only cereal that accumulates a substantial amount of lipids in the endosperm. This gives it potential as an oil crop, which could address both the nutritional and environmental concerns of modern society. To develop oat with increased oil content, thorough investigations of its lipid metabolism and tools for genetic manipulations are needed.

Analyses of lipids in seeds of wild and cultivated oat species revealed variation in wild oat accessions in both oil content and quality. This variation should allow for development of new oat varieties for diverse applications. However, to develop oat as an oil crop, a level of 20% of the seed dry weight as oil is required and the range of oil content in the studied accessions was 4-10%. Another feature which showed almost no deviation was the amount of omega 3 fatty acid, α-linolenic acid (0.6-2.1%) (Leonova *et al*., 2008).

Lipids in oat endosperm have been reported to exist, not enclosed in oil bodies, but as non-structured oil smears. In this study, we also observed oil smears, a phenomenon probably correlated with the reduced number of oil body-associated proteins in the endosperm, as revealed by microscopic and staining methods. This was supported experimentally by SDS-PAGE separation of oil-body proteins and immunoblotting and immunolocalization with antibodies against a 16 kD oil body protein (Heneen *et al*., 2008).

Biochemical studies of lipid mobilization during oat seed germination demonstrated efficient utilization of oil reserves from the starchy endosperm; these results were corroborated by microscopy. An oat cultivar which is capable of accumulating high amounts of oil in the endosperm was also shown to be efficient in utilizing these reserves upon germination (Leonova *et al*., 2010).

References

Heneen, W. K., G. Karlsson, K. Brismar, P. O. Gummeson, S. Marttila, S. Leonova, A. S. Carlsson, M. Bafor, A. Banas, B. Mattsson, H., & S. Stymne (2008). Fusion of oil bodies in endosperm of oat grains. Planta 228(4):589-599.

Leonova, S., Å. Grimberg, S. Marttila, S. Stymne, & A.S. Carlsson (2010). Mobilization of lipid reserves during germination of oat (*Avena sativa* L.), a cereal rich in endosperm oil. Journal of Experimental Botany 61(11):3089-3099.

Leonova, S., T. Shelenga, M. Hamberg, A.V.Konarev, I. Loskutov, & A.S.Carlsson (2008). Analysis of oil composition in cultivars and wild species of oat (Avena sp.). Journal of Agricultural and Food Chemistry 56(17):7983-7991.

Pure Porridge Puzzle – People, Process, Purity and Price

Beth Armour

Cream Hill Estates, Montreal, Quebec, Canada

Correspondence: beth.armour@bellnet.ca

Getting a gluten-free product to market can often be challenging as it requires many people, processes, monitoring and testing to ensure the purity of the product. It is particularly challenging when it comes to gluten-free oats. In our five step purity process, starting from the seed until the package is ready for shipping to the customer, every step requires a commitment to ensuring there is no cross-contamination with gluten-containing items. Even though all of this comes at a price and with some challenges, the demand for gluten-free oats has increased in many parts of the world, in part due to the increasingly important health benefits of oats.

Oat-Rice Processing and Quality Evaluation

Xinzhong Hu[1], Xiaoping Li[1], Yang Xu[2], Qiong Zhao[2]

[1] College of Food Engineering and Nutrition Science, Shaanxi Normal University, Xian, Shaanxi 710062, China; [2] College of Food Science and Engineering, Northwest A&F University, Yangling, Shaanxi, China, 712100, China

Correspondence: hxinzhong@126.com

Oat-rice is a new kind of oat food that has appeared in the Chinese market, but current oat-rice products have many disadvantages, such as coarse taste, short shelf life, and longer cooking time. These disadvantages have hindered the acceptance of oat-rice by consumers. To overcome these obstacles, we used Chinese naked oats as the raw materials, combined with the abrasive milling and infrared roasting, and mixed with rice to produce the better mouth-feel oat-rice. This research evaluated the quality of the oat-rice and the mixture (oat-rice and rice) by nutritive index, amino acid pattern, sensory evaluation, texture profile analysis, appearance, color, and peroxidase activity. In addition, the obese-mouse model was used to evaluate the blood glucose and fat reducing functionality of oat-rice. Our results showed that the nutritional value of oat-rice is higher than rice alone. As the proportion of oat-rice was increased in an oat-rice/rice mixture, the protein and lipid contents increased gradually, but the taste became coarser. The critical control points of oat-rice are kernel size screening (20-25g/thousand kernel weights), debranning with an abrasive mill, steam treatment, and infrared roasting. The lipase activity and peroxidase activity were deactivated by these treatments. The final oat-rice has a lighter color, more pleasant taste, shorter cooking time, longer shelf life and more balanced amino acid value by steaming the oat component compared with rice treated for the same amount of time. The amino acid evaluation, TPA, and sensory evaluation indicated that the optimum ratio of oat-rice and rice is 30%.

The animal experiments were conducted with three different proportions of oat-rice added to a normal mouse diet, fed to obese mice, and compared to normal mice on a normal diet or obese mice on a normal diet. When compared to the obese-mice on a normal diet, the weight gain (assessed by Lee 's index) of mice from low oat-rice group, medium oat-rice group and high oat-rice group, was significantly reduced ($P<0.05$). The concentration of blood glucose, total cholesterol and low density lipoprotein were also reduced ($P>0.05$), while insulin content and insulin sensitivity were significantly increased ($P<0.05$) and steatosis of the liver was significantly decreased. When the oat-rice addition was 20%-30% of the diet, the effect of reducing weight for the obese mice was the most obvious.

American Oat Workers Conference 2014

Monday, July 14

Session 3: Agronomy and Physiology

High yield input systems and impact on yield and β-glucan levels*

Spyridon Mourtzinis, Shawn P. Conley, and John M. Gaska

Department of Agronomy, University of Wisconsin-Madison

Correspondence: spconley@wisc.edu

Oat (Avena sativa L.) is an important crop in the U.S. The primary uses for oat in Wisconsin are for establishing alfalfa underseedings, livestock forage, grain, and straw production, and for human nutrition. Therefore, the quantitative and qualitative characteristics of oat are of great importance. The effects of variety, seeding rate, seed treatment, and foliar fungicide on total grain yield, groat proportion, test weight, plant height, lodging severity, and β-glucan content were examined in two separate trials established from 2011 to 2013 at the University of Wisconsin Arlington Agricultural Research Station. The results from the two three-year studies highlight the importance of selecting an appropriate oat variety with superior yield and quality characteristics. The use of a high seeding rate had no effect on any of the examined characteristics. However, treated seeds exhibited increased total yield compared to untreated. An important finding of this study is that the use of a foliar fungicide increased total and groat yields, reduced lodging severity without impacting β-glucan content. The results of this study indicate that the use of a superior variety such as Badger and BetaGene, use of Rancona Crest seed treatment, and use of Headline foliar fungicide can greatly increase oat yields in Wisconsin without reducing the crops' quality characteristics.

Data used for this abstract and conference report is currently in review by the Journal Crop Science; Mourtzinis, S., S. P. Conley, J.M. Gaska (2014). Agronomic Management and Fungicide Effects on Oat Yield and Quality. (In review: Crop Sci.).

* The full report from this presentation is available in the Oat Newsletter, 2014, Volume 1

β-Glucan, Oil, and Protein of Oats as Affected by Variety, Location, and N Application

Bao-Luo Ma[1], Judith Fregeau-Reid[1], Denis Pageau[2], Cecil Vera[3], and Weikai Yan[1]

[1]AAFC-ECORC, Ottawa, ON K1A 0C6; [2]AAFC, Normandin, QC G8M 4K3; [3]AAFC, Melfort, SK S0E 1A0

Correspondence: Baoluo.Ma@agr.gc.ca

Oat (*Avena sativa* L.) has been cultivated increasingly as a healthy food crop due to its high dietary fibre (β-glucan in particular) content. High yielding oat cultivars usually do not have the desired levels of dietary fibre, or vice versa. A field experiment was conducted in 2013 to study the effects of nitrogen (N) fertilization on the yield and quality characteristics of ten oat cultivars important in western and eastern Canada. The experiment was conducted at three locations in Canada: 1) The Central Experimental Farm, AAFC in Ottawa, Ontario, 2) The Normandin Research Farm, AAFC in Normandin, Quebec, and 3) The Melfort Research Farm, AAFC in Melfort, Saskatchewan. At each site the experiment was arranged in a split-plot design with three or four replications, with four levels of N (0, 50, 100 and 150 kg ha^{-1}) as the main plots and ten cultivars (twelve in Ottawa) as the subplots. The plots were seeded at a density of approximately 300 plants m^{-2} from late April to early May at each site. At maturity, the plots were combined for grain yield. A subsample from each plot was taken to determine groat (oat grains after removing the hulls) content. The groat was then ground and used to determine protein, β-glucan, and oil concentrations using near-infrared reflectance spectroscopy (FOSS NIRS 6500, Eden Prairie, MN, USA) using calibration equations developed in-house, based on wet chemistry.
The data showed that the protein, oil, and β-glucan concentrations were affected by location, genotype, and N application. Ottawa had the highest β-glucan, Normandin the highest protein, and Melfort the highest oil concentrations. Cultivar CDC Morrison had the highest β-glucan (5.7%) and protein (15.1%), followed by Summit (5.5% and 14.2%, respectively). CDC Seabiscuit had the highest oil concentration (8.2%), while Dieter had the lowest (6.0%). Partial correlation analysis of the data showed that the β-glucan level was positively correlated with protein concentration ($P < 0.01$) and grain yield ($P < 0.01$), and negatively correlated with oil concentration ($P < 0.07$) across all sites, genotypes, and N treatments. In general, increasing N application increased protein and β-glucan, but decreased the oil concentrations. Therefore, the result suggests that N application can be used to improve the quality profiles of oat genotypes.

The Effect of Nitrogen and Fungicides on Oat Yield and Quality

Bill May

Agriculture and Agri-Food Canada, Indian Head, SK

Correspondence: bill.may@agr.gc.ca

Oat (*Avena sativa* L.) yields in Saskatchewan typically exceed 90 bu/ac and yields of 200 bu/ac are possible. Crop removal of nitrogen from soil is slightly more than 0.6 lb/bu meaning that a 150 bu/ac crop would remove more than 100 kg ha-1 of N. Past research indicated that oat yield was often optimized at N rates between 30 and 60 kg ha-1 with N rates above 60 kg ha-1 reducing the test weight. Recently, fungicides have been promoted to increase yield through a general increase in plant health in addition to protecting the crop when significant injury occurs from a fungal disease. Many producers with a desire to maximize oat yields are trying a combination of products to increase yield. For these reasons, growers who target high oat yields often apply in excess of 90 kg ha-1 of fertilizer N. and use foliar fungicides for leaf disease control. The objective of this experiment was to examine the effects of combining higher nitrogen rates with fungicides in oat. Three fungicide treatments (no fungicide, Headline or Stratego) and eight nitrogen fertilizer rates (5, 20, 40, 60, 80, 100, 120 and 140 kg ha-1) were used in a split plot design with 4 replications at Indian Head and Melfort in 2012 and 2013. The cultivar Triactor was used at all four site years. Leaf disease development was low especially for crown rust (*Puccinia coronata* Corda f. sp. *avenae* Eriks.). The yield potential at all four site years was above average with the yield of the 5 kg N ha-1 rate ranging between 3707 to 6350 kg ha-1 (96 to 166 bu/ac). There was no interaction between the fungicide and applied N fertilizer for any of the variables measured at either location in either year. The oat was more responsive to higher N rates than expected with yield increasing as N rate increased to 140 kg N ha-1 at Melfort in 2012, 100 kg N ha-1 at Melfort in 2013 and Indian Head in 2012 and 2013. Test weight declined as the N rate increased at all four site years; however, the only decline to be large enough to result in a lower grade was at Indian Head in 2012. In conclusion, the grain yield of Triactor responded to N rates up to 100 kg N ha-1 with very little impact on test weight. This response requires further study to determine if it is stable over various environmental conditions. Triactor has enough disease resistance that a fungicide application did not increase yield and fungicide application did not benefit the oat crop in the absence of disease or improve the responsiveness of oat to N rates.

