

2006 American Oat Workers' Conference Program Book

July 23-26
2006

Fargo
North Dakota



USDA-NRCS PLANTS Database / Britton, N.L., and A. Brown. 1913.
Illustrated flora of the northern states and Canada. Vol. 1: 218.

2006 American Oat Workers' Conference
Organizing Committee

Douglas C. Doehlert, USDA-ARS Fargo, ND
Michael S. McMullen, North Dakota State University, Fargo, ND
Edith Nelson, North Dakota State University, Fargo, ND

2006 American Oat Workers Conference

We thank our sponsors for their generous
support.

The Quaker Oats Company (PepsiCo)

General Mills

Can-Oat Milling

Grain Millers Inc.

ConAgra Food Ingredients

Farmers Grain Dealers Inc., Des Moines, IA

North Dakota State University Plant Sciences Department



Program
2006 American Oat Workers' Conference

Sunday, July 23, 2006

10:00 am: Registration open

10:00 am-12:00 noon: Poster setup

1:00: Hosts: Welcome, Introduction, and Housekeeping.

Session #1: Industry Needs: Moderator, Sam Weaver

1:20: Jay Brandau, Grain Millers: *Supply and Demand*

1:30: Bill Bonner, ConAgra Food Ingredients: *New Product Development, Value-Added Products*

1:40: Bruce Roskens, PepsiCo/Quaker Oats: *Agronomic Management*

1:50: Kelley Henderson, Can-Oat Milling: *Milling Quality*

2:00: Joe Lutz, General Mills: *Health and Wellness*

2:10: Panel Discussion

2:30 Break

Session #2: Oat Breeding Session: Moderator, Fred Kolb

2:50: Christopher Green, SW Seed Ltd, UK: *Enhancing the Value for Oats: A European Perspective*

3:10: Michael S. McMullen, North Dakota State University, Fargo, ND: *North Dakota State Oat Breeding*

3:30: Deon Stuthman, University of Minnesota, St. Paul, MN: *Alternatives to Single Major Gene Crown Rust Resistance*

3:50: Brian Rosnagel, University of Saskatchewan, Saskatoon, SK: *Pure lining of Breeder Seed for molecular variety identification in oat*

4:10: Jennifer Mitchell Fetch, AAFC, Winnipeg, MB: *Breeding Milling Oat for the Rust Area of Western Canada*

6:00-9:00pm: Social: Free food and drinks!!!!

Monday, July 24, 2006

6:00-7:30am: Buffet Breakfast

Session #3: Production: Moderator, Mike Gartner

8:00: David Livingston, USDA-ARS and North Carolina State Univ. Raleigh, NC: *Survival of frozen tissue in winter oat crowns*

8:20: Bill May, AAFC, Indian Head, SK: *Milling Oat Production*

8:40: Dwain Meyer, North Dakota State Univ., Fargo: *Forage Yield and Quality of Oat Hays at Fargo*

9:00: Pat Carr, North Dakota State Univ, Dickinson, ND: *Oat Variety Comparisons on Fields Managed Organically in Minnesota and North Dakota*

9:20: Steven Shirliffe, University of Saskatchewan, Saskatoon, SK: *Controlling Wild Oat in Tame Oat*

9:40 Break

Session #4: Pathology: Moderator, Jean-Luc Jannink

10:00: James Chong, AAFC, Winnipeg, MB: *In Search of New Effective Resistance to Crown Rust in *Avena sterilis**

10:20: Angela Sebelius, NDSU, Fargo, ND: *Linkage relationships among factors that affect groat oil concentration, crown rust resistance, stem rust resistance and the naked character in oat*

10:40: Mike Bonman, USDA-ARS, Aberdeen, ID: *Crown rust resistance of oat germplasm from the ARS-Aberdeen program*

11:00: E.W. Jackson, USDA-ARS, Aberdeen, ID: *Qualitative and Quantitative Characterization and Mapping of Oat Crown Rust Resistance Using Phenotypic Data from Three Assessment Methods*

11:20: Hedera Porter, USDA-ARS, St Paul, MN: *Intogression of Oat Crown Rust Resistance from Diploid *Avena strigosa* and Tetraploid *A. murphyi**

11:40: Joe Anderson, USDA-ARS, West Lafayette, IN: *Barley Yellow Dwarf Virus in Oats: A Field and Laboratory View*

12:00-1:20 Catered Lunch

Session #5: Genetic Markers: Moderator, Howard Rines

1:20: Steve Molnar, AAFC, Ottawa, ON: *PCR Markers for Beta-glucan, Oil and Protein in Oats*

1:40: Nick Tinker, AAFC, Ottawa, ON: *An Allele Survey of North American Oat Varieties*

2:00: Charlene Wight, AAFC, Ottawa, ON: *Oatgenes: A Comprehensive Database of Oat Markers and QTLs*

2:20: Panel Discussion: *Oat Molecular Markers*

Howard Rines, UDSU-ARS, St. Paul, MN: *Oat Molecular Markers: Status and Opportunities*

Jean-Luc Jannink, Iowa State University, Ames, IA: *Use of Breeding Populations to Detect and Use QTL*

Shiaomon Chao, USDA-ARS, Fargo, ND: *Application of Molecular Marker Technologies on Cereal Crops Improvement*

3:00- 5:00 Break and Poster Session

Dinner on your own

Tuesday, July 25, 2006

6:00-7:30 am Buffet Breakfast

Session #6 Processing and Chemistry: Moderator, Vernon Youngs

8:00: Doug Doehlert, USDA-ARS, Fargo, ND: *Oat Kernel Density and the Physical Basis of Test Weight*

8:20: Nancy Ames, AAFC, Winnipeg, MB; *Enhancing Oat End Product Quality*

8:40: Mitchell Wise, USDA-ARS, Madison, WI: *Avenanthramides in Oat (Avena sativa), a Value Added Phytonutrient*

9:00: Alona Chernyshova, Iowa State Univ., Ames IA: *β -Glucan Content and Variance in Crosses Between High β -Glucan and Elite Agronomic Lines*

9:20: Kathryn Begeal, Organic Grain and Milling, Inc., Clyde, ND: *Organic Market Opportunities: Value-added Marketing for High Beta-glucan Oat Varieties*

9:40 Break

Session #7 Special Topics: Moderator, Brian Rossnagel

10:00: Greg Lardy, North Dakota State Univ., Fargo, ND: *Feeding Value of Oats in Livestock Diets*

10:20: Ginger Rich, Rich Equine Nutrition, TN,

10:20: Massiel Orellana, Iowa State Univ., Ames IA: *Bayesian Modeling Of Heterogeneous Error and Genotype By Environment Interaction Variances: Model Assessment*

10:40: Christoph U. Germeier, Federal Centre of Breeding Research on Cultivated Plants, Braunschweig, Germany: *Towards a Global Strategy for the ex situ Conservation of Oat Genetic Resources*

11:00: Axel Diederichsen, AAFC, Saskatoon, SK: *Results of a Phenotypic Characterization of a Large Avena sativa Germplasm Collection*

11:20: Yong-Bi Fu, AAFC, Saskatoon, SK: *AFLP Variation in Cultivated Oat Germplasm Collection*

12:00 noon -1:20pm Catered Lunch

1:20 pm-4:20 pm Field Trip

Demonstration oat plots at Casselton Seed Farm and Fargo nurseries

6:00pm-9:00pm Banquet and Awards Ceremony

Wednesday, July 26, 2006

6:00 am-7:30 am Buffet Breakfast

8:00 am-10:00am American Oat Workers' Conference Business Meeting

10:00 am Break- box lunches available

10:30 am: Oat Crop Germplasm Committee Meeting (lunch served)