Modelling β-glucan content in oat using data from variety trials

Steven J. Shirtliffe

Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, S7N 5A8.

Correspondence: steve.shirtliffe@usask.ca

Despite years of concentrated effort in plant breeding, in some years oat β-glucan content is often low. The environmental variables that drive oat β-glucan are not completely known. The effect of environmental variables on oat β-glucan content was modeled using correlation analysis and stepwise multiple linear regression on 49 site years of oat variety trials constituting over 1600 data entries. The data from the Western Cooperative Oat Registration Trials (WCORT) from 2001 to 2010 was used exclusively to parameterize of the model. The environmental parameters considered were precipitation, average maximum temperature, average minimum temperature, cooling degree-days (days with average temperature above 18C), and days with maximum temperature above 30 C. Using these values we then calculated average monthly temperatures (average of maximum and minimum temp), monthly temperature range (maximum T – minimum T), and growing season precipitation (May – August). The model was then simplified in a stepwise fashion using multiple linear regressions. A final model was developed that described 40% of the non-genetic variation of β-glucan with only 5 environmental variables. In general, hot temperatures in May and July resulted in the highest β-glucan. Growing season precipitation had a negative effect on β-glucan. Hot temperatures in August along with cool nights also appear to result in high β-glucan. If successfully validated, this model has the potential to predict oat β-glucan levels in western Canada on a geographic and temporal basis.

Phenotypic analysis of abiotic stress tolerance in Australian oat

Klaus Oldach[1,2], Yusuf Genc[1,2], Mahmood Hassan[1], Tim March[2], John Harris[1], Pamela Zwer[1].

[1]South Australian Research and Development Institute, Plant Genomics Centre, Waite Campus, Urrbrae, SA 5064, Australia; [2]School of Agriculture, Food, and Wine, University of Adelaide, Waite Campus, Urrbrae, SA 5064, Australia

Correspondence: john.harris2@sa.gov.au

Boron toxicity affects about 50% of the neutral-alkaline soils of the South Australian and Victorian grain belt and dryland salinity affects 67% of all cropping areas in Australia. These sub-soil constraints can result in yield losses under conditions of water deficit that are prevalent in the Australian cropping environment. Selection for tolerances to these abiotic stresses in oat would be enhanced by the development of molecular markers for trait selection. However, a prerequisite for marker development is an initial accurate phenotypic analysis to establish the closest possible linkage between trait and molecular marker. In this project our aims were to benchmark Boron and salinity tolerance of oat to wheat and barley and translate marker technologies to oat for use as selection tools for agronomically important traits.

American Oat Workers Conference 2014

Tuesday, July 15

The Oat Newsletter: where we've been and where we're going

Charlene P. Wight[1], Michael McMullen[2], Gabe Gusmini[3], Gerard R. Lazo[4], S. Shea Miller[1], Jennifer Mitchell Fetch[5], Jean-Luc Jannink[6], Mark E. Sorrells[7], and Nicholas A. Tinker[1].

[1]ECORC, Agriculture and Agri-Food Canada, Ottawa, ON, Canada; [2]Dept. Plant Sciences, North Dakota State University, Fargo, ND, USA; [3]Corporate R&D, PepsiCo, Inc., Hawthorne, NY, USA; [4]USDA-ARS Western Regional Research Center, Albany, CA, USA; [5]Brandon Research Centre, Agriculture and Agri-Food Canada, Brandon, MB, Canada; [6]USDA-ARS and Cornell University, Ithaca, NY, USA; [7]Dept. Plant Breeding and Genetics, Cornell University, Ithaca, NY, USA

Correspondence: nick.tinker@agr.gc.ca

The first Oat Newsletter was published by the National Oat Conference in 1950. It was published once a year and mailed out to "oat workers" only. The newsletter was designed to supplement the Uniform Nursery reports by providing short research updates, meeting information, community information, and reports from oat research stations concerning yields, disease outbreaks, etc.. Past issues contain a fascinating history, and are well worth reading.

Starting in 1998, the newsletter was hosted online by the USDA GrainGenes website. The last issue was published in 2006, but, by this time, the newsletter was in decline. This was not surprising, as people had begun taking advantage of email, cheap long-distance phone calls, and easy access to the Internet to keep in touch. On-line databases were also making research information more readily available, and GrainGenes and POOL (**P**edigrees **O**f **O**at **L**ines), for example, had become important resources for people working on oats.

So why continue with the Oat Newsletter? E-mail and voice conferencing may function well to keep smaller groups of people together, but do not allow for input from outside the group. Fewer people work solely on oats and many are unable to attend oat conferences or meetings. AOWC proceedings will continue to be published in the Newsletter, and other conferences, including the IOC, will be encouraged to submit conference reports for inclusion as well. There is also still a need to discuss project options, share preliminary information, and keep each other updated concerning a myriad of things, including personal stories.

The new Oat Newsletter, linked to the Oat Global portal on GrainGenes, is being designed to make it easier to post and view information. While there will continue to be an editorial process for formal Newsletter submissions, there will also be a direct discussion forum with minimal moderation. Those who subscribe will receive notifications when new material is available. At the end of each year, articles published during that year will be collected and archived in a volume. All previous issues of the newsletter, from 1950 onwards, will also be available. To quote K.S. Quisenberry in the inaugural edition of the Oat Newsletter, "Its success will depend on the cooperation of all workers." The same holds true today, and we look forward to receiving your contributions.

American Oat Workers Conference 2014

Tuesday, July 14

Session 4: Pathology

Effect of timing of inoculation and *Fusarium* species on the development of Fusarium head blight and deoxynivalenol contamination in oat*

A.G. Xue[1], Y.H. Chen[1], G. Marchand[1], W. Guo[1], C.Z. Ren[2], M. Savard[1], and A. McElroy[3]

[1]AAFC-ECORC, Ottawa ON, K1A 0C6, Canada; [2]Heilongjiang Bayi Agricultural University, 5 Xinfeng Road, Daqing Heilongjiang, 163319, China; [3]Baicheng Academy of Agricultural Sciences, 17 Sanhe Road, Baicheng Jilin, 137000, China; [4]PhytoGene Resources Inc., 1855 Rue des Arbres, Orleans ON, K1E 2T7, Canada

Correspondence: allen.xue@agr.gc.ca

Fusarium head blight (FHB) is a destructive disease of oats in Canada. To assist the development of FHB-resistant cultivars, the influence of timing of inoculation and pathogenicity of four *Fusarium* spp. causing FHB were examined on 12 oat genotypes under controlled environmental conditions. Early inoculations with *F. graminearum* at or before the complete emergence of ears resulted in little or no visible FHB symptoms but deoxynivalenol (DON) contents ranging from 0.9 to 3.7 ppm were detected in the harvested grain. Severe levels of FHB were observed on these genotypes with infected spikelets (IS) ranging from 40 to 75% and DON concentrations, from 6.3 to 10.2 ppm, when plants were inoculated at or after the 50 % anthesis stage. Inoculation at the 50 % anthesis was considered the most appropriate timing as it allowed sufficient time for disease development and assessment prior to physiological maturity of the plant. Of the four *Fusarium* spp., *F. culmorum* and *F. graminearum* were equally highly pathogenic, having areas under the disease progress curve (AUDPC) of 45.3 and 47.3, and DON content in the harvested grain of 10.4 and 14.3 ppm, respectively. *Fusarium sporotrichioides* resulted in the lowest AUDPC (31.2) and was significantly less pathogenic than the two highly pathogenic species. *Fusarium avenaceum* was intermediate and the resulting AUDPC (36.7) was not significantly different from those of either the highly pathogenic or the weakly pathogenic species. The oat genotype and *Fusarium spp*. interaction was not significant, suggesting that breeding for resistance to *F. graminearum* may also confer enhanced resistance to other *Fusarium* spp.

* The full report from this presentation is available in the Oat Newsletter, 2014, Volume 1

Effects of cropping factors and health promoting compounds in different oat cultivars on *Fusarium* species infection and mycotoxin contamination*

Torsten Schirdewahn[1], Charlotte Martin[2], Fabio Mascher[2], Thomas D. Bucheli[1], Mario Bertossa[3], Romina Morisoli[3], Tomke Musa[1], Susanne Vogelgsang[1]

[1]Agroscope, Institute for Sustainability Sciences, Reckenholzstrasse 191, 8046 Zurich, Switzerland; [2]Agroscope, Institute for Plant Production Sciences, Route de Duillier 50, 1260 Nyon 1, Switzerland[3;] Agroscope, Institute for Plant Production Sciences, A Ramél 18, 6593 Cadenazzo, Switzerland

Correspondence: susanne.vogelgsang@agroscope.admin.ch;

Small-grain cereal varieties differ substantially with respect to their content in health promoting compounds (HPCs). The various HPCs found in wheat, barley and oats include substances with antioxidant potential such as phenolics, tocopherols, arabinoxylans and carotenoids, as well as ß-glucan. Compounds with antioxidant potential are considered to prevent human diseases such as cancer, cardiovascular diseases and Parkinson. The polysaccharide ß-glucan on the other hand is a soluble dietary fibre associated control of cholesterol and attenuation of insulin levels. Apart from containing HPCs, cereals must be safe and thus free of health threatening substances. Contamination of cereals with mycotoxins, especially through different *Fusarium* species, constitutes a substantial risk to human health. Interestingly, fungal growth and/or toxin production can be inhibited by different plant endogenous HPCs.

Funded by a National Research Programme (www.nrp69.ch) of the Swiss National Science Foundation, the project "Are healthy cereals safe cereals? - Ensuring the resistance of small grain cereals to *Fusarium* diseases" (HEALTHY & SAFE) was launched at the end of 2013. The overall objective of HEALTHY & SAFE is to reduce the risk of contamination of small-grain cereals by *Fusarium* toxins while developing value added varieties containing HPCs. Using a systematic approach, the occurrence and frequency of toxigenic *Fusarium* species on oat and barley are assessed in grains from all over Switzerland. In parallel, the resistance against Fusarium head blight (FHB) and mycotoxin accumulation in grains of novel genotypes with enhanced content in HPCs and potentially improved resistance traits are currently evaluated.

We will present results from the first year of work, including the *Fusarium* species occurrence and effect of cropping factors on infection from a monitoring on oat harvest samples. Furthermore, we will give an overview on current experiments and upcoming activities such as resistance experiments with artificial infections, epidemiology, forecasting and implementation.

* The full report from this presentation is available in the Oat Newsletter, 2014, Volume 1

Quantitative trait loci from two genotypes of oat (*Avena sativa* L.) conditioning resistance to *Puccinia coronata*

Ebrahiem M. Babiker[1], Tyler C. Gordon[1], Eric W. Jackson[2], Shiaoman Chao[3], Stephen A. Harrison[4], Martin L. Carson[5], Don E. Obert [6], J. Michael Bonman[1]

[1]USDA-ARS, Small Grains and Potato Germplasm Research Unit, Aberdeen, ID 83210; [2]General Mills Inc., 150 Research Drive, Kannapolis, NC, 28081; [3]USDA-ARS, Cereal Crops Research, 1605 Albrecht Blvd., Fargo, ND 58102; [4]Louisiana State University Agricultural Center, 104 M.B. Sturgis Hall, Baton Rouge, LA 70803; [5]USDA-ARS, Cereal Disease Laboratory, St. Paul 55108; [6]Limagrain Cereal Seeds, 9020 Grant Road, Battle Ground, IN, 47920

Correspondence: Mike.Bonman@ars.usda.gov

Developing oat cultivars with partial resistance to crown rust would be beneficial for disease management. Two recombinant inbred line (RIL) populations were derived by crossing the susceptible cultivar 'Provena' with two partially resistant sources, 'CDC Boyer' and breeding line 94197A1-9-2-2-2-5. The populations were evaluated for crown rust severity in the field at Louisiana State University (LSU) in 2009 and 2010 and at the Cereal Disease Laboratory (CDL) in St. Paul, Minnesota in 2009, 2010, and 2011. An iSelect platform containing assays for 5744 oat single nucleotide polymorphisms (SNPs) was used to genotype the populations. From the 2009 CDL test, linkage analyses revealed two QTL for partial resistance in the Provena/CDC Boyer population on chromosome 19A. One of the 19A QTL was also detected in the 2009 LSU test. These QTL explained 10-15% and 11-20% of the phenotypic variation. Another QTL for partial resistance, explaining 10-11% of the phenotypic variation was detected in on chromosome 12D in the CDL 2009 test. In the Provena/94197A1-9-2-2-2-5 population, only one QTL for partial resistance was detected on chromosome 13A in the CDL 2011 test. This QTL explained 19-35% of the phenotypic variation. Only the 13A QTL from the Provena/94197A1-9-2-2-2-5 population was validated in CDC Boyer /94197A1-9-2-2-2-5 population in the CDL 2010 and 2011 tests. This QTL explained 18-19% and 28-53% of the phenotypic variations respectively. To find candidate genes for resistance within each of the detected QTL, the significant SNP markers sequences were used as queries for BLASTN searches against the rice genome database. Fifteen candidate genes were identified on chromosomes 4 and 6 of rice. These genes could be potential targets for further marker develop and gene identification from the two resistant parents.

Development of SNP Markers for Breeding Disease Resistant Oat Varieties

Belaghihalli N Gnanesh[1], Curt A McCartney[1], Jennifer W Mitchell-Fetch[2], Yang Lin[3], James Chong[1], Aaron D Beattie[3], Pete E Eckstein[3], Jim G Menzies[1], Taye Zegeye[1], Tom Fetch[1,2], Randy Kutcher[3] and Eric W Jackson[4]

[1]Agriculture and Agri-Food Canada, Cereal Research Centre, 101 Route 100, Morden, MB, R6M 1Y5, Canada; [2]Agriculture and Agri-Food Canada, Brandon Research Centre, 2701 Grand Valley Road, Brandon, MB, R7A 5Y3, Canada; [3]Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, S7N 5A8, Canada; [4]General Mills Agriculture Research, 150 N. Research Campus Dr., Kannapolis, NC, 28081, USA

Correspondence: gnaneshbn@gmail.com

Oat (*Avena sativa* L.) is an important cereal crop grown world-wide for human and livestock consumption. Oat production can be adversely affected by major diseases such as crown rust and stem rust. Recently developed genomic tools allow new approaches to improve breeding for resistance to these diseases based on a more efficient use of genetic resources. Here, we discuss the successful identification of important oat crown and stem rust resistance genes. Race-specific seedling resistance genes are the primary means of controlling crown and stem rust of oat in Canada. We developed DNA markers linked to crown rust resistance genes (*Pc91*, *Pc94*, and a temporally designated gene *PcKM*) and a stem rust gene (postulated to be *Pg12*), and assigned chromosomal locations to the identified resistance genes. In addition, the molecular identification of loci conferring quantitative resistance (or trait) in oat has made important progress, although none of such loci has been cloned. A major QTL, designated *QPc.crc-14D*, was identified that explained up to 76% of the phenotypic variance of adult plant resistance (APR) to crown rust. The QTL was located on oat chromosome 14D flanked by two SNP markers, GMI_GBS_90753 and GMI_ES14_c1439_83. *QPc.crc-14D* was significant in three bi-parental mapping populations evaluated during this study. Analysis of synteny between oat and wheat suggests that *QPc.crc-14D* is orthologous to the stripe rust APR gene *Yr16* in wheat. Even at this early stage, it can be foreseen that this new knowledge of SNP markers for major QTL might revolutionize oat breeding for durable rust resistance in the near future. The progress made towards high-throughput molecular marker techniques in oat provides a completely new perspective on resistance breeding against these two important rust diseases.

American Oat Workers Conference 2014

Tuesday, July 14

Session 5: Breeding/Germplasm

Structure of the oat genepool at Plant Gene Resources of Canada

Axel Diederichsen

Plant Gene Resources of Canada, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada

Correspondence: axel.diederichsen@agr.gc.ca

Canada started as a leader in oat genetic resources research

Oat as a crop for short growing seasons and cooler temperate climates is important for Canada. While global oat production has declined considerably since the 1960s, it has remained relatively stable in Canada. Oat research and breeding in Canada has included a fruitful and close cooperation among Canadian plant breeders, pathologists, cytologists, taxonomists and genebank curators from Plant Gene Resources of Canada and international genebanks starting back in the 1960s. Canadian scientists organized and participated in many collecting missions for oat germplasm in the Mediterranean Region, the Near East and Central Asia between 1964 and 1982, resulting in more than 7000 unique oat accessions at PGRC of nearly all known *Avena* species. New species were described and the systematics of the genus *Avena* were reviewed based on this material (Baum 1977). Intensive characterisation for disease resistances of rust diseases and steady transfer of monogenic resistances from the wild progenitor *Avena sterilis* L. to the common hexaploid oat *A. sativa* are a unique success story in collaboration among dedicated scientists to make use of crop wild relatives in plant breeding. The relevance of crop wild relatives was emphasised more than 100 years ago (Baur 1917) and today this strategy gains momentum again (Loskutov and Rines 2011).

The world base collection of oat at PGRC

In 1977, PGRC was assigned the task to preserve the base collection of oat germplasm by the International Board for Plant Genetic Resources (IBPGR, today Bioversity International) (Thormann and Engels 2001). Many world genebanks deposited back-up duplicates of oat samples at PGRC and today the PGRC collection has more than 27,000 accessions of 29 *Avena* species, the largest oat collection in the world (FAO 2010). During recent years, PGRC has focused on regeneration and characterisation of the *Avena* material to ensure that seeds and information about the material are available. The PGRC website (www.agr.gc.ca/pgrc-rpc) is used to disseminate information to order seed material from PGRC. The passport data has been improved and geo-referenced for producing distribution maps. Recent research at PGRC has focused on molecular, morphological and seed quality diversity to better understand the structure of the genepool (Diederichsen 2008, 2009; Fu et al. 2003, 2005). Recent acquisitions of oat occurred during collection missions to Ukraine and Italy. A set of 350 world oat cultivars was

added due to collaboration with N. Tinker of Ottawa. Between 1998 and 2013, PGRC distributed a total of 16,061 *Avena* accessions of all species to 29 countries in the world. This underlines the impact the PGRC oat collection has on world- wide oat research and breeding.

Outlooks for the PGRC oat collection

It is presently required to make strategic decisions regarding the PGRC oat collection. None of the International Research Centres (CGIAR Centres) has a mandate for oat, underlining the global relevance of the PGRC oat collection. International coordination could be improved to enhance conservation and utilization of *Avena* diversity in the spirit of the International Treaty on Plant Genetic Resources for Food and Agriculture. Additional collecting of wild and landrace *Avena* material from central Asia may be warranted. PGRC continues to enter Canadian cultivars in the collection; a principal decision is whether PGRC should strive to update the world base collection of *Avena* by adding more recent material from international sources.

References

Baum B.R. (1977) Oats: wild and cultivated, a monograph of the genus *Avena* L. (Poaceae). Canada Department of Agriculture, Ottawa.

Baur, E. (1917) Die Bedeutung der primitiven Kulturrassen und der wilden Verwandten unserer Kulturpflanzen für die Pflanzenzüchtung. [The relevance of primitive crop types and the wild relatives of our cultivated plants for plant breeding]. Jahrbuch DLG (Saatzuchtabteilung), pp. 145-154.

Diederichsen A. (2008) Assessments of genetic diversity within a world collection of cultivated hexaploid oat (*Avena sativa* L.) based on qualitative morphological characters. Genetic Resources and Crop Evolution 55, 419-440.

Diederichsen A. (2009) Duplication in Nordic *Avena sativa* accessions at the Canadian national genebank. Genetic Resources and Crop Evolution 56, 587-597.

FAO (2010) The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture. http://www.fao.org/agriculture/crops/thematic-sitemap/theme/seeds-pgr/sow/sow2/en/

Fu Y.B., Peterson G.W., Scoles G., Rossnagel B., Schoen D.J., Richards K.W. (2003) Allelic diversity changes in 96 oat cultivars released from 1886 to 2001. Crop Science 43:1989–1995.

Fu Y.B., Peterson G.W., Williams D., Richards K.W., Mitchell Fetch J. (2005) Patterns of AFLP variation in a core subset of cultivated hexaploid oat germplasm. Theoretical and Applied Genetics 530:530–539.

Loskutov, I.G. and Rines H.W. (2011) Chapter 3 *Avena*. In: Kole C. (ed.) Wild crop relatives: genomic and breeding resources cereals. Springer, Berlin Heidelberg, pp. 109-183.

Thormann, I. and Engels, J. (2001) IBPGR/IPGRI Register of Base Collections. In: Anonymous (2001) Development of a scientifically sound and financially sustainable global genebank system. Final report on the technical research phase. IPGRI, Rome, Italy. 32 pp.

SNP and DArT diversity in European oat germplasm

Alf Ceplitis, Pernilla Vallenback

Lantmännen Agriculture, Breeding & Technology, SE-26881 Svalöv, Sweden

Correspondence: alf.ceplitis@lantmannen.com

The recently developed oat 6k SNP chip represents a major breakthrough in terms of genomic tools for oat research and breeding. The SNP markers were developed from mainly North American germplasm and their performance in material from other regions has been less investigated. Here, we report results from SNP genotyping of a panel of 261 oat varieties of European origin. Nearly 3,000 SNP loci were polymorphic in the panel as a whole, with some differences in the number of polymorphic markers and levels of diversity between European regions (i.e. North, South, East & West). While Southern European varieties were more divergent, there was nevertheless little population substructure within the European panel. Of the total number of SNP markers polymorphic in the European material, 455 are included in the recent oat consensus map (Oliver et al. 2013) and occur on all 21 linkage groups. Among these markers, there was an almost 3-fold difference in the level of diversity between linkage groups. Comparisons of the amount and structure of genetic diversity in the European panel estimated from SNP vs. DArT markers will also be presented.

References

Oliver, R.E., N.A. Tinker, G.R. Lazo, S. Chao, E.N. Jellen, et al. (2013). SNP Discovery and Chromosome Anchoring Provide the First Physically-Anchored Hexaploid Oat Map and Reveal Synteny with Model Species. PloS ONE 8: e58068.

Genetic structure of a Chilean oat core collection based on GBS SNPs

Mónica Mathias-Ramwell[1], María-Elena Reyes[1], Francisco Bustamante-Gutierrez[3], Javier Flores-Vera[3], Iván Maureira-Buttler[2], Haroldo Salvo-Garrido[1,2].

[1] Instituto de Investigaciones Agropecuarias, INIA, km 10 camino Cajón-Vilcún, Región de La Araucanía, Chile; [2] Agriaquaculture Nutritional Genomic Center, CGNA, km 10 camino Cajón-Vilcún, Región de La Araucanía, Chile; [3] Universidad de Concepción Campus Los Ángeles, Juan Antonio Coloma #0201, Región del Bío Bío, Chile

Correspondence: hsalvo@inia.cl

Oat is the major agricultural export product of the "La Araucanía" region, Chile. The continuous increase in oat cropping area has transformed Chile into the fourth ranked oat food exporting country. Oat, as most crops, must be better adapted to new environmental conditions, such as climate changes and global warming, in order to increase, or at least maintain, grain yields, pest resistance, industrial quality, and healthy food quality traits.

To overcome these challenges, oat breeding at INIA has generated several genetic and genomic strategies to aid in the introduction of novel favorable genetic variation, and to facilitate pre-breeding and selection of better-adapted oat genotypes. In this study, we show the use of a set of SNP markers, generated by Genotyping by Sequencing-GBS, to understand genetic diversity within our oat core collection. A set of 190 diverse oat accessions was included in the analyses, and 370 out of 20,475 SNPs were used for a genetic population structure analysis. The most likely number of subpopulations was eight, with allele frequency divergence among them ranging from 0.23 to 0.43. Fst values for each subpopulation were high (0.65-0.98), as expected in a self-pollinated species. Currently, the whole set of SNPs is being used for association studies using a large set of phenotypic data collected in multi-environment evaluations, in order to discover QTLs associated with agronomic, industrial and food quality-related traits.