Posters

- 01 **A Graphical Web-Based Database of Oat Molecular Markers**; Diane Bergeron, Charlene Wight, Hai Pham, Nick Tinker. ECORC, AAFC, 960 Carling Ave. Ottawa ON K1A-0C6 Canada.
- 02 **Evaluation of Oats for Reaction to Fusarium Head Blight**; W. Cao, G. Fedak, A. Xue and M. Savard, ECORC, Agriculture and Agri-Food Canada, 960 Carling Ave. Ottawa, ON Canada K1A 0C6.
- 03 **Virulence in US crown rust populations from 2001-2005**; M. L. Carson and G. E. Ochocki, USDA-ARS Cereal Disease Lab, St. Paul, MN 55108.
- 04 **Molecular Mapping of the *Dw6* Dwarfing Locus**; Julie Chapados, Solomon Kibite, Bonnie Bancroft, and Stephen J. Molnar. Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, Central Experimental Farm, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada (JC, BB, and SJM) and Lacombe Research Centre, Agriculture and Agri-Food Canada, 6000 C & E Trail, Lacombe, AB T4L 1W1, Canada (SK in memoriam).
- 05 **Pedigrees of Oat Lines (POOL): Updates and Usage**; Jitka Deyl and Nick Tinker, Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, Central Experimental Farm, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada.
- 06 **Molecular markers for the oat stem rust resistance gene *Pg16***; P. Eckstein, T. Fetch, D. Hay, T. Zatorski, B. Rossnagel, and G. Scoles. Department of Plant Sciences/Crop Development Centre, University of Saskatchewan, Saskatoon, SK, CANADA, S7N 5A8 (PE, DH, TZ, and BR) and Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB, CANADA, R3T 2M9, (TF)
- 07 **Enlargement of PCR-based marker resources in oat by surveying genomic-derived SSRs from barley and wheat**; Gongshe Hu, Robert Campbell, Eric Jackson, and J. Michael Bonman, USDA-ARS, Small Grains and Potato Germplasm Research Unit, 1691 South 2700 West, Aberdeen, Idaho 83210 USA.
- 08 **Stabilizing naked oats with infrared roasting and the effects on groat quality**; Xin-Zhong Hu, J. Fréreau Reid and V. Burrows. College of Food Science & Engineering, Northwest A & F University, Yangling, Shaanxi, P R China, 712100 (XZH) and Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-food Canada, KW Neatby Building, 960 Carling Avenue, Ottawa, Ontario K1A 0C6 Canada (JFR and VB).
- 09 **A detached leaf method for cereal rust disease studies**; E. W. Jackson, J. Chong, J. B. Avant, and J. M. Bonman. USDA-ARS, Small Grains and Potato Germplasm Research Unit, 1691 S. 2700 W., Aberdeen ID 83210 USA (EWJ, JBA, and JMB) and Cereal Research Centre, Agriculture & Agri-Food Canada, Winnipeg, MB, Canada R3T 2M9 (JC).
- 10 **Oat Information in GrainGenes**; Gerard R. Lazo, David E. Matthews, Victoria Carollo, and Olin D. Anderson. USDA-ARS, Western Regional Research Center, Albany, CA 94710-1105 USA (GRL DEM, VC, and ODA), USDA-ARS, Dept. of Plant Breeding, Cornell University, Ithaca, NY 14853 USA (DEM), and Plant Science & Plant Pathology, Montana State University, Bozeman, MT 59717 USA (VC).
- 11 **QTLs Affecting Heading Date in Oat Under Short Day Conditions**; Ana Locatelli, Luiz C. Federizzi, Sandra C. K. Milach, Charlene P. Wight, Stephen J. Molnar, Julie T. Chapados, and Nicholas A. Tinker. Pioneer Sementes Ltda., Paissandú 582,

- P.O.Box 72, Passo Fundo, 99.010-100, Brazil (AL and SCKM), Federal University of Rio Grande do Sul, Caixa postal 776, CEP 91.501-970, Porto Alegre, RS, Brazil (LCF), and AAFC, CEF, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada (CPW, SJM, JTJ, and NAT).
- 12 **Managing wild oat in tame oat through the seeding date and seeding rate of tame oat**; W.E. May, S.J. Shirliffe, G.P. Lafond, and D. McAndrew. AAFC, Indian Head Research Farm, Box 760, Indian Head, SK, S0G 2K0.
- 13 **Altering the competitiveness of tame oat verses wild oat with phosphorous and seeding rate**; W.E. May and G.P.Lafond. AAFC, Indian Head Research Farm, Box 760, Indian Head, SK, S0G 2K0.
- 14 **Oats with Maize Chromosome and Chromosome Segment Additions**; Matthew D. Walch, Howard W. Rines, Ronald L. Phillips, Richard V. Kowles, Adrian O. Stec, Ralf G. Kynast, Ron J. Okagaki, Morrison Jacobs, Mark W. Galatowitsch, Christina M. Schmidt, Paul A. Huettl. Department of Agronomy and Plant Genetics, University of Minnesota (WDW, HWR, RLP, AOS, RGK, RJO, MJ, MWG, and PAH), USDA-ARS, 1991 Upper Buford Circle, St. Paul, MN 55108, USA (HWR), and St. Mary's University, Winona, MN, USA (RVK).
- 15 **Identification of Molecular Markers for Aluminum Tolerance in Diploid Oat Through Comparative Mapping and QTL Analysis**; Charlene P. Wight, Solomon Kibite, Nicholas A. Tinker, and Stephen J. Molnar. Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, Central Experimental Farm, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada (CPW, NAT, and SJM). Lacombe Research Centre, Agriculture and Agri-Food Canada, 6000 C & E Trail, Lacombe, AB T4L 1W1, Canada. (SK, in memorium)
- 16 **Release of a high yielding forage oat for subtropical Australia**; B. Winter, L. Song and R. Uebergang. Leslie Research Centre, PO Box 2282, Toowoomba, Queensland, 4350, Australia (BW and LS), and Heritage Seeds, 22 Suscatand St, Rocklea, Queensland, 4106, Australia (RU).
- 17 **Oatlink - progress in molecular marker identification at IGER**; Tim Langdon, Joana Dulawa, Robert Hasterok, Sandy Cowan, John Valentine, Catherine Howarth. Institute of Grassland & Environmental Research, Plas Gogerddan, Aberystwyth SY23 4UJ, UK (TL, SC, CH), Faculty of Biology and Environmental Protection, University of Silesia, Jagiellonska 28, 40-032 Katowice, Poland (JD, RH).
- 18 **Quantitative Trait Loci for Winter Hardiness Component Traits in Oat**; David R. Wooten Jr., David P. Livingston, III, H. Jeanette Lyerly, and J. Paul Murphy, Department of Crop Science, North Carolina State University, Raleigh NC 27695 USA.
- 19 **Development of a Rapid Detection Method for Yellow Dwarf Viruses**; Mahua Deb and Joseph M. Anderson, Agronomy Department (MD) and USDA-ARS (JMA), Purdue University, West Lafayette, IN 47907.
- 20 **The Susceptibility Response to BYDV in *Avena sativa*: Using the Wheat Gene Microarray as a Tool for Measuring Gene Expression in Oat in Response to BYDV Infection**; Joseph M. Anderson, USDA-ARS, Purdue University, West Lafayette, IN 47907.
- 21 **Near-Infrared Reflectance Spectroscopy for the Determination of Fiber and β -Glucan in Oats**; N. Ames, C. Rhymer, and J. Mitchell-Fetch. Cereal Research Centre, Agriculture & Agri-Food Canada, 195 Dafoe Rd., Winnipeg, MB, Canada, R3T 2M9.

- 22 **Genotype and Environment Effects on Oat β -glucan, Total Dietary Fiber and Antioxidant Activity**; N. Ames, C. Rhymer, and B. Rossnagel. Cereal Research Centre, Agriculture & Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB, Canada, R3T 2M9 (NA and CR). University of Saskatchewan, Crop Development Centre, Saskatoon, SK, Canada (BR).
- 23 **Development of a Microsatellite Library for *Puccinia coronata***; Hattie Dambroski and Martin Carson, USDA-ARS-Cereal Disease Laboratory, St. Paul, MN, USA

Abstracts for the 2006 Oat Workers' Conference

Supply and Demand

Jay Brandau

Sr. Vice President, Grain Millers, Inc., Cabriole Center-suite 400, 9531 West 78th Street
Eden Prairie, MN 55344

This presentation examines the changes in supply and demand of oats over the last few years and outlook at futures changes. We will discuss the Canadian supply and demand, the US supply and demand, the big four supply and demand trends, current and historical prices, and forward trends in oat milling. We will also discuss current supply and demand for new crop oats and what effect weather might have in the next three months.

Value Added Oat Products

William A. Bonner

Director R&D/Technical Services
ConAgra Food Ingredients

The original healthy whole grain has been available for centuries and our industry has taken the opportunity to expand it across a variety of applications. Oatmeal as a hot cereal has been flavored and sweetened for palatability. It has been shortened in cook time from hours to minutes with even more convenience added through heatable precooked products.

Oatmeal has gone from this staple hot cereal that sticks to your ribs to ready to eat breakfast cereals on to baked and formed cereal bars - even viscous drinks from time to time. Each format simplifies the consumer's preparation and time requirements and in general have probably offered unique sensory properties through appearance, taste and texture.

Offering up comments on the above product types, other conventional oat based food products, pet food applications cosmetic and other industrial applications, we continue to see the perceived health value to products labeled to contain oats. Functional process limitations, current and potential component concentrations and future potential uses will be reviewed.

Agronomic Management of Oats

A. Bruce Roskens

Senior Manager – Ag Research and Commodity Development
PepsiCo/Quaker Oats

Changes in crop rotations and patterns, crop disease pressures, new technologies in other crop breeding, and new farming equipment have created a multitude of new issues, as well as perhaps some new opportunities for profitable oats production. Unfortunately, just as oats acreage has declined in North America, so have agronomic studies for profitable oats production. The majority of agronomic data available for oats production today is based on research projects conducted over 20 years (or more) ago. It is obvious that cropping patterns have changed dramatically in most of North America in the past 20 years. Tillage practices have been altered and reduced and are performed with much larger equipment. Herbicide, insecticide, and fungicide formulations and use have dramatically changed. The availability of GMO varieties and hybrids in other crops has altered production practices and tactics.

But what has changed in oat agronomy? We are still discussing many of the same issues in oats production we encountered 50 years ago. Plant diseases, lodging, low test weights, maturity issues at harvest, effective weed control, and damaged kernels/grain at harvest are just a few examples of old problems with few new solutions. Oats breeders have made significant genetic improvements to yield, quality, and some lodging problems, but very little effort has been expended to investigate “system” approaches to many agronomic issues with oats. Current crop management efforts from both private companies and public institutions in North America are focused on row crop (corn) and oil crop (soybean and canola) improvements, with little regard to small grain crop management systems, including oats. With the exception of some wheat varietal work – focused on scab control - this narrow focus is driven by market prices, government farm support and marketing programs, and expected returns of sales of new chemicals and hybrids or varieties.

Crop input and grain handling companies, as well as farmers, researchers, and processors and food manufacturers need to address this “widening gap” in agronomic management if we expect oats to maintain any degree of competitiveness. We cannot expect new varietal improvements to be the sole answer to declining oats acreage and production in North America. We must, as an industry, address the need for improvements in oats production agronomy that considers and leverages the vast changes in other crops. We need to investigate and capitalize on advancements such as:

Benefits of oats in crop rotations to control specific weed and insect issues in all crops

Improved yields and lodging control through new targeted fertility programs including micronutrient use. New cropping patterns have altered fertility use and availability in the soil. Disease control via not only genetic resistance, but integrated systems controls, including effective and safe use of fungicides and multiple variety mixes. Improvements in seeding, harvesting, and grain handling using new equipment and technologies now available to the producer and grain handler. Oats benefits in the conservation program initiatives in both Canada and U.S. agriculture policies.

There is no one simple answer to improved oats production. However, unless we investigate and leverage improvements in other crops as well as opportunities these crops present, we will continue to see the trend of yield and agronomic gaps widen between oats and other crops.

Oat Milling Quality

Kelly Henderson

Technical Services Manager – Can-Oat Milling
#1 Can-Oat Dr. – Portage la Prairie, MB – Canada – R1N 3W1

Consumer interest in nutrition and palatability has kept oats in the fore front as a desirable food ingredient. Oat products are increasingly being used in food formulations because of their soluble and insoluble fiber levels. The mild pleasing conditioned oat flavor is complimentary to many other ingredients and allows the incorporation of oats into many different food formulas.

Along with these factors, there is the need to meet or exceed common milling grade requirements. Meeting the raw oat specification criteria is the starting point for procuring oats. There still are many physical attributes important to millers which could be influenced through breeding. Certain aspects such as groat yield and breakage, groat size, trichome hairs, and flake strength could be improved. The health aspects of oats are also vital to a mill operation and β -glucan, fat, antioxidants and disease susceptibility/effects could be further manipulated to have a greater positive impact on oat consumption.

Additional useful areas of study would be, reducing the need for fertilizers and pesticides, improving milling efficiencies, developing new tests for grading, sensory analysis, and controlling processes that provide useful and timely results. Not to be forgotten, it is also imperative to do innovative food product development, finding new uses for oat products, ensuring the flavor, texture, and visual characteristics are not compromised.

All these aspects are associated with, and shape the oat milling process. We need to identify and disregard short term trends and focus on sustainable trends. We must continue to make improvements, be more efficient, and provide more value to our customers.

Key Words: oat specification, milling efficiencies, groat, health

Health and Wellness

Joe Lutz

General Mills Ag Research
1201 North 4th Street
LeSueur, MN 56058

The health benefits of eating oats are widely known by consumers today. Food manufacturers and marketers in the US have a number of FDA regulated health claims they can use to promote sales and brand equity. To use these health claims the product must meet certain criteria listed in the Code of Federal Regulations which in turn places requirements on the oat crop used in that product. For example the use of the “Soluble fiber from certain foods and the risk of coronary heart disease” health claim (CFR101.81), sets the requirements for whole oats or oat flour by definition at least 4.0% beta-glucan (BG) and at least 10% total dietary fiber (TDF). The product must also meet the “low fat” claim which depending on the serving size would require approximately less than 7.5% oil. The addition of other non-oat ingredients to the product formula can increase the requirement for BG and TDF. Oat bran can be used to raise the level of BG and TDF in the product, however oat bran also has increased oil levels. In general, food manufacturers would like to see oat varieties with higher BG and TDF and perhaps more importantly lower oil.

Enhancing the Value for Oats: A European Perspective

Christopher Green

SW Seed Ltd, Great Abington, Cambridge CB1 6 AS
christopher.green@swseed.com

The agricultural supply chain is both outdated and disconnected, and this has given rise to one of its fundamental problems, that of value migration.

The challenge to the oat industry is to stimulate sustained wealth along the supply chain, thereby attracting reinvestment, and encouraging innovation to maintain crop competitiveness on the farm and consumer appeal in the market.

The concepts of value and supply chain were popularised in the late eighties, but the ideas are only now cascading through to agriculture. The particular problem with agriculture is that it is a commodity based industry producing a standard low value product, which can easily be substituted on price. This problem becomes accentuated with oats, where, despite their excellent brand potential, are overshadowed by the globalisation of alternative cereals. The fragmented and volatile nature of oat production, the fierce crop competition and general absence of a consistent consumer driven market, strains the chain.

As in any chain the oat value chain is only as strong as its weakest link. It is therefore incumbent upon us as crop developers to reinforce our link and ensure that, regardless of end point market, it is robust and in so doing secure an appropriate value for onward investment.

In the search for a more cohesive and connected value approach to marketing we are adopting a branding strategy, linking the field production of oats to end market use. In practice this is easier to achieve in niche areas, but the principle needs to be adopted on a wider scale if we, as an oat industry, are to optimise the brand goodness and value contained in our beloved cereal grain.

This presentation will cover some of the principles and challenges and provide examples of our initiatives and brand approaches, setting this against the harsh realities of a competitive market, where lowest unit cost of production distorts functional values.

North Dakota State University Oat Breeding

Michael S. McMullen¹, Douglas Doehlert², and R.R. Baumann¹

¹Department of Plant Sciences, North Dakota State University, Fargo, North Dakota 58105-5051, email: michael.mcmullen@ndsu.edu. ²USDA-ARS, Fargo, ND, USA.

Changing cropping patterns in North Dakota often are accompanied by a reduction in oat production area. Economic return to oat production may be improved by developing cultivars with increased yield, improved production stability, and improved forage and grain quality so that oats will remain an economically viable alternative in cropping systems.