Acknowledgments: Quaker Oats, Agriaquaculture Nutritional Genomic Center (CGNA), "Alimentos El Globo S.A." Company, "Corporación de Fomento de la Producción" – CORFO (INNOVA 12IDL2-13628).

Management of Oat Germplasm in China

Zongwen Zhang[1,2], Bin Wu[1]

[1] Institute of Crop Science of Chinese academy of Agricultural sciences, Beijing, China; [2] East Asia Office of Bioversity International, Beijing, China

Correspondence: Zhangzongwen@caas.cn or z.zhang@cgiar.org

Oat (*Avena* L.) is a minor grain crop in China. It is widely cultivated in north, northwest and southwest parts of the country. Oat, particularly naked oat serves as staple food for many local people in producing areas. In the long history of cultivation, various types of local oat varieties were derived and remained under different agroecological environments. Since 1980s, over 4220 accessions of oat germplasm have been collected and conserved by the national genebank in China, including 2200 accessions of naked type and 2020 accessions of hulled type. Morphological characterization of Chinese oat collection was carried out for the traits of plant, panicle, flower and grains. Data on accessions were documented and shared in National Information System of Crop Germplasm Resources. Genetic diversity of oat collection was assessed with molecular markers, such as AFLP, SSR, etc. The ploidy levels of oat species were distinguished with special SSR markers. With the constructed genetic linkage maps, QTLs related to useful traits such as β-glucan content and grain size were mapped. Attempts were made to identify accessions with resistance to drought and salt, and strong adaptability to different environments, which have high potential to meet the need for climate change. With all efforts above, the conservation and sustainable use of oat germplasm has been secured, which will contribute and support to the research and development of oat industry in China.

American Oat Workers Conference 2014

Tuesday, July 14

Session 6: Breeding/Molecular Tools I

A shiny new state-of-the-art oat consensus map: where to next?

A. Shawn Chaffin[1†], Yung-Fen Huang2[2†], Scott M. Smith[3†], Adriano de Bernardi Schneider[1], Robert Reid[4], Ebrahiem Babiker[5], Gnanesh Nanjappa[3], Bradley Foresman[9], Stephen Blanchard[4], Jeremy Jay[4], Charlene P. Wight[2], Rebekah Oliver[6], Shiaoman Chao[7], Emir Islamovic[8], Kathy L. Klos[5], Fred L. Kolb[9], Curt A. McCartney[2], Jennifer Mitchell Fetch[2], J. Michael Bonman[5], Cory Brouwer[4], Eric N. Jellen[10], Jesse Poland[11], Tzung-Fu Hsieh[2], Ryan Brown[12], Joe Lutz[12], Eric Jackson[12‡], Nicholas A. Tinker[2‡], Jessica A. Schlueter[1‡]

[1]Department of Bioinformatics and Genomics, University of North Carolina at Charlotte, 9201 University City Blvd., Charlotte, NC, 28025, USA; [3]Department of Plant and Microbial Biology, North Carolina State University, N.C. Research Campus, 600 Laureat Way, Kannaplis, NC, 28081, USA; [2]Agriculture and Agri-Food Canada, Bldg. 20, 960 Carling Ave, Ottawa ON, K1A0C6, Canada; [4]Bioinformatics Services Division, University of North Carolina at Charlotte, 150 North Research Campus Drive, Suite 3333, Kannapolis, NC, 28081, USA; [5]Small Grains and Potato Germplasm Research, USDA-ARS, 1691 S 2700 W, Aberdeen, ID, 83210; [6]Department of Plant Sciences, North Dakota State University, P.O. Box 6050, Fargo, ND, 58108-6050; [7]Cereal Crops Research, USDA-ARS, 1605 Albrecht Blvd N, Fargo, NC, 58102-2765; [8]Department of Plan and Microbial Biology, University of California at Berkeley, 311 Koshland Hall, Berkeley, CA, 94720; [9]Department of Crop Sciences, University of Illinois, AE-120 Turner Hall, 1102 S. Goodwin, Urbana, IL, 61801; [10]Department of Plant and Wildlife Sciences, Brighman Young University, 4105 LSB, Provo, UT, 84602; [11]Department of Agronomy, Kansas State University, 4011 Throckmorton Plant Sciences Center, Manhattan, KS, 66506; [12]General Mills Crop Biosciences, Center for Wheat Innovation, Manhattan KS, 66506

Correspondence: jschluet@uncc.edu; [†]equal contribution; [‡]senior authors

Here we present the improved construction of the oat consensus linkage map. This map was developed from 12 populations genotyped by the oat Infinium assay as well as a subset genotyped by sequencing. This consensus map represents the 21 chromosomes of hexaploid oat as well as variants of chromosomes that have translocations. Individual component maps were cleaned for duplicated markers and them merged into a single consensus map. Linkage groups were assigned and anchored to physical chromosomes using monosomic hybrid lines. These consensus map, as well as two of the individual population maps, are being used to anchor the assembly of the oat genome zipper.

Genetic diversity among oat lines of the North American Collaborative Oat Research Enterprise (CORE)

Kathy Esvelt Klos, Yung-Fen Huang, Nicholas Tinker, CORE collaborators

USDA-ARS, Aberdeen, ID, USA

Correspondence: Kathy.Klos@ARS.USDA.GOV

Characterization of population structure and genetic diversity is a critical first step in association mapping of genes controlling complex traits. It can also assist plant breeders with parent selection aimed at maximizing the potential for effective new gene combinations in lines under development. Using 9,615 polymorphic markers genotyped on 514 lines, we found evidence of population structure at a level which may inflate the type I error rate of genome-wide association analyses (λ=2.2). Examination of the eigenvalues of the first 25 principal components also suggested the presence of sub-population groups in this sample. However, incorporation of the first three principal components as covariates in a mixed linear model should generally prove sufficient to account for population structure in genotype-phenotype association analyses. Visualizing patterns of genetic diversity by plotting the first three principal coordinates revealed clustering of lines according to growth habit. Bayesian model-based analyses also identified patterns of allelic similarity suggestive of sub-populations defined by breeding program and region of adaptation. These analyses suggest that oat lines originating from different breeding programs differ in their allele frequency distributions. Thus they may also differ in allelic composition at genes controlling important complex traits.

What can we learn from diploid oats: The IBERS Diploid *Avena* Genomics Resource (DAGR) and its application to hexaploid oat breeding?

Catherine J Howarth[1], Rob Vickerstaff[1], Tim Langdon[1]

[1]IBERS, Aberystwyth University,

Correspondence: catherine.howarth@aber.ac.uk

An *Avena* A-genome zipper has been constructed based on sequencing of parents and inbred progeny from an interspecific cross between wild and domesticated diploid species (*Avena atlantica x A. strigosa*). Synteny with other grass and cereal genomes has been established based on sequencing and mapping of over 26000 annotated genes (high confidence predictions based on combined *ab initio* and database alignment approaches). This genome zipper is being used for gene discovery, for anchoring high density hexaploid maps, and as a reference for other wild and cultivated *Avena* sequence assemblies. Examination of the relationship of the A genome with barley indicate clear patterns of synteny. Comparison with hexaploid oats shows a more complex picture. Further sequencing of a C-genome diploid (*A. ventricosa*) and additional A-genome species (*A. damascena, A. longiglumis*) is being conducted to provide references to aid assembly of the hexaploid oat genome, and to shed light on the evolution of lineage specific pathways underlying agronomically important traits. For example, common genomic regions associated with the control of flowering time have been found in both the diploid and in a number of hexaploid mapping populations developed in Aberystwyth. Near-isogenic lines containing QTL of interest have been developed in hexaploid oats using marker assisted back-crossing. In addition, we are using a panel of land races and old varieties as well as our nested association mapping panel and MAGIC populations for novel allele discovery and to dissect the genetic control of traits of interest. The breeding programme is then used to test and validate marker-trait associations and to develop new varieties by marker assisted selection and genomic selection.

American Oat Workers Conference 2014

Tuesday, July 14

Session 7: Breeding/Molecular Tools II

Development of protein-rich tetraploid oat, current state and prospects

Gideon Ladizinsky

The Hebrew University of Jerusalem, Israel

Correspondence: Zafrira7@bezeqint.net

Of all oat species, *Avena magna* (2n=28), has the highest groat protein content. This may range from 23% to 30%. Transferring that protein content to common oat cultivars, (*Avena sativa*, 2n =42) is barred by the difference in chromosome numbers and the polygenic inheritance of protein content. In fact, hybrids between the two are self-sterile. However, by massive back crossing of such hybrids using pollen of either parent, a few seeds may be obtained, but they are too few for transferring traits of a quantitative nature.

An alternative approach for exploiting the high protein content of *A. magna* is domesticating that wild oat. This can be achieved by transferring the domestication syndrome of the common oat to *A. magna*. In oat, the most crucial character of that syndrome is non-shattering seed, together with glabrous and yellow lemmas, reduction of awn number and size and erect growth. Each of these characters is controlled by a single gene.

After more than 25 years, and following five hybridization cycles with the common oat, crossed firstly with *A. magna* and later with the resultant 2n=28 hybrid derivatives we possess a number of 2n=28 lines that are morphologically indistinguishable from the common oat. Some of them have a protein content ranging from 16% to 25%. For maximizing the protein content, crosses were made between elite lines and wild A. *magna*. Domesticated F_2 derivatives with the highest protein content were crossed with one another followed by single seed descent (now at F_4). An attempt is also being made to introduce stiffer straw, semi-dwarf stature, naked seed and day length insensitivity to the 2n=28 germplasm.

Undoubtedly, collaborative effort is needed for making the tetraploid oat a viable option for oat growers and perhaps marking the beginning of a new era in oat breeding.

What does *CslF6* gene sequence and expression tell us about genome relationships in polyploid *Avena*?

*Eric N. Jellen, Melissa C. Fogarty, Peter J. Maughan, Eric W. Jackson, Douglass C. Brown and Veronica Cepeda-Cornejo

*Brigham Young University, Provo, UT

Correspondence: rick_jellen@byu.edu

We sequenced *CslF6* from a range of hexaploid, diploid and tetraploid genotypes of *Avena* and putative A-, C-, and D-genome diploid lines. Comparison of the diploid sequences with sequences from the hexaploids allowed for a putative determination of genome origin. Similarity of one *CslF6* gene variant in *A. canariensis* suggests a close relationship between this diploid taxon and the D-genome donor to hexaploid oat. Sequences cloned from *A. insularis* and *A. magna* resemble D-genome sequences more closely than A-genome sequences, leading to us to conclude that they are both likely CCDD. RNAseq was used to determine homeologue-specific expression of *CslF6* and a negative correlation was observed between *CslF6-C* and high β-glucan grain content. Though it is well known that the absolute level of expression of a certain gene is important to a trait, our data suggest an important caveat in gene expression; namely, that the proportion of gene expression attributable to each homologue can have a dramatic effect on phenotype. This and other work in our lab on an unrelated allotetraploid, *Chenopodium berlandieri*, for the *GBSSI* gene suggest several interesting models of how epistasis in a polyploid might affect gene expression.

Discrimination of new dwarf oat lines by allelism tests, SSR markers and plant height components

Toshinobu Morikawa, Shinya Uemura and Satoshi Kuriyama

Graduate School of Life and Environmental Sciences, Osaka Prefecture University, Sakai, Osaka 599-8531, Japan

Correspondence: morikawa@plant.osakafu-u.ac.jp

One of the breeding objectives for oat is to reduce plant height, improving the lodging resistance. Allelism tests of the recessive and dominant dwarfing genes of oat have been carried out, and seven independent loci have been identified. Four new dwarfing genes were introduced from six accessions of the wild oat *Avena fatua* into the cultivated form, *A. byzantina* cv. 'Kanota'. In total, seven dwarfing genes are available for oat plant breeding programs. In this study, SSR (Single Sequence Repeat) analysis was performed to trace the transmittance of the genomic region around the dwarfing genes in the inbred lines and wild accessions during extended breeding programs. Genetic variation in wild and cultivated oat and the effect of gene introduction were clarified.