Grain quality often limits market opportunities and many oat growers consider stability of quality characteristics such as test weight to be as important if not more important than grain yield potential in selecting a cultivar for production. Since test weight is an important factor in determining value of oats, growers prefer cultivars that produce stable high test weight even under unfavorable growing conditions. High test weight white oats command premiums for the racehorse oat market. Milling industry quality requirements are mostly compatible quality characteristics of oats grown for livestock feed. Milling yield is closely related to hull percentage so that cultivars with high milling yield will likely provide increased energy for livestock feed. Other characteristics that lead to improved milling efficiency are being evaluated. Livestock producers may prefer higher groat oil concentration as an energy source than is acceptable for the milling industry, which leads to some divergence of objectives for the two markets. Naked oats continue to find use in the livestock industry and offer opportunities to increase the value of oats in some production systems. Low oil naked oats may become useful to the milling industry.

The health benefits associated with beta-glucan soluble fiber has driven consumer demand for oat food products. Genetic variation for soluble fiber concentration in oats allows development of cultivars with increased soluble fiber concentration that should increase the value of oat products to health-minded consumers.

Oats are grown on approximately 60,000 ha as annual forage in ND and research has demonstrated substantial variation among oat cultivars for both forage yield and quality. Indicators of forage quality have been identified that should allow development of cultivars with improved relative forage value to increase the worth of forage oats to livestock producers.

Stability of oat yield and quality requires protection from oat diseases important in ND that include crown rust, stem rust, and to a lesser extent, barley yellow dwarf virus. Each disease may require a different strategy to provide effective resistance for the oat crop.

**Oat Breeding at Aberdeen, Idaho:
Shuttle Breeding to Improve Disease Resistance.**

D.E. Obert, J.M. Bonman, and E. W. Jackson

USDA-ARS Small Grains and Potato Germplasm Research Unit, 1691 South 2700 West,
Aberdeen, ID 83210.

The USDA-ARS oat breeding program at Aberdeen, ID was very successful under the leadership of Darrell Wesenberg, producing cultivars such as Otana, Monida, Ajay, Provena, and Lamont, and more recently Maverick and Monico. Although the yield potential and quality of these lines are superior in the Intermountain West, their lack of resistance to crown and stem rust prevented their use in the Midwestern US.

We have instituted a ‘shuttle breeding program’ to introgress resistance to crown and stem rust resistance into germplasm of the Aberdeen breeding program. Sources of resistance from oat breeding programs at Texas A&M University, University of Arkansas, University of Minnesota, North Dakota State University, Louisiana State University, and the University of Florida are being crossed with elite lines and cultivars from the ARS-Aberdeen program and F₂ populations are grown at Castroville, TX under natural infection by the two rust pathogens. Panicles from resistant F₂ plants are harvested and bulked by pedigree for generation advance at Aberdeen, ID as F₃ plots. F₄ seed from individual panicles are harvested at Aberdeen and head rows are planted at Castroville. Once again these rows are evaluated for disease resistance and agronomic characteristics, and panicles from resistant rows are harvested. F_{4.5} rows are then planted at Aberdeen and multiple plants are pulled from superior rows based on maturity, height, disease resistance (stem rust), and lodging resistance. These F_{5.6} selections are then planted at Castroville, TX for further disease evaluation. Based on disease reaction, superior (resistant) selections are planted as 2-row plots at Aberdeen and evaluated for maturity, height, lodging resistance, yield, and test weight. The use of the ‘winter nursery’ in Texas provides both disease evaluation and generation advance. We hope to derive superior cultivars and germplasm by introgressing better levels of rust resistance into our breeding program.

Alternatives to Single Major Gene Crown Rust Resistance

Deon D. Stuthman

University of Minnesota
St. Paul, Minnesota, USA

Five different reports published about a century ago shaped the oat breeding agenda for much of the 20th century. M.A. Carleton in 1894 first recorded differences for rust infection in different varieties. Next in 1900 came the rediscovery of Mendel's classical work first published in 1866. Soon thereafter Johannsen published his 'pure line theory' to explain why continued selection in 'pure lines' would not produce continued improvement. A few years later, Norton, in 1907, wrote, 'Oat breeding in the United States in general is a question of breeding for resistance.' Lastly, Barrus, in 1911, described the concept of physiological races of bean-anthracoze. Collectively, over the next 50+ years, these reports instructed much of the oat breeding efforts which mainly emphasized disease resistance, especially for crown rust. (Later in 1963, Van der Plank would coin the term "vertifoliar effect" to describe the isolation and use of single genes with large effects, especially for, but not limited to, disease resistance.) Along the way, there were several serious disease epidemics, but usually discovery and utilization of a new resistance gene would keep the new pathogen population in check, at least for some period of time. Unfortunately, the phenomenon of gene defeat is still with us today, i.e., the almost total defeat of Pc68 in much of Canada and parts of the United States just this past summer.

There were two most notable exceptions for oat researchers to focus on the 'vertifoliar effect' for crown rust resistance. First, Parker, in 1918, described 'early telia' as an alternative form of resistance. Then Hoerner (1919) and Parker (1920) described rust reactions which they called moderately resistant (MR) and moderately susceptible (MS), which were less than immune reactions, but superior to fully susceptible. Unfortunately, almost all U.S. oat researchers mostly ignored these novel ideas for nearly 30 years.

In 1953, my now departed colleague and mentor, Matthew Moore, established a unique crown rust screening nursery by planting several rows of buckthorn bushes alongside his rust screening plot area. His rationale was that these alternate host (for crown rust) plants would provide inoculum that would be a much better representation of the potential diversity of the pathogen population than what might occur naturally in any one location. Also, in the mid 1950s Simmons described 'adult plant' resistance, and Stanton described 'late rusting' in the cultivar 'Red Rustproof.' A decade later in the 1960s, three prominent pathologists, Van der Plank, Hooker, and Caldwell gave considerable support to alternative approaches of single gene, seedling evaluated crown rust resistance. Another decade later, Luke and colleagues described horizontal crown rust resistance in 'Red Rustproof.' However, for the most part, again few oat researchers paid much attention, or, only except in minor ways, utilized these alternative approaches to develop more permanently resistant genotypes. A somewhat different alternative approach to crown rust resistance, multi-line varieties, was first described by Browning and his colleagues in 1964. The approach utilized backcrossing up to a dozen or more individual crown rust resistance genes into a common background genotype. These multi-line varieties were quite successful in stabilizing crown rust resistance, but were not competitive for other important characteristics of ever improving, commercial oat varieties.

Several possible strategies to achieve more durable resistance will be presented. In general, the goal of such will be to match the complexity of the virulence in the pathogen, thereby establishing equilibrium between the two.

Pure lining of Breeder Seed for Molecular Variety Identification in Oat.

B. Rossnagel, P. Eckstein, T. Zatorski, G. Scoles.

Department of Plant Sciences/Crop Development Centre, University of Saskatchewan
Saskatoon, SK, CANADA, S7N 5A8, e-mail: graham.scoles@usask.ca

In Canada, the protection of a variety under Plant Breeders Rights requires the candidate be shown to be distinct, uniform and stable (DUS). To demonstrate that a variety meets these requirements, the variety is described by a series of morphological/botanical characteristics. The combination of phenotypic characteristics unique to a variety becomes the legal basis to assess its distinctiveness, uniformity and stability. The limitations to the current system are many. Phenotypic descriptions need to be determined by experienced personnel at varying times throughout the season, and need to be duplicated over at least two field seasons. The process is long and expensive. Since descriptions are comparative in nature (to two or three reference varieties chosen by the Plant Breeder) the descriptions are often subject to interpretation and may be described differently in subsequent evaluations. If variety identity is challenged, the material needs to be grown either in the field or a growth facility along with the reference varieties included at registration, and the characteristics may appear different when grown under different conditions.