PCR amplification using 25 SSR primer pairs was carried out. Fourteen primer pairs amplified a single band and six primer pairs produced double bands, while four primer pairs failed to provide a clear band. Therefore, 26 SSR loci were detected. Five loci out of 26 were monomorphic among the lines tested. Two plants of AV21 and a plant of AV198 had a novel allele neither recurrent parent nor donor parent had. Based on Nei's genetic distance and using SSR polymorphism, a dendrogram of 16 lines was constructed. *A. byzantina*, *A. sativa* and *A. fatua* were separated clearly into different groups and all inbred lines were clustered with 'Kanota' at the same species level. In the *A. fatua* cluster, there was no correlation between geographic and genetic distances.

The parental dwarf accessions had alleles differing from 'Kanota' at 15 or 16 loci, and one to five alleles were still maintained in the dwarf inbred lines. Although the expected ratio of inherited differential alleles in the BC_1 generation was 25%, inbred lines other than AV208

showed lower ratios than expected. As a result of pedigree selection, wild genomic segments might be dropped effectively. However, AV21 (BC4) has inherited 25% of the differential alleles. In cluster analysis, it was farthest from 'Kanota' in terms of inbred lines. Some wild gene clusters from the donor parents were inherited together with the dwarfing genes. SSRs can be used successfully for studying the inheritance of genomic segments within pedigree breeding programs.

Eight dwarf oat lines identified as having different dwarfing genes and genetic backgrounds were discriminated using allelism tests, SSR markers and plant height components (each inter-node length). The dwarf oat lines were classified into four groups; i.e., ordinary (Do), extreme (De), semi (Ds) and compact (Dc) dwarf types, according to the inter-node lengths. The wild dwarf accessions (*Avena fatua*) showed highly variable inter-node lengths and the new dwarfing genes were transferred to cultivated oats. Two different recessive dwarfing genes controlling Do-type (*dw9b*) and De-type (*dw10*) were involved in the same L169 dwarf line. The *dw10* dwarfing gene rendered all inter-node lengths much shorter than *dw9b* did. The Ds-type was controlled by a single semi-dominant gene, *Dw11*. This unique dwarfness was characterized by short peduncle length, unilateral panicle, stiff inter-node and large grains, producing high yield because of strong resistance to lodging. The new allele *dw9a* was found in dwarf line L812 (Av213 and Av214), which showed the same De-type dwarfness as *dw10*. The phenotypic expression of *Dw12* was similar to the Dc-type dwarfness of *Dw7*, which was located at an independent locus. The PCP analysis for plant height components clearly distinguished each dwarfing gene among the similar De- and Do-type dwarf lines, *dw9b*, *dw10* and *dw9a*. *Dw12* was also separated from the same Dc-type, *Dw7*, in the scatter diagram. The plant height components of the four new dwarfing genes (*dw9, dw10, Dw11* and *Dw12*) were different from each other and *Dw6*, *Dw7* and *Dw8*, which have been already reported.

Genetic variation in oat panicle structure and grain quality

I.M. Griffiths, A.A. Cowan, C.J. Howarth, T. Langdon, M.J.P Martinez Martin and A. H. Marshall

IBERS, Aberystwyth University, UK

Correspondence: igg@aber.ac.uk

With 70% of oats grown in the UK being utilised in the human food sector, one of the major breeding targets for UK oats is the improvement of milling quality. Developing oat varieties with high milling quality is constrained by a lack of detailed information on how genetic differences and environmental/management factors impact on grain quality and yield. Important parameters include specific weight, kernel content (KC), hullability and thousand grain weight (TGW). The complex architecture of the panicle directly influences grain quality. A replicated field trial was conducted into the diversity of panicle structure in 12 IBERS-bred winter oats. A wide range of traits both pre- and post-harvest were measured. After harvest, panicles were hand-dissected and the distribution of single-, double- and triple-grained spikelets was recorded, along with grain number and weight. Using multivariate analysis, the twelve cultivars could be divided into two groups: one with early flowering time, high KC and TGW, long grains, low grain numbers per panicle, and the other with late flowering time, low KC and TGW, short grains, high grain number per panicle.

A comparison of primary and secondary grains was conducted. Due to the arrangement of the grains within the spikelet, the husk of primary grain is larger than the husk of secondary grain. TGW, KC and grain size and shape measurements were conducted on primary and secondary grain separately. The TGW of primary grains was higher than the TGW of secondary grains. However, the KC of secondary grains was higher than the KC of primary grains. These results suggest that secondary grain would have a higher mill performance. Although there is high variation in between primary and secondary grain and across the panicle, the overall quality of harvest samples is stable between field seasons. Considerable variation in grain size was found across the panicle, particularly between primary and secondary grain. This could be a contributing factor to performance in the mill. From these results, cultivars which have a more uniform grain distribution can be identified. Kernel shape is an additional criterion in oat selection. Oat millers prefer plump kernels over long, thin kernels. Non- destructive image analysis tools have been developed at IBERS to quantify grain and kernel size parameters accurately. These have been used to characterise both varietal differences and also within-panicle differences in grain size, shape and weight.

American Oat Workers Conference 2014

Wednesday, July 16

Breeders

Breeding Oats for Western Washington

Winkler LR, Jones SS, Lyon SR and Inglis DA.

Washington State University, Northwestern Washington Research & Extension Center

Correspondence: louisa.winkler@email.wsu.edu

Western Washington, the fertile area between North America's Cascade mountain range and the Pacific Ocean, has a diverse and colourful agricultural landscape from which the oat crop is noticeably absent. Historical records show that the region once was richly populated by highly productive oat fields, but these disappeared along with much of the USA's oat acreage over the second half of the twentieth century.

During the period of the oat crop's decline, there has been no regional oat breeding or testing of available cultivars. An opportunity now exists to provide farmers with region-specific performance information and adapted cultivars, reintroducing the crop as an option for rotation with bulbs, vegetable seed and specialty potatoes and addressing multiple end-uses within the region. Farmers have expressed interest in oat grain as a locally-grown substitute for wheat and maize in GM-free and organic poultry diets, as well as adding value through milling for human food consumption.

Western Washington's climate is characterised as Oceanic (Köppen Csb), with warm, dry summers and wet winters. Precipitation recorded at Washington State University's Mount Vernon Research & Extension Center between 2007 and 2013 reached an annual average of 767mm, of which 43.9 per cent fell between January and April (WSU AgWeatherNet). The persistence of rainfall into March and April can impede machine access to fields and the timely planting of spring crops, and many farmers therefore prefer to plant crops in the fall. Fall-sown crops must be able to tolerate the high precipitation and freeze-thaw cycles which can occur during the region's winters.

In WSU Northwestern Washington Research & Extension Center's newly established oat programme, classical breeding techniques are being used to work towards regionally adapted and winter-tolerant oat cultivars. Germplasm drawn primarily from European and North American collections of new and old cultivars, landraces and breeding lines is being screened for winter-tolerance, and a population of spring-by-winter crosses will be used to investigate associations between winter-tolerance and grain quality traits. Regionally selected advanced-generation spring breeding material also is being developed with a view to the release of a milling quality cultivar in the near future. At the same time, multi-location replicated nurseries of commercially available spring oat cultivars will be used to explore the possibility of reliably producing oat grain in western Washington which meets with milling and animal feed quality specifications, either industry standard or custom.

Oat breeding in Argentina: public and private partnership

Wehrhahne L.[1], Moreyra F.[2]

[1]EEAI INTA Barrow, P.Box 50, 7500 Tres Arroyos, Buenos Aires, Argentina, [2]EEA INTA Bordenave, P.Box 44, 8187 Bordenave, Buenos Aires, Argentina

Correspondence: wehrhahne.liliana@inta.gob.ar

At the beginning of the 1920s, oat breeding in Argentina was carried out by private and public institutions. Among them were the breeding firms Buck, Massaux, Klein, Tomé and the public establishments Livestock Agricultural Experiment Institute of Santa Fe, La Plata National University, La Previsión Experimental Station and INTA (National Institute of Livestock and Agricultural Technology). They achieved registrations of 40 oat varieties.

At present only INTA Barrow and INTA Bordenave maintain the program, having released 16 cultivars between them, which represent 40% of the total number. Both of them have exchanged germplasm with the Quaker Oat Program for Breeding in Developing Countries for years. On the other hand, seed companies have introduced and registered oat seeds from Brazil and Uruguay.

Cereal breeding programs and the oat program in particular, began when Barrow was named La Previsión Experimental Station. The station was founded by local farmers in 1923; its property passed to the Buenos Aires Province in 1942; in 1962 realized an agreement with INTA and nowadays is named Barrow Integrated Experimental Station (EEAI). It represents an example of integration between the Ministry of Land Affairs of Buenos Aires Province and INTA (a federal Institute), a model that enables strengthening of research activities in cereals, oilseeds, quality, livestock and the communication of the information obtained. As for Bordenave Station (EEA), its first oat field experiments date from 1934, seven years after its foundation by the South Railway Company.

Up to 1970 most of the oat area was covered with *Avena byzantina*, but the situation changed with the appearance of the cultivar Suregrain; today, the majority of the 2 million hectares sowed with oat in Argentina are *Avena sativa.*

The main goal of present public programs is the development of forage, forage-grain (double purpose) and high quality cultivars suitable for the food industry. For the last objective is important to select grains with high test weight, protein, groat percentage and beta-glucan content.

Cultivars obtained are commercialized by agreements between INTA and private enterprises. Funds generated by royalties are turned over to research programs. At present, INTA has Technology Transfer Agreements involving cultivar licenses with the private companies Buck Seeds and SeedAr.

Another way to sell oat varieties is by means of Cooperative Associations of the mentioned Experimental Stations. These associations are integrated by institutions such as cooperatives, professionals and farmers, and its objective is to generate and administer resources to be applied in investigation.

Oat breeding in Chile

Mónica Mathias-Ramwell, María-Elena Reyes, Adolfo Montenegro-Barriga, Haroldo Salvo-Garrido.

Instituto de Investigaciones Agropecuarias, INIA, camino Cajón-Vilcún km 10, Región de La Araucanía, Chile.

Correspondence: monica.mathias@inia.cl

Oat production in Chile is located mostly in the southern part of the country in the "La Araucanía" region, which is the leader in oat food processing. Oat grain is the major agricultural export product in this region, whose grain production has helped Chile become the fourth largest exporter of oat-food in the world.

Since 1965, oat breeding has focused on food industry and agriculture-related traits. During this ~50 year period, the Chilean Agricultural Research Institute (INIA) has delivered 15 oat cultivars using several genetic strategies, and generated a prolific germplasm exchange collaboration with different countries and institutions, such as the Quaker International Oat Nursery-QION (from 1975) and the USDA International Oat Rust Nursery-IORN (until 1985).

Supernova INIA is our latest released cultivar and possesses high yielding genetic potential (14 t ha-1), and industrial (70% groat) and physical grain quality. Its improved industrial and yielding traits has made it the most used oat in Chile, covering ~80% of the Chilean cropping area. Our current challenges focus on making Chilean oats a suitable product for both agriculture and healthy food markets, adapted to climatic challenges and an environmentally-friendly type of agriculture. To overcome these challenges, several genetic strategies are being used, together with multi-environment agronomic field evaluations.

Acknowledgments: Quaker Oats, Agriaquaculture Nutritional Genomic Center (CGNA), "Alimentos El Globo S.A." Company, "Corporación de Fomento de la Producción" – CORFO (INNOVA 12IDL2-13628).

Oat Breeding at IBERS

A A Cowan, I M Griffiths, C J Howarth, T Langdon, T Cooper and A H Marshall

IBERS, Aberystwyth University, UK

Correspondence: syc@aber.ac.uk

Aberystwyth University has a long and successful record in breeding oats. When George Stapledon started the Welsh Plant Breeding Station as part of the University in 1919, the aims were to breed varieties which improved agriculture. These aims are still valid today. IBERS has successful winter and spring oat breeding programmes producing varieties primarily for the UK market. The general targets are to produce economically competitive varieties which are high yielding, disease resistant, easy to crop and meet end user requirements. In the UK, approximately 70% of oats are used for human consumption and we have an expanding market for cereal products. For the milling industry, the goals are high yielding varieties that are easy to dehull combined with high specific weight and high kernel content. For the animal feed sector, targets include high oil content and good protein content with balanced amino acids. Specifically for the ruminant market, we are developing low lignin husked varieties with high groat oil. The programme has strong links with the UK milling industry, which provides validation of breeding targets and will undertake analysis of the milling quality of selected material.