Since the advent of DNA fingerprinting technology, the opportunity exists to replace the current phenotypic description of a plant variety with molecular characterizations as descriptors for crop variety registration, PBR, and commercial identity preservation requirements. Several technologies exist that could serve the purpose, all with inherent advantages and disadvantages. The advantages of all of these technologies however are the non-subjective nature of the descriptive data, and the stability of molecular data. We have assessed the ability of molecular markers to distinguish closely related oat varieties, as well as all 24 currently registered Canadian hulless barley varieties. Hulless barley was chosen as a “model” because of the simple genetics of this crop species, the relatively small number of varieties in this class registered in Canada, and availability of Breeder Seed of all varieties. In addition, we have investigated the uniformity of molecular banding patterns in oat varieties. Options for dealing with potential non-uniformity in new varieties include the purification of a candidate variety for a molecular pattern (pure lining), as has been done for CDC Weaver.

Key Words: variety identification, distinct, uniform, molecular, DNA fingerprint

Breeding Milling Oat for the Rust Area of Western Canada

Jennifer Mitchell Fetch, Nancy Ames, James Chong, Tom Fetch, Steve Haber, Jim Menzies,
Andy Tekauz

Agriculture & Agri-Food Canada Cereal Research Centre, 195 Dafoe Road, Winnipeg, Manitoba
R3T 2M9 CANADA. E-mail: jfetch@agr.gc.ca

Milling oat production has shifted to the eastern prairies of western Canada due to mill locations, sourcing for exports to mills in the USA, and removal of transportation subsidies for agricultural commodities in 1995. There has also been an increase in local (eastern prairie) processing. The need for a breeding program located in the eastern prairies became evident to the Cereal Research Centre (CRC) and the local and international industry. Therefore, in 1996, a consortium of Agriculture and Agri-Food Canada and industry partners was set up as the Prairie Oat Breeding Consortium (POBC) at the CRC.

The objectives of the POBC are to develop oat varieties adapted to the Canadian prairies with enhanced disease resistance, superior food quality for milling and other processing, and superior agronomic performance including higher yield. The CRC conducts disease resistance, quality and biotechnology research that also benefits the oat industry. These scientists collaborate with the oat breeding program to transfer their outputs to the clients in the form of superior oat cultivars.

In the eastern prairie region, disease pressure is usually increased due to favorable environmental conditions. Resistance to crown rust, stem rust, smut, barley yellow dwarf virus, Fusarium head blight, and leaf spotting diseases is critical for this region, which will ensure the food safety and food quality in oat as required by North American and international consumers. Genetic resistance to these diseases is optimum, as this provides producers with a non-chemical disease control method, which reduces adverse impacts on the environment and lowers crop inputs. Resistant and agronomically superior cultivars will ensure production sustainability, market growth, grade protection, and reduction of risk for producers and end users in this region. Increased domestic processing in this region may lead to development of value added processes and novel uses for oat and oat products, thereby increasing available business opportunities for local producers and processors. These innovations could eventually provide additional options for Canadian and international consumers as well.

Oat has been shown to provide improved health benefits to consumers. One means is by reducing blood cholesterol levels due to the presence of beta-glucan fibre in the grain. Research and breeding to increase the beta-glucan levels in prairie-grown oats would provide nutritional benefits to consumers and additional marketing opportunities for oat producers and processors. New end uses such as functional foods and fractionation products would fit in with the increasing interest around the world in low glycemic diets, where the emphasis is on slow-release carbohydrates such as those provided by oat and other whole grains. Functional foods designed with the cholesterol-lowering benefit in mind are being developed in other areas of the world, and this potentially lucrative and health-promoting market is under consideration in Canada.

Survival of frozen tissue in winter oat crowns

David Livingston, Shyamalrau Tallury

USDA-ARS and North Carolina State University, Raleigh, NC.

The part of oat that over winters, known as the crown, is a complex organ composed of numerous cell types distributed in seemingly random patterns. Winter oats, like other winter cereals, survive freeze conditions during winter by various protective mechanisms within this vital tissue. The lower part of the crown is composed of xylem and phloem vessels that are flanked by numerous large parenchyma cells. The center of the lower crown, called the crown core, is the tissue that provides continuity from the roots to the upper part of the crown called the apical meristem. This apical region is the tissue that is most susceptible to freezing in plants that have not been cold acclimated. During cold acclimation the apical region rapidly becomes more freezing tolerant than the rest of the crown and after 3 weeks of cold acclimation is the most freezing tolerant tissue in the crown. Paraffin embedded sections that were triple stained were photographed to illustrate the recovery of various tissues and cell types within the crown after freezing. The crown was then fractionated into 2 regions and analyzed to quantify biochemical differences between the tissues. Percent moisture, the percentage of water freezing, carbohydrate concentrations and invertase activities differed significantly between the 2 regions. These differences will be discussed in relation to the survival of the tissues. In addition, the survival of specific tissue within oat crowns was compared to more winter hardy cereals (barley, wheat and rye). Differences in tissue survival between species will be the basis of a metabolomics study to determine why oats are the most susceptible winter cereal to freezing conditions.

Milling Oat Production

William May

AAFC, Indian Head Research Farm, Box 760
Indian Head, SK, S0G 2K0

Producers growing oats strive to attain the quality needed to derive a premium price for their crop. Currently, oats used for race horses and for human consumption are two markets that provide a premium price. The human consumption market has processor-dependent specifications for kernel moisture, test weight, groat colour, percentage of sound kernels, percentage of thin seed, and admixtures. The producer can alter a number of his production practices to increase the probability of achieving a high level of quality and yield. Production practices that tend to increase yield and quality are cultivar, early seeding, moderate nitrogen fertilizer rates, increased seeding rate in the presence of wild oats.

Key Words: *Avena sativa*, *Avena fatua*, seeding date, seeding rate, test weight, yield

Forage Yield and Quality of Oat Hays at Fargo

Dwain W. Meyer, Michael S. McMullen, and Robert D. Nudell

North Dakota State University, Fargo, ND 58105

Oat (*Avena sativa* L.) hay acreage has increased over the last 5 years to nearly 125,000 acres annually. We therefore evaluated several oat hays to determine which cultivar that should be recommended for hay production. Twelve oat cultivars/genotypes were seeded each year during 2002 to 2005, but only nine were included each year. The nine cultivars/genotypes included two early maturing cultivars, Jerry and Killdeer, one mid-maturing cultivar, HiFi, two late-maturing cultivars, Ebeltoft and AC Assiniboia, two forage-type cultivars, Ensiler and ForagePlus, one naked cultivar, Paul, and one low lignin dwarf naked genotype, ND000461. AC Ronald, Stark (naked cultivar), and ND001306 (low lignin, dwarf, naked genotype) were included in 2004 and 2005. The field design was a randomized complete block with three replicates. An experimental unit was 6 by 22 feet and consisted of six rows spaced 12 inches apart. Soil test indicated adequate P and K, and N was applied so soil test N plus fertilizer was at least 125 lb/acre. Seed of all entries were planted at 1 million seeds/acre as early as possible each year. Weeds were controlled by hand weeding. Each entry was harvested for yield and quality sample taken when five consecutive random panicles had the tip spikelet just beginning soft dough stage. Quality samples were ground in a Wiley mill to pass a 1-mm screen and sealed in glass bottles until chemical analysis. Standard wet chemistry analyses were performed for crude protein (CP), acid-detergent fiber (ADF), neutral-detergent fiber (NDF), acid-detergent lignin (ADL), and in vitro dry matter digestibility (IVDMD) and hemicellulose, cellulose, and relative feed value (RFV) calculated using standard formulas.

Significant cultivar effects for forage yield and each quality component measured were detected even though the cultivar by year interaction was significant. Forage yield was highest from the late-maturing naked-oat genotypes, ND000461 and Paul. AC Assiniboia, Ensiler, Killdeer, and Jerry were the lowest yielding cultivars. Forage yield of the two forage oats were similar to the early maturing cultivars. Forage quality of late-maturing cultivars/genotypes generally was higher than early maturing and forage cultivars. Paul had significantly lower NDF, ADF, hemicellulose, and cellulose and higher IVDMD than the other eight cultivars/genotypes tested over the 4 years. The forage cultivars generally were high in ADF and ADL, and low in IVDMD and CP. ND000461 and Ebeltoft were highest in IVDMD while ND000461 and AC Assiniboia were lowest in ADL. High IVDMD was negatively associated with ADL with Ebeltoft and Stark notable exceptions.