The Aberystwyth oat breeding programme is also used to integrate new approaches to genetic improvement into a successful plant breeding programme and to test hypotheses associated with yield formation, grain quality and composition and sustainability traits. We are mainly using pedigree selection and have incorporated marker-assisted technology to identify parents for crossing and validate crosses through to selection of lines with desired alleles. High throughput phenotyping using NIRS to screen rapidly on a whole groat basis for oil, protein and beta glucan has been developed. We are also investigating the potential of developing doubled haploid technology in oats. The breeding programme is funded through partnerships between government and industry (QUOATS, www.quoats.org) and is often used as an example of how "public good" plant breeding should function. Government funding enables a research-led approach to breeding, incorporating a wide range of genetic diversity into the programme and the development of novel techniques, whereas industry funding ensures that stakeholder demands drive breeding objectives and that new varieties are used by farmers. The programme has a track record of translating outputs from fundamental research into agronomic performance and quality improvements.

Oat Breeding Efforts in Turkey

Ziya Dumlupinar[1], Erdem Aslan[1], Hatice Kübra Gören[1], Sevgi HEREK[2], Ali Tekin[1], Tevrican Dokuyucu[2] and Aydın Akkaya[2]

[1]Kahramanmaras Sutcu Imam University, Department of Agricultural Biotechnology, Turkey

[2]Kahramanmaras Sutcu Imam University, Department of Field Crops, Turkey

Correspondence: zdumlupinar@ksu.edu.tr

Oat (*Avena* spp.) is one of the cereal crops grown for its grain and hay in Turkey. At the beginning of the 20th century, oat was one of the major cereal crops, due to its importance in horse feeding. Although oat production has been gradually decreasing in recent years, its health benefit claims make it a popular ingredient for healthy foods.

Oat breeding studies started in the early 1950s in Turkey. In these studies, landraces from across Turkey were collected, identified and tested for grain yield in different environments. Experiments located in higher regions, however, failed because of hard winter conditions. Therefore, those projects started in the early 1950s did not continue for too long. However, those projects pointed out the importance of winter hardiness for winter cultivars and the importance of non-lodging, non-shattering, and simultaneous maturation, as well as high grain and hay yield for spring cultivars, which would be planted in the fall along coastal areas.

Since the millennium, oat breeding projects have started to emerge at some universities and agricultural research institutes in Turkey. Turkey is one of the centers of origin of the cultivated oats *Avena sativa* L. and *Avena byzantina* Koch. Our oat breeding program has been established for the molecular and phenotypic characterization of oat genotypes. To date, 772 oat landraces have been characterized in our program and 174 of 772 oat landraces have been genotyped using 6k SNP bead chips, with the huge contribution and collaboration of colleagues in the US.

After phenotypic and genotypic characterization, parental selections were made and oat hybridization studies were initiated. Besides hybridization, mutation breeding projects were also started and chemicals were used to induce mutations in oat genotypes. Additionally, yield trials in several locations have been carried out.

As a result of these studies, one genotype, which is distinguished for its non-lodging, non-shattering and especially early maturing traits, will be registered as a spring oat cultivar.

In future studies, screening will be continued and the data obtained will be associated with marker data by using association mapping analysis.

Forage oat breeding in Morocco

Shaimi N, Al Faiz C, Saidi N, Salih Idrissi A and A. Souihka

Institut National de la Recherche Agronomique. Rabat. Morocco

Correspondence: shaimi_naima@yahoo.fr

In Morocco, oats are grown essentially in rainfed areas, almost exclusively for forage, mainly for hay, cultivated in pure stand or in mixture with vetch. Since its introduction in Morocco in the beginning of last century, the most used varieties originated from Europe. Due to the harsh ecological conditions of the south Mediterranean region, these varieties elicited little interest from Moroccan farmers. Thereafter, the *byzantina* types were introduced from Algeria, and constituted the genetic basis of the first Moroccan selected varieties. Some of these varieties are still grown. These varieties are now very susceptible to the common diseases and cannot cover all the potential ecological zones for oats. Local oat seeds are mainly a mixture of these varieties with some imported ones.

INRA-Morocco, the public Moroccan research institution, initiated a breeding programme in the 1980s to select new oat varieties. This programme was essentially based on the International Quaker Oat nursery (ION). Currently, around 16 cultivated oat varieties have been registered in the Official Catalogue. Most of the selected varieties are more adapted to biotic and abiotic stresses than the European ones and have very good forage and grain yields.

The Quaker nurseries are a valuable resource since they contain highly diversified genetic material from which we could select many lines for different target regions. Our objective in the future is not only to focus on disease resistance or high yielding genotypes but to select for seed quality with high content of protein, oil and β-glucan. With climatic change, droughts became more frequent and longer. Earliness as a drought escape mechanism should take high priority in genotype screening.

Oat Breeding at AAFC Winnipeg since 2010

Jennifer Mitchell Fetch

AAFC, Brandon, MB, Canada R7A 5Y3

Correspondence: jennifer.mitchellfetch@agr.gc.ca

Oat breeding is an important AAFC mandate in western Canada, with the support of the Growing Forward II Agri-Innovation Program proposal from the Prairie Oat Growers Association to the Government of Canada. The Prairie Oat Breeding Consortium project continues to develop oat cultivars for the Canadian prairies for diverse end markets and uses. The objectives of the program continue to be good yield capacity and end-use quality characteristics desired by the industry. The cultivars developed carry genetic resistance to major diseases, pests and adverse environmental conditions prevalent in the production areas, adding to the adaptability and sustainability of Canadian agriculture and the environment.

The POBC project invested in recent innovations in molecular marker technology to increase the pace at which superior oat cultivars can be developed for the production areas and end-use markets. This will lead to enhanced economic growth for the oat agri-food and agri-feed industries as new end-use markets become viable. Oat productivity can be enhanced through identification of cultivars that perform best under adverse environmental conditions and resist a wide variety of biotic and abiotic stresses. Molecular markers associated with these traits will enhance the capability to select germplasm carrying those traits. The pathologists affiliated with this project provide pathogen surveys to detect changes in virulence and to assist in identifying suitable genes for resistance. Chemists provide research into new methods for evaluating important quality traits and provide strong evaluations of the end-use quality in germplasm moving through the breeding program. A network of several Agriculture and Agri-Food Canada research centres and Universities across western and eastern Canada is evaluating oat germplasm under a wide variety of environmental conditions (agronomic adaptation trials) to effectively identify superior genotypes.

These cultivars are developed to address evolving needs of the agri-based industries in order to respond to market demands, enable economic resiliency, enable commercialization in new market opportunities, and maintain Canada as the competitive supplier of oat around the world. The entire oat value chain will be strengthened. These oat cultivars will be utilized to greatly improve the health and well-being of Canadians and all types of oat consumers around the world.

During the past 4 years 3 oat cultivars from the breeding program at Winnipeg have gained support for registration including Stride, AAC Justice and an organically-developed milling-quality cultivar (OT8003).

American Oat Workers Conference 2014

Posters

Genotyping-by-sequencing facilitates whole genome visualization of Canadian oat cultivars

Benazir K. Marquez[1,2], Charlene P. Wight[1], Jennifer Mitchell Fetch[3], Aaron D. Beattie[4], Douglas A. Johnson[2], Jesse Poland[5], Nicholas A. Tinker[1]

[1]Agriculture and Agri-Food Canada, Bldg. 20, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; [2]Department of Biology, University of Ottawa, 30 Marie Curie Private, Ottawa, ON K1N 6N5, Canada [3]Agriculture and Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB R7A 5Y3, Canada [4]Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada [5]Department of Agronomy, Kansas State University, Manhattan, KS 66506, USA

Correspondence: nick.tinker@agr.gc.ca;

Neutral genetic variation can remain as residual heterogeneity within a cultivar. Genotyping-by-sequencing (GBS) was applied to DNA from 160 seeds of four Canadian cultivars ('AC Morgan', 'Jordan', 'Leggett', and 'Ronald') to evaluate its utility for detecting intra-cultivar variation. Each cultivar subset included equal amounts of breeder seed, certified seed, seed harvested from a cultivar increase, and seed harvested from a registration or Plant Breeder's Rights trial. The universal network-enabled analysis kit non-reference pipeline was used to find 2212 SNPs, of which 1344 have been mapped on the oat consensus framework. Principal component analyses with these SNPs revealed that the majority of seeds clustered by cultivar; however, cultivar-specific analyses showed all four contained some allelic variation. This detected variation did not appear to be limited to a specific seed source. Only 21.8% of all GBS loci showed substantial polymorphism (PIC > 0.3) within one or more oat cultivars. The genome of each cultivar was visualized using graphical genotyping, and this allowed for physical contamination to be distinguished from true genetic heterogeneity/heterozygosity. Heterogeneity was represented by allelic variation that fell within distinct map regions and showed allele frequencies of between 40% and 60% in the cultivar in which polymorphism was observed. Contamination was characterized by consistent, non-localized variation. This method of data interpretation would be suitable for breeders as an efficient tool for selection, and for inspectors as a method of discovering possible seed contaminants.

European Avena genetic resources: characterization for quality and agronomic traits

Giorgio Tumino[1], Fulvia Rizza[1], Franz Badeck[1], Caterina Morcia[1],Matthias H. Herrmann[2], Christoph U. Germeier[2], Zofia Bulinska-Radomska[3], Lena Dimberg[4], Jean Koenig[5], Gerard Branlard[5], Danela Murariu[6], Nadezhda Antonova[7], Ivana Polišenská[8], Rita Redaelli[9], Valeria Terzi[1]

[1] CRA – GPG, Genomics Research Centre, Via San Protaso 302, 29017-Fiorenzuola d'Arda (PC), Italy. [2] Julius Kühn Institute, Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Agricultural Crops, Erwin-Baur-Str. 27, D-06484 Quedlinburg, Germany. [3] Plant Breeding and Acclimatization Institute (IHAR) - PBAI National Plant Genetic Resources Centre (NPGRC), Radzików, PL-05-870 Blonie, Poland. [4] Sveriges Lantbruksuniversitet, Dept. Food Science; Division of Plant Products, Ullsväg 29C, PO Box 7051 SE_750 07 Uppsala, Sweden. [5] INRA, UMR Amélioration et Santé des Plantes, 234 avenue du Brézet, 63100 Clermont-Ferrand, France. [6] Vegetal Genetic Resources Bank of Suceava, B-dul 1 Mai nr. 17, 720237 Suceava, Romania. [7] Institute of Plant Genetic Resources "K. Malkov", Druzhba No 2, 4122 Sadovo, Bulgaria. [8] Agrotest Fyto, Ltd., Havlickova 2787/121, 767 01 Kromeriz, Czech Republic. [9] CRA – MAC, ex Istituto Sperimentale Cerealicoltura, Via Stezzano 24, 24126 Bergamo, Italy.

Correspondence: valeria.terzi@entecra.it

In the AveQ European cooperative project genebank material and oat varieties have been evaluated for traits considered important for future oat breeding in a European premium market. Six hundred fifty five oat accessions were selected- including current commercial cultivars as well as cultivated, marginally cultivated and wild genebank material- representing twelve *Avena* species, more than 100 years of breeding history and more than 30 countries of origin. All the accessions were evaluated in two-year field trials in seven European locations (Estonia, Sweden, Poland, France, Italy, Romania and Bulgaria) for some morphological and agronomic traits – including yield and disease resistance. Variability for cold tolerance was evaluated in open field trials in three environments (Italy, Romania and Bulgaria). In addition, chlorophyll fluorescence analysis in controlled environments was used to confirm cold tolerance of a subset of the germplasm collection. Variability for Fusarium Head Blight resistance was evaluated through dedicated field experiments, under both artificial and natural inoculum conditions.