We conclude that Paul should be selected for oat hay since it had the highest forage yield and quality of released cultivars. Of entries tested, late-maturing cultivars/genotypes were higher in forage yield and quality than early maturing cultivars.

Forage oat cultivars were at best equal to early maturing cultivars in forage yield and quality. AC Assiniboia and AC Ronald were the best dual forage or grain cultivars of those tested. ND000461 has good potential for release as a forage cultivar with high forage yield and quality.

Oat Variety Comparisons on Fields Managed Organically in Minnesota and North Dakota

Patrick M. Carr¹, Herman J. Kandel², Paul M. Porter³,
Richard D. Horsley⁴, and Steve F. Zwinger⁵

¹North Dakota State Univ., Dickinson Res. Ext. Ctr., 1133 State Ave., Dickinson, ND 58601-3267; ²Univ. Minnesota, Crookston Res. Ext. Ctr., 251 Owen Hall, 2900 Univ. Ave., Crookston, MN 56715-5001; ³Univ. Minnesota, Dep. Agron. Plant Gen., 411 Borlaug Hall, St. Paul, MN 55108-6026; ⁴North Dakota State Univ., Dep. Plant Sci., P.O. Box 5051, Fargo, ND 58105-5051; ⁵North Dakota State Univ., Carrington Res. Ext. Ctr., P.O. Box 219, Carrington, ND 58421.

Modern oat (*Avena sativa* L.) cultivars generally are developed and selected in environments where synthetic agrichemicals are used to minimize nutrient deficiencies and pests. Our objective was to determine the adaptability of spring oat cultivars for production in certified organic environments. Single seed lots for 10 cultivars released since 1986 were evaluated for grain yield and kernel volume weight on four certified organic fields in Minnesota and North Dakota in 2003 and 2004. Kernel weight along with seedling vigor and density, plant canopy development, plant height, propensity to lodge, and panicle density were determined for cultivars in most but not all environments. Interactions between environments and cultivars existed for all three grain parameters ($P < 0.05$), but some cultivars ranked high consistently for yield, along with kernel and volume weight. For example, the cultivars Ebeltoft and Sesqui produced as many as 44 and 59 bu/acre more, respectively, than other selected cultivars, depending on the environment. Differences in seedling vigor and other phenotypic growth traits occurred between cultivars but failed to explain much of the variability in grain yield that was detected. Modern oat cultivars adapted to production in certified organic environments were identified as a result of this study. However, the phenotypic growth traits that were considered are not suited as primary selection criterion for grain yield among spring oat cultivars in certified organic environments.

References

1. Carr, P.M., H.K. Kandel, P.M. Porter, R.D. Horsley, and S.W. Zwinger. 2006. Wheat cultivar performance on certified organic environments in Minnesota and North Dakota. *Crop Sci.* In press.
2. Richards. M.C., and V. Heppel. 1990. p. 147-155. *In* Anonymous (ed.) Cereal varieties for the organic and low input grower. Proc., Symp. Organized by the British Crop Protection Council, Churchill Coll., Cambridge, UK. 4-6 Sep. BCPC, Farnham, UK.

Key Words: Organic farming; ecological farming; variety trials

Controlling Wild Oat in Tame Oat

Steven Shirtliffe¹, Chris Willenborg² and Jeffrey Wildeman³

¹Department of Plant Sciences, University of Saskatchewan; ²Department of Plant Science, University of Manitoba, Winnipeg, MB; ³Cargill-AgHorizons, Regina, SK.

Wild oat and green foxtail are the two most common weeds in western Canada. As there are no herbicides to control these weeds in tame oat, yield and quality reductions occur whenever it is present. Therefore the primary way to control wild oat and green foxtail in oat is through cultural methods. Our group has spent eight years investigating cultural weed control of wild oat in oat.

Most commonly grown varieties of tame oat do not differ in yield and quality loss from wild oat. However, the semi-dwarf oat line OT288 had its yield reduced the most from wild oat. In contrast the forage oat variety, CDC Bell, has relatively little yield loss from wild oat, probably attributable to its height and wide, lax leaves. Unfortunately, CDC Bell is selected for forage use and has poor seed quality and maximum yield. The oat breeding program has recognized the competitive ability of this variety and has used it as a parent to cross with lines with better seed quality and agronomics. These crosses will be evaluated for competitive ability as well as seed yield and quality in the future.

We have also found that increasing seeding rate is a very effective way to reduce the yield loss by wild oat. Increasing oat seeding rate of oat from 250 to 500 plants m⁻² always resulted in higher oat yield when wild oats were present. Seeding large sized oat seed is another possible way of increasing the competitive ability of oat with weeds. In a green house study we have found that seed with large careopsis yielded higher both in the presence of wild oats and weed free. Nevertheless, in the field seed size does not affect the yield of weed-free oats grown at any density. However, under competition with wild oat, oats seeded from larger seed has less yield loss.

The yield loss that wild oat causes in oat depends upon the relative timing of the wild oat emergence. The relative growth stage of the oats and wild oats is very important because latter emerging weeds are much less competitive than early emerging ones. For example, 25 wild oats m⁻² will cause 10% yield loss when they emerge at the same time as the crop. If wild oat emerges one leaf stage later than the oats, 85 wild oat seedlings m⁻² are needed to cause the same 10% yield loss. We are currently developing a model to assist producers to determine if an oat crop should be destroyed because of wild oat contamination and reseeded. Preliminary simulations indicate that often the best decision is to leave the oat crop and accept the yield loss from the wild oat rather than re-seeding and risk yield and quality loss from a late flowering crop. In this situation, farmers can avoid excess wild oat contamination by delaying windrowing or harvesting until most wild oats have shed. An individual wild oat will shed most of its seed within a two week period.

A common method of weed control in organic crop production is in-crop harrowing. However, there have been recommendations that in-crop harrowing should not be used in oat. We have found that oats are as tolerant to in-crop harrowing as barley is and more tolerant than oat. In summary, we have found that yield and quality losses from wild oat can be managed in the absence of herbicides.

In Search of New Effective Resistance to Crown Rust in *Avena sterilis*

James Chong and Gang Chen

Cereal Research Centre, Agriculture & Agri-Food Canada
Winnipeg, Manitoba, Canada R3T 2M9. jchong@agr.gc.ca

Crown rust, caused by *Puccinia coronata* f. sp. *avenae*, is an economically important disease of oat in North America. While losses of the crop have been minimized through resistance breeding, the disease continues to be a major threat to oat production. During the early years of oat breeding, resistance to crown rust was obtained primarily from cultivated oat introduced into North America. By the end of the 1950s, all deployable sources of resistance from cultivated oat had been overcome. The discovery in the 1960s of a large pool of genes for resistance to crown rust in wild populations of *Avena sterilis* in the Middle East and North Africa marked the beginning of a new era for resistance breeding, as subsequent effort depended almost entirely on resistance from this wild relative. However, as with the genes from cultivated oat, many of the genes from *A. sterilis* that were highly effective at the time of release have all been overcome by the pathogen within a relatively short time. In North America, *P. coronata* can reproduce sexually, evolving new virulence phenotypes in the process due to sexual recombination. Presently, only a few available genes are effective against crown rust. Thus, finding adequate sources of resistance for developing cultivars with more durable resistance to new virulent phenotypes remains a real challenge. During 1999-2003, we evaluated over 4,000 accessions of *A. sterilis* from the National Small Grains Collection, Plant Gene Resources of Canada and Vavilov Institute, for crown rust reaction. The accessions were tested with a composite of *P. coronata* isolates collected each year from annual surveys in western Canada during 1999 and 2004. Sixteen accessions which were either immune or had very low crown rust severities in the field were selected for studies to determine the genetics of their resistance to crown rust. These were either crossed or crossed and then backcrossed to the susceptible cultivars, 'Harmon' or 'AC Morgan'. Segregation of the progenies for resistance to specific crown rust isolates in greenhouse tests showed that resistance in all accessions was complex and generally conferred by at least two or more genes. Accessions that were susceptible to an isolate at the seedling stage and resistant to the same isolate at the adult-plant stage were considered to possess adult-plant resistance. Resistance-gene suppressors appeared to be common in *A. sterilis*. Five of the 16 accessions were shown to possess a suppressor gene that inhibited the expression of a resistance gene. The combined greenhouse and field tests with composite isolates appeared to be useful for identifying the effective crown rust resistance gene(s) among those that were not effective within the same accessions. The effective seedling and adult-plant resistance genes identified in the study have been individually isolated into single-gene lines, allowing these putative new genes to be further tested for identity, verified their effectiveness to crown rust, and determined their linkage/allelic relationships with other crown rust resistance genes.