All harvested samples were analysed for protein, fat and total ß-glucan, and a subset of about 80 accessions were additionally analysed for soluble ß-glucan, starch, dietary fibre components (uronic acids, Klason lignin, and non- starch polysaccharides) and antioxidants (tocols and avenanthramides).

With the aim to complement phenotyping data with molecular ones, a subset of about 150 accessions, including standard cultivars, was genotyped using the Illumina 6K Oat Array. Data were filtered to eliminate failed and monomorphic markers, and population structure was investigated. This genotyping work represents a preparatory study for a future Genome-Wide Association Scanning.

Acknowledgements: AveQ project was funded by the European Commission under Council Regulation (EC) No 870/2004.

Naked oat growing in the Czech Republic

Jan Moudrý[1], Jan Moudrý Jr.[1], Petr Konvalina[1]

[1]University of South Bohemia in Ceske Budejovice, Faculty of Agriculture, Studentska 13, Ceske Budejovice, 37005, Czech Republic

Correspondence: jmoudry@zf.jcu.cz

The paper introduces briefly the history and current status of naked oat breeding and cultivation in the Czech Republic. The varieties of naked oat spring forms from Czech provenance are world leaders in terms of yield and quality. Many European countries have expressed their interest in buying varieties, seed or production. Current varieties originated from an old variety called "Chinese". In Czechoslovakia during the 2nd World War, the collection of Canadian and Chinese oat varieties was built up and supplemented by a set of local landraces. In 1960, the “Krukanicky naked oat” variety was recognized, but its use was soon restricted because of the low yield. In 1988, in Krukanice, the excellent variety of naked oat “Adam” was cultivated and afterwards even better varieties such as “Abel”, “Izak”, “Saul” and others were cultivated. Current varieties of naked oat are characterized by a high number of grains in a panicle (42), large grains (proportion of grain over 1,8 mm sieve is 91-94%) and relatively high Thousand-Grain Weight (27g). The average grain yield in comparative tests is 4,7 t/ha. The quality of grain is high not only because of a high content of nitrogenous substances (4,5-14,7%) and fat in dry matter content (5,5-7,1%), but also thanks to their composition. The share of solid glumes is only 0,3%, and the beta glucan content is 5.0-5.8%. These varieties are less additional input-intensive, resistant to pathogens, and tolerate poor soil and site conditions. For these reasons, they are suitable for production systems with limited inputs (organic farming, low input systems) and environmentally sensitive areas.

Phenotypic analysis of abiotic stress tolerance in Australian oat

Klaus Oldach[1,2], Yusuf Genc[1,2], Mahmood Hassan[1], Tim March[2], John Harris[1], Pamela Zwer[1].

[1]South Australian Research and Development Institute, Plant Genomics Centre, Waite Campus, Urrbrae, SA 5064, Australia; [2]School of Agriculture, Food, and Wine, University of Adelaide, Waite Campus, Urrbrae, SA 5064, Australia

Correspondence: john.harris2@sa.gov.au

Boron toxicity affects about 50% of the neutral-alkaline soils of the South Australian and Victorian grain belt and dryland salinity affects 67% of all cropping areas in Australia. These sub-soil constraints can result in yield losses under conditions of water deficit that are prevalent in the Australian cropping environment. In this project our aims were to benchmark boron and salinity tolerance of oat to wheat and barley. Results suggest that oat is relatively tolerant to boron and typical visual symptoms such as necrotic lesions are uncommon. The measurements on salinity tolerance and ion homeostasis in oats and comparisons to wheat and barley suggest that the three cereal species engage different physiological mechanisms to cope with high saline conditions. In contrast to wheat, oat shows high levels of Na^+ and Cl^- implying that improved salinity tolerance in oat might be achieved by selection of oat germplasm with greater exclusion of these ions.

A Tale of Forgotten Splendour: The Oat Crop in Pacific Northwest History

Winkler, LR, Jones, SS, Lyon, SR, Inglis, DA and Brouwer, BO

Washington State University, Northwestern Washington Research & Extension Center

Correspondence: louisa.winkler@email.wsu.edu

Located in the American Pacific Northwest between the Cascade mountain range and the Pacific Ocean, western Washington once was noted for its bountiful oat crops, extolled in the writings of early settlers and visitors to the area. The oat plant (*Avena sativa* L.) is well adapted to the weather conditions characteristic of the region's coastal climate, and USDA archive data attest to the regional predominance of oats over wheat in terms of both yield and acreage until the mid twentieth century. Subsequently, however, the crop underwent a rapid decline in importance parallel to a contraction of the oat acreage across the USA: oats almost completely vanished from western Washington, such that today's farming community has little knowledge and experience of growing the crop, and access to only a limited spectrum of cultivars. This poster presents historical photographs, narrative accounts and production data which chronicle the story of oats in western Washington from their illustrious peak to their near-disappearance. A confluence of social, economic, technological and cultural change is revealed. Among these, factors including mechanisation of agriculture, development of increased regional specialisation in agricultural production and altered practices in livestock husbandry can be identified which may explain the regional and continental redistribution of oat production.

Historic data demonstrate the agronomic potential for production of oats in western Washington, while recent shifts in the availability and price of feed grains along with growing consumer demand for GM-free and local products may reopen markets for oat producers in the region. A programme of breeding and testing has been initiated at Washington State University's Northwest Washington Research & Extension Center to enable farmers to respond to these opportunities with regionally adapted cultivars.

Does Oat Possess a Grain Hardness Locus?

Michael A. Tanchak[1], Martin J. MacInnis[1,2], Kelcie A. Lahey[1,3], Alicia M. Currie[1],

Charlene P. Wight[4] and Stephen J. Molnar[4]

[1]Dept. of Biology, Cape Breton University, P.O. Box 5300, Sydney, NS B1P 6L2, CANADA; [2]Current Address: School of Kinesiology, University of British Columbia, 210-6081 University Boulevard, Vancouver, BC V6T 1Z1, CANADA; [3]Current Address: Dept. of Physiology and Pharmacology, University of Calgary, 3310 Hospital Drive NW, Calgary, AB T2N 4N1, CANADA; [4]Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, Central Experimental Farm, 960 Carling Ave., Ottawa, ON K1A 0C6, CANADA

Correspondence: michael_tanchak@cbu.ca

The *Ha*-locus or Hardness locus of wheat [*Triticum aestivum* L.] is located on the short arm of chromosome 5D and contains genes that encode for puroindoline a, puroindoline b, and grain softness protein 1. The puroindolines are the major determinants of grain texture/hardness, a major agronomic and quality trait in wheat. All three proteins and/or synthetic peptides derived from them have demonstrated antimicrobial properties. Existing genetic markers for oat homologues of *Ha*-locus genes were identified by using the ESTs for the Umn series of RFLP markers developed at the U. of Minnesota as query sequences in BLASTN searches of the NCBI NUCLEOTIDE database. Umn287, Umn360, and Umn856 were identified as markers corresponding to the genes of the *Ha*-locus by virtue of significant sequence identity with sequences encoding puroindolines, their homologues from other species [*e.g.*, oat tryptophanins/vromindolines, and hordoindolines,] or grain softness protein. Umn162, Umn249, and Umn753 were also identified as potential markers for the *Ha*-locus based on significant sequence identity with the *Ha*-locus region in a BAC [BAC 37D5] from *Brachypodium sylvaticum*. Umn162, Umn249, and Umn753 are essentially identical in sequence and show limited sequence identity with sequences from other cereals. Data mining of the NCBI EST database identified ESTs developed at the U. of Saskatchewan that appear to encode a novel oat tryptophanin [OT154], predicted to be 154 amino acids in length, and including a novel tryptophan-rich domain. Three basic variants of this sequence, represented here by NCBI accession numbers GO581309, GO581838, and GO582063, were identified. Cleaved amplified polymorphic sequence [CAPS] markers were developed for GO582063 and GO581838. Mapping data placed a GO582063 locus on the Kanota X Ogle (KxO) DArT map [Tinker *et al*. 2009, BMC Genomics 10: 39] at 165 cM in linkage group (LG) 22_44+18 in proximity with Umn287, Umn360A, and Umn856A; on the Terra X Marion (TxM) map [De Koeyer *et al*. 2004, Theor. Appl. Genet. 108: 1285-1298] at 13 cM in LG 15 in proximity with Umn360A and Umn856A; and on the small LG 31 consisting of two other markers in the Dal X Exeter map [Hizbai *et al.* 2012, The Plant Genome 5: 164-175]. Mapping of the CAPS for GO581838 establishes an association between it and the unlinked Umn360X locus in the TxM map. Tinker *et al.* [2009] also mapped Umn360 [Umn360brv] and Umn856 [Umn856b] within 1cM of one another on KxO LG 29_43. These mapping results strongly suggest that, in oat, there are at least two gene assemblages resembling the single *Ha*-locus found in wheat.

Organic oat seed quality

Petr Konvalina[1], Ivana Capouchová[2], Hana Honsová[2], Evženie Prokinová[2], Dagmar Janovská[3], Jan Moudrý Jr. [1], Jan Moudrý[1]

[1] University of South Bohemia in České Budějovice, Faculty of Agriculture, Studentská 13, 37005 České Budějovice, Czech Republic
[2] Czech University of Life Sciences, Kamýcká 129, 16521 Praha 6-Suchdol, Czech Republic
[3] Crop Research Institute, Drnovská 507, 161 06 Praha 6-Ruzyně, Czech Republic

Correspondence: konvalina@zf.jcu.cz

It is extremely difficult to get high-quality certified organic seeds. However, organic farmers are not allowed to use any seeds other than the certified organic ones. Certified organic seeds are rare and organic farmers usually have to use conventional untreated seeds or farm seeds in order to establish their crop stands. For this reason, we studied and evaluated the health and biological characteristics of four varieties of common oat (the hulled form) and naked oat during a three-year trial. The experimental crop stands were established in three different localities within the Czech Republic. Results of the trial have shown sufficient quality of all the tested seeds. However, they must come from farms applying high-quality agrotechnologies. There were minimum differences in the level of seed contamination with colonies of the most frequent pathogens (*e.g.*, *Fusarium* spp., *Alternaria* spp.).

Collaborative Oat Research Enterprise (CORE): outcome, progress, and beyond

Yung-Fen Huang, Nick Tinker, Eric Jackson, and CORE members[1]

[1]A list of CORE members and key collaborators will be presented on the poster

Correspondence: nick.tinker@agr.gc.ca

The Collaborative Oat Research Enterprise (CORE) was initiated in 2009 and brought together oat workers from across North America and Europe. CORE partners have developed a suite of new tools to support molecular breeding and the genetic dissection of key oat traits. At the foundation of CORE was a set of diverse oat germplasm, comprising six bi-parental mapping populations (407 progeny), 109 oat lines representing oat diversity worldwide (AFRI109), and 564 oat lines nominated by breeders to represent germplasm from fourteen spring oat and four winter oat breeding programs in the United States (393), Canada (138), Norway (15), Sweden (11), and the United Kingdom (6). One major outcome of CORE was the development of an Illumina SNP assay (approx. 3,600 markers), which is now available for the whole community to use (Tinker *et al*., 2014). Genotyping-by-sequencing (GBS) has also been applied successfully to CORE germplasm (Huang *et al.*, 2014). Data from SNP assays of the six bi-parental mapping populations led to the release of the first chromosome-anchored oat consensus map (Oliver *et al*., 2013). A refined oat consensus map, constructed from twelve mapping populations and more than 14,000 SNP and GBS markers, will be reported by Schlueter *et al*. at this conference. AFRI109 and 564 breeding line sets have been genotyped and phenotyped at multiple locations. Analysis of genetic diversity has shed light on the structure of oat cultivars (Klos *et al*., reported at this conference). Genetic mechanisms underlying traits of interest are being studied through association mapping by CORE members. To continue the collaborative dynamics and invigoration of oat molecular breeding provided by CORE, an open database will be a crucial tool to enable exchanges between oat workers. We are developing such a tool based on CORE data and the database structure of The Triticeae Toolbox (T3; Jannink *et al.*, reported at this conference). Five years from the initiation of CORE, we would like to summarise the outcome, progress, and future opportunities provided by CORE and to acknowledge all of the people who have made it possible.