Key Words: *Avena sterilis*, crown rust, *Puccinia coronata*, resistance, suppressors

Linkage relationships among factors that affect groat oil concentration, crown rust resistance, stem rust resistance and the naked character in oat

Diego Vilaro, Angela Sebelius and Michael McMullen

North Dakota State University, Fargo ND, 58105

Crown rust resistance (CRR), derived from IAB 605X, is apparently conferred by a single dominant gene and is responsible for CRR of 'Morton'. We gave the CRR gene a designation of B during these studies. Observations of breeding populations suggest B resistance may be associated with low groat oil concentration. Stem rust resistance (SRR) conferred by a source designated 'pg-a complex', is conferred by at least two recessive genes. Lines with pg-a and IAB in the homozygous condition have not been identified in breeding populations suggesting that B is associated with one of the components of *pg-a* complex. A component of *pg-a* stem rust resistance in the naked cultivar 'Paul' appears to be associated with a gene conferring the multifloret or naked character. The naked character and the multiflorous spikelet always occur together, and in Paul a single dominant gene confers naked trait. This study attempts to genetically describe these relationships. F₂ populations from the CR susceptible/resistant 'Otana'/Morton cross were evaluated for resistance to composite comprised of prevalent crown rust races in North Dakota. B CRR was conferred by one dominant gene and possibly one suppressor gene as the 13:3 ratio indicated. Progeny of crosses involving Morton, and Paul or ND873126 as the susceptible recurrent parent suggested a single dominant gene conferred resistance to crown rust. Testcrosses obtained involving the *pg-a* SRR line ND873126 and Morton indicated that the model that best fits the data describes the relationship between one factor of B and one factor of *pg-a* being linked in coupling (B_Pg-A). Morton and ND873126 differ by a single factor relative to resistance conferred by *pg-a*. BC₁F₂ families from this cross suggested strong linkage of CRR and SRR factors. The relationship between CRR from the IAB source and oil concentration was evaluated in a field experiment involving 15 pairs of F_{5,6} sister lines with and without crown rust resistance. Interaction between lines and oil concentration was detected, however IAB and low oil concentration were not significantly associated. *Pg-a* is controlled by one factor in the cross between Morton and Paul as BC₁F₁ and BC₁F₂ data suggested. *B* and *pg-a* were always linked and *N* was linked to *B* and *A*, but with less intensity than *B* with *A*. The gene order in this chromosome region is described as *N-B-A*.

Crown Rust Resistance of Oat Germplasm from the ARS-Aberdeen Program

J. M. Bonman¹, D.E. Obert¹, E. W. Jackson¹, S.A. Harrison² and M. L. Carson³.

¹USDA-ARS, Small Grains and Potato Germplasm Research Unit, 1691 S. 2700 W., Aberdeen ID 83210; ²Louisiana State University, AgCenter Agronomy Department, 104 MB Sturgis Hall, Baton Rouge, LA 70803; ³USDA-ARS Cereal Disease Laboratory, 1551 Lindig Ave., St. Paul, MN 55108.

Previously oat breeding at ARS-Aberdeen primarily targeted the Intermountain West. However, with the recent reduction in oat breeding effort at some land grant institutions, there is a greater need for ARS materials to be more widely adapted. Crown rust resistance has thus become a breeding target for the ARS-Aberdeen oat enhancement program. Since crown rust resistance was previously not a high priority, we began by assessing the crown rust resistance of cultivars previously released from Aberdeen and of elite breeding lines from 2003. Field experiments were conducted against natural *Puccinia coronata* populations in LA and TX under highly-conducive conditions and using specific pathogen races in ID. Greenhouse experiments were conducted to test for compatibility to *P. coronata* isolates from throughout the US. In the field, all cultivars were highly susceptible to pathogen populations in TX and LA and to compatible isolates in Aberdeen trials. Similarly, the cultivars were susceptible to most of the US isolates in the greenhouse tests. Elite lines 99Ab12179 and 99Ab11862 showed only about 20% disease severity relative to the check Provena in TX and LA and were resistant to about half of the US isolates. Experiments are underway to determine if the lower disease levels in the field were due to partial resistance in these two lines. Our experiments have shown the vulnerability of the Aberdeen cultivars and lines to crown rust and work is currently underway to improve the disease resistance within the program by crossing with resistant lines and selecting under high disease pressure in south Texas.

Qualitative and Quantitative Characterization and Mapping of Oat Crown Rust Resistance Using Phenotypic Data from Three Assessment Methods

E. W. Jackson¹, D. E. Obert¹, M. Menz², G. Hu¹, J. Chong³, and J. M. Bonman¹

¹USDA-ARS, Small Grains and Potato Germplasm Research Unit, 1691 S. 2700 W., Aberdeen ID 83210; ²Department of Soil and Crop Sciences and The Institute for Plant Genomics and Biotechnology, Texas A & M University, College Station, TX 77843-2123; ³Cereal Research Centre, Agriculture & Agri-Food Canada, Winnipeg, MB, Canada R3T 2M9

Accurate characterization and mapping of disease resistance loci depends on the type and precision of phenotypic measurements. For cereal rust diseases, such measurements are commonly based on qualitative or quantitative visual ratings of disease reactions and diseased leaf area. Since phenotypic data collected this way are dependent upon the skill of individual raters, data accuracy would also be affected by rater experience. This study compared a new quantitative (q) PCR assay, estimating fungal development in oat tissue, to visual and digital assessments of oat crown rust resistance in the Ogle/TAM O-301 (OT) mapping population. Resistance was characterized and mapped both qualitatively and quantitatively using the three assessments of OT recombinant inbred lines inoculated with a single *P. coronata* isolate (CR185) in the greenhouse and field. Based on the qualitative approach all three assessment methods identified a major gene from Ogle on linkage group OT6. Data from the q-PCR assay, however, allowed more precise mapping of the major gene. Quantitative mapping based on q-PCR data also identified QTL conferred by TAM O-301 on OT32 and OT2, neither of which were detected by digital assessment and only the QTL on OT32 was detectable using data from visual ratings. Overall, using q-PCR to precisely phenotype oat crown rust reactions in two environments provided an enhanced means of mapping resistance in the OT mapping population. Similar methods should be applicable to the study of other cereal rust pathosystems.

Intogression of Oat Crown Rust Resistance from Diploid *Avena strigosa* and Tetraploid *A. murphyi*

Howard W. Rines¹, Hedera L. Porter¹, Martin L. Carson² and Gerald E. Ochocki²

¹USDA-ARS and Department of Agronomy and Plant Genetics, University of Minnesota, 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108; ²USDA - Cereal Disease Lab, 1551 Lindig Street, St. Paul, MN 55108. E-mail: porte205@umn.edu

Accessions of a diploid oat ($2n = 2x = 14$) *Avena strigosa* L. (CI 6954SP) and a tetraploid oat ($2n = 4x = 28$) *Avena murphyi* Ladiz. (P12) were identified as potential new sources of resistance to oat crown rust (*Puccinia coronata* f. sp. *avenae*) for introgression into cultivated hexaploid oat ($2n = 6x = 42$) *Avena sativa* L. *A. strigosa* served as the female parent in crosses to *A. sativa* cv. Black Mesdag and *A. murphyi* P12. Embryo rescue was required in crosses with Black Mesdag but was unnecessary in crosses with *A. murphyi*. Viable seed was also produced from crosses between *A. sativa* cv. Ogle and *A. murphyi* when Ogle was the female parent. Colchicine doubling was utilized with all F₁ plants, allowing for partial self-fertility in the C₁ generation.