References

Huang, Y.-F. *et al.* (2014) Using genotyping-by-sequencing (GBS) for genomic discovery in cultivated oat. PLoS ONE, in press.

Oliver R.E., *et al.* (2013) SNP Discovery and Chromosome Anchoring Provide the First Physically-Anchored Hexaploid Oat Map and Reveal Synteny with Model Species. PLoS ONE 8:e58068

Tinker, N.A. *et al.* (2014) A SNP genotyping array for hexaploid oat (*Avena sativa* L.) The Plant Genome, in press.

Mapping the *Pc58* complex with SNPs in an expanded Ogle/TAM O-301 oat (*Avena sativa* L.) population

Kathy Esvelt Klos[1], Ebrahiem M. Babiker[1], Tyler C. Gordon[1], Shiaoman Chao[2], Stephen A. Harrison[3], Bryan E. Simoneaux[4], J. Michael Bonman[1]

[1]USDA-ARS, Small Grains and Potato Germplasm Research Unit, Aberdeen, ID 83210 USA; [2]USDA-ARS, Cereal Crops Research, 1605 Albrecht Blvd. N., Fargo, ND 58102 USA; [3]Louisiana State University Agricultural Center, 104 M.B. Sturgis Hall, Baton Rouge, LA 70803 USA; [4]Texas A&M University, Dept. Of Crop and Soil Science, College Station, TX 77843 USA

Correspondence: kathy.klos@ars.usda.gov

Oat crown rust caused by the fungus *Puccinia coronata* f.sp. *avenae* Eriks. (*Pca*) is a persistent threat to oat production and can cause yield reductions of 20 to 50% (Simons, 1985). Identification and deployment of genes conferring resistance to a wide-range of *Pca* pathogen races is an important and cost-effective means of minimizing crop losses. A broad-spectrum crown rust resistance gene complex, *Pc58*, was previously characterized in the Ogle/TAM O-301 mapping population using 136 RILs with RFLP and AFLP markers (Hoffman *et al*., 2006; Jackson *et al*., 2008, Jackson *et al*., 2010). In this study, we further characterized the *Pc58* complex in an expanded Ogle/TAM O-301 oat mapping population of 283 RILs using the Illumina iSelect Infinium annotated SNP array (Oliver, 2013). Our results indicate that the previously published *Pc58* complex is composed of at least two distinct loci located on chromosomes 9D and 15A. These mapping results may i) enable identification of diagnostic SNP markers that can determine the presence of the *Pc58* complex in cultivars with unknown resistance, ii) expand annotation of the oat genome with previously published RFLP markers, iii) assist in efficient introgression of these resistance QTL into established oat cultivars, and iv) provide baseline information for positional cloning of the *Pc58* gene complex.

References

Hoffman, D.L., J. Chong, E.W. Jackson, D.E. Obert (2006). Characterization and Mapping of Crown Rust Resistance Gene Complex (*Pc58*) in TAM O-301. Crop Sci. 46:2630-2635.

Jackson, E.W., D.E. Obert, M. Menz, G. Hu, J.M. Bonman (2008). Qualitative and quantitative trait loci conditioning resistance to *Puccinia coronata* pathotypes NQMG and LGCG in the oat (*Avena sativa* L.) cultivars Ogle and TAM O-301. Theor Appl Genet. 116:517-527.

Jackson, E.W., D.E. Obert, J.B. Avant, S.A. Harrison, J. Chong, M.L. Carson and J.M. Bonman (2010). Quantitative Trait Loci in the Ogle/TAM O-301 Oat Mapping Population Controlling Resistance to *Puccinia coronata* in the Field. Phytopath. 100:484-492

Oliver, R.E., N.A. Tinker, G.R. Lazo, S. Chao, E.N. Jellen, M.L. Carson, H.W. Rines, D.E. Obert, J.D. Lutz, I. Shackelford, A.B. Korol, C. P. Wight, K.M. Gardner, J. Hattori, A.D. Beattie, Å. Bjørnstad, J. M. Bonman, J-L. Jannink, M.E. Sorrells, G.L. Brown-Guedira, J.W. Mitchell Fetch, S.A. Harrison, C. J. Howarth, A. Ibrahim, F.L. Kolb, M.S. McMullen, J.P. Murphy, H.W. Ohm, B.G. Rossnagel, W. Yan, K.J. Miclaus, J. Hiller, P. J. Maughan, R.R Redman Hulse, J.M. Anderson, E. Islamovic, E.W. Jackson. (2013). SNP discovery and chromosome anchoring provide the first physically-anchored hexaploid oat map and reveal synteny with model species. PLoS One 8 (3): e58068.

Simons, M.D. (1985). Crown rust. *The cereal rusts, 2*, 131-172.

Beta-glucan content in Southern Brazilian oat cultivars and environments[§]

Marcelo T. Pacheco[1], Martim Fogaça Severo[2], Luiz C. Federizzi[1]

[1]Federal University of Rio Grande do Sul (UFRGS), Av. Bento Gonçalves, 7712, Porto Alegre, RS, 91540-000, Brazil [2]Master's student at the time the research was conducted, currently at Pioneer Hybrid Seeds Brazil [§]Part of the Master's dissertation of the second author

Correspondence: marpac@ufrgs.br

Beta-glucans are the main soluble fiber in oats, and are one of the constituents of the cell wall. Beta-glucans are associated with human health benefits, such as the reduction of blood cholesterol and heart disease risk. Beta-glucan content in oats is known to be affected by the environment, even though how the environment affects it is not well understood. This work aimed to measured beta-glucan content in Brazilian oat (*Avena sativa* L.) genotypes under different Southern Brazilian environments and to study stability and adaptability parameters for these genotypes and this trait. Beta-glucan content measurements were based on near-infrared reflectance (NIR) analysis, using ground groats. On the one hand, no genotype-by-environment interaction was found under the study conditions. On the other hand, beta-glucan content fluctuated considerably for the same genotypes across environments or among replicates within environments. The mean beta-glucan content was around 6.0 %, varying between 3.95 and 7.62 % for values based on environmental means and between 3.64 and 8.66 % for values based on single replicates. The oat cultivar URS Guapa had the highest mean (6.55 %) but the largest linear regression deviation, with a regression coefficient (*b*) not different from zero. The cultivars URS Guará, URS Tarimba and URS Guria showed high beta-glucan means, around 6.50 %, and *b* not different than 1.0, but the coefficients of determination (R^2) for the first two genotypes were not high. In general, genotypes revealed adequate levels of beta-glucan content, showing adaptability and stability in the tested environments. The main exception was UFRGS 049001-1, which was the only hulless oat line in the study. It exhibited low beta-glucan content and *b* not different from zero. Considering all of the parameters together (mean, adaptability (*b*), stability (σ_d^2) and predictability (R^2)), the best oat genotypes were URS Charrua, UFRGS 14, URS Corona and URS Guria.

AOWC Demonstration Plots - Delegates

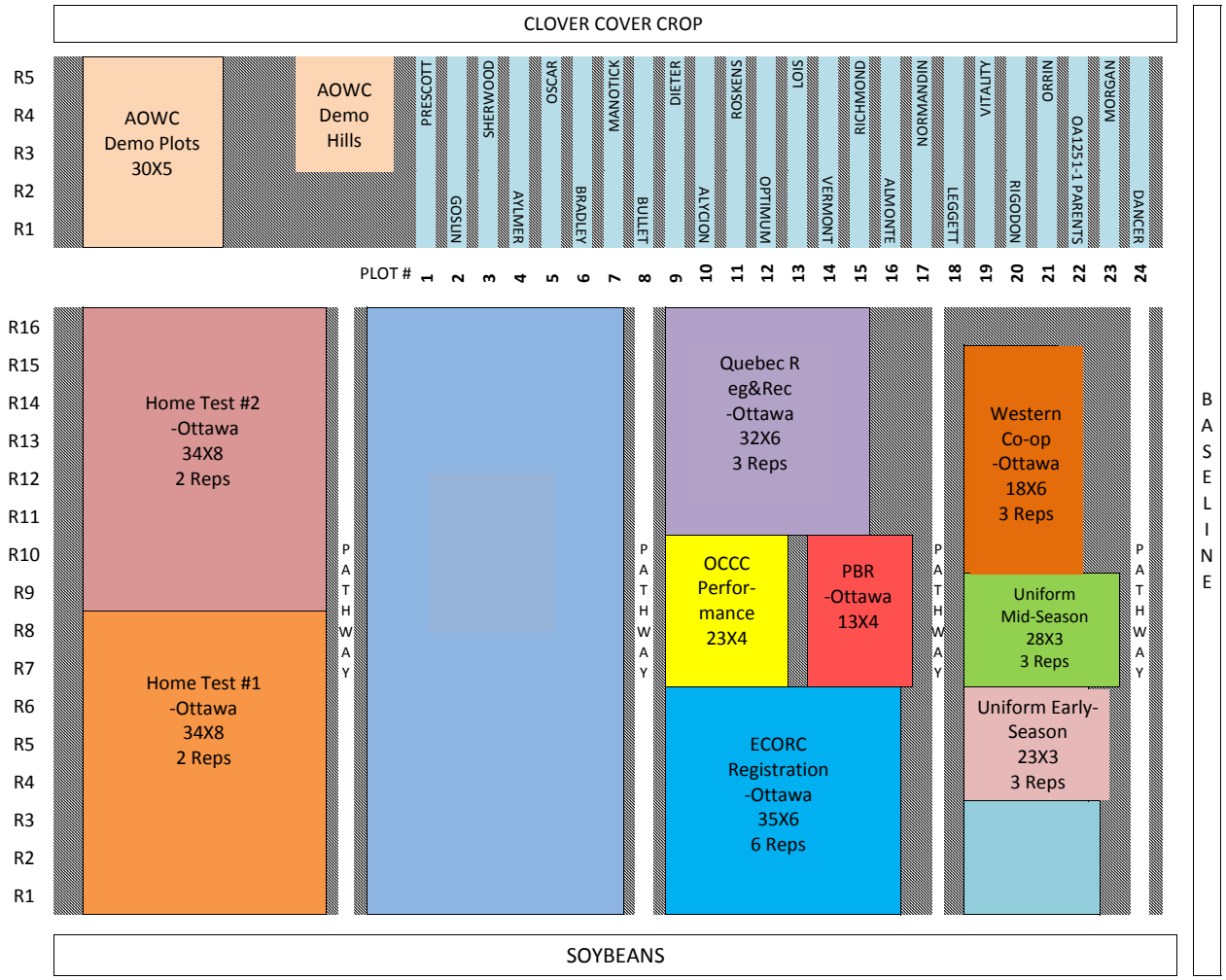
Plots	Sponsor
101 – 130	UWOYN
201 - 224	Sungrain
301 – 320	Saskatoon
401 – 412	California
414 – 416	Turkey
417 – 422	Edelhof
423 – 426	UK
501 – 520	China

AOWC Demonstration Plots – Diversity

Wight Selections	Diederichsen Selections	
	Taxon	Name
Bountiful	*Avena brevis*	SAIA 2
Novojatkovo	*Avena strigosa*	454
Aveia	*Avena nuda*	Avena strigosa nuda 8
CN 57896	*Avena nuda*	Brevis nudi
Ford Early Giant	*Avena sativa*	HA 70-81-3
Wisc. X-1588	*Avena sativa*	Multigrap
WAOAT2133	*Avena sativa*	Avoine Nue-Nue Noise
Pony	*Avena sativa*	Brighton
Caleche	*Avena abyssinica*	
Landhafer	*Avena abyssinica*	AB0008
VAO-08		
Victor		
Bullion		
S147		
Rustproof		
Avena strigosa AVE 128		
Avena sterilis CAV 4501		
Avena abyssinica Ciav 2113		

Complete electronic field book: **http://aowc.ca/fieldplan.html**

2014 YIELD PLOTS



ECORC OAT CREW 2014