Screening for oat crown rust resistance was conducted using a bulk inoculum collected from the buckthorn nursery on the St. Paul campus. *A. strigosa* x *A. sativa* cv. Black Mesdag C₁ plants were all susceptible, while both crosses with *A. murphyi* resulted in an intermediate resistance response. Subsequent backcrosses to the *A. strigosa* x Black Mesdag and *A. strigosa* x *A. murphyi* crosses with rust susceptible *A. sativa* cv. Ogle have produced progeny segregating for a range of crown rust resistance and susceptibility. Selection in each generation has been for resistant phenotypes. The BC₃F₁ generation of crosses involving *A. strigosa* with Ogle as recurrent parent are segregating approximately 1 resistant : 1 susceptible regardless of whether Ogle is the female or male parent. Root tips of plants with moderate to high rust resistance are being analyzed for chromosome number.

Key Words: interspecific crosses, oat crown rust resistance, disease resistance

Barley Yellow Dwarf Virus in Oats: A Field and Laboratory View

Joseph M. Anderson¹ and Herbert W. Ohm²

¹USDA-ARS and ²Agronomy Department, Purdue University, West Lafayette, IN 47907

Barley and Cereal Yellow Dwarf Viruses continue to be a major disease problem in the Midwest and Southeastern parts of the US. A number of lines developed in the small grains breeding programs at Purdue University and University of Illinois do have significant resistance to these viruses. However, when the disease pressure is high the level of resistance within these lines does not appear to be sufficient. Also this resistance is most likely due to the pyramiding of a number of genes, which individually do not provide high levels of resistance. Moving this multi-gene resistance into adapted material for this wide growing region requires a significant amount of testing over multiple generations. Consequently, we are currently testing in the greenhouse and field a set of *Avena strigosa* and *Avena sterilis* accessions to identify lines which contain high levels of B/CYDV resistance. Preliminary analyses suggest that several of these lines are quite resistant. Those lines which contain significant levels of virus resistance will be used as resistance donors in the breeding program.

PCR Markers for Beta-glucan, Oil and Protein

Stephen J. Molnar, Winson Orr, Shan He, Julie Chapados, Anissa Lybaert,
Charlene Wight, and Nick Tinker

Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada,
Central Experimental Farm, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada.

Polymerase Chain Reaction (PCR) based markers tightly linked to Quantitative Trait Loci (QTLs), or to the target locus for a single gene trait, are well suited for marker assisted breeding. Although extremely useful in other crops, we and others have had limited success in mapping microsatellite or Simple Sequence Repeat (SSR) markers in oat due to low frequencies of polymorphism. Therefore, Randomly Amplified Polymorphic DNA (RAPD) and other molecular markers associated with QTLs for beta-glucan, oil and protein content were redesigned as Sequence Characterized Amplified Region (SCAR) or Cleaved Amplified Polymorphic Sequence (CAPS) markers (Orr and Molnar). PCR-based markers have also been developed by designing primers to consensus sequences for metabolic genes in the requisite biochemical pathways. A few Single Nucleotide Polymorphism (SNP) markers are now also available in oat and such markers may well be developed for oil, beta-glucan and protein in the near future. Analysis of homologous and homeologous relationships between such markers using the Kanota x Ogle (Wight et al 2003) or other reference maps, suggests strategies for finding additional QTLs and additional linked markers. The expanding collection of PCR-based markers constitutes a valuable resource for the oat breeder. Validation of markers on breeding lines is establishing parameters for their use in marker-assisted selection.

Wight et al. (2003) A molecular marker map in Kanota x Ogle hexaploid oat (*Avena* spp.) enhanced by additional markers and a robust framework. *Genome* 46: 28-47.

Orr and Molnar (2006) Development and mapping of PCR based SCAR and CAPS markers linked to oil QTLs in oat. Submitted to *Crop Science*.

An Allele Survey of North American Oat Varieties

Nick Tinker, Steve Molnar, Charlene Wight, Jitka Deyl, Weikai Yan, Klaus Jakubinek, Diane Bergeron, Art McElroy, Shan He, Winson Orr, Julie Chapados, Hai Pham.

ECORC, AAFC, 960 Carling Ave. Ottawa, ON K1A 0C6, Canada.

A survey attempts to represent a type of information about an entire population by sampling a subset of its members. In this study, the population is the “working germplasm of breeders in North America” and the information is the “diversity of molecular marker alleles”. The population was sampled by breeders, who each nominated recent varieties that would contain alleles that were representative of their region of adaptation. This list of nominees was then stratified, and lines with high redundancy of known co-ancestry were eliminated. The resulting set of 35 lines is diverse and inclusive, but not random. Pairs of PCR primers were screened across this germplasm to reveal polymorphisms. Of these, 55 were based on sequence characterized amplified regions (SCARS) and 17 were based on microsatellites. Biplots of the allele-by-variety matrix revealed a high degree of structure in both varieties and markers. Much of the allele redundancy is due to over-sampling of alleles from certain QTL regions, while redundancy of germplasm may reveal previously unknown genetic relationships. The resulting database can be used to predict whether given markers are likely to reveal polymorphism in a given type of germplasm. Furthermore, a limited amount of gene association analysis may be possible once further phenotypic analysis has been performed on this germplasm. Marker scores in this database will be presented using a graphical web-based software tool called “GELATO”.

Oatgenes: A Comprehensive Database of Oat Markers and QTLs

Charlene P. Wight, Diane S. Bergeron, and Nicholas A. Tinker

Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada,
Central Experimental Farm, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada.

Molecular markers, linkage maps, and quantitative trait loci (QTLs) are essential components of genetic discovery and molecular breeding. Increasingly, new results build on cumulative information from previous studies. For example, comparative analysis of gene sequence and position among and between species is now a routine method for gene discovery, and cumulative evidence from previous studies is used to strengthen inferences regarding QTLs. Databases such as NCBI, GrainGenes, and Gramene are valuable tools for gathering this type of evidence. However, existing resources have two limitations with respect to oat. Firstly, the genetic maps of oat have not been integrated into a single consensus map. Secondly, numerous QTL reports with different degrees of statistical support have not been integrated into a single reference.

To address these issues, we have assembled two new composite oat frameworks: a hexaploid framework based on the Kanota x Ogle (KxO) map, and a diploid framework based on the *Avena atlantica* x *A. hirtula* (AxH) map. The hexaploid framework brings together information from 38 maps (3401 markers); the diploid one information from 8 maps (1117 markers). A single tetraploid map from *A. barbata* was also incorporated as a separate framework. Framework markers represent chromosome regions, similar to the “bins” used on other maps, into which all other markers are placed. Marker names are appended with a suffix to reflect the map whence they came. The centiMorgan distances along each framework linkage group are those of the base map, with negative numbers representing regions that extend beyond the first framework marker in the base map. If a group is known to be homologous to one of the base map groups but cannot be oriented with respect to the base map, it is incorporated into the framework as an auxiliary group. Groups with no known homology to the base map groups are appended to the framework.

These composite maps provided the framework for the construction of a comprehensive QTL database for oat, incorporating information from 640 QTL reported in the primary literature. Each QTL was assigned to one of the chromosome regions and given a “confidence index” that ranged from 1 (most evidence) to 3 (least evidence) depending on the type and degree of evidence used to infer the QTL. This indexing system was as objective as possible, incorporating an approximation of genome-wide error control, but adjustments were made if additional evidence proved compelling; e.g., the QTL was present in a number of different environments. In addition, 38 loci mapped as single genes were incorporated into the same database by giving them a default confidence index of “1”.

A web-based interface has recently been added to the database, allowing users to search for information concerning specific traits, regions of the genome, markers, or mapping populations. Information concerning the original references and notes concerning each locus are included in the search results, as are graphical representations of each linkage group with icons marking the approximate location of QTLs. This database will be accessible at the following location: <http://avena.agr.gc.ca/oatgenes/>.

Oat Molecular Markers: Status and Opportunities

Howard W. Rines

USDA-ARS and Department of Agronomy and Plant Genetics, University of Minnesota, 1991
Upper Buford Circle, St. Paul, MN 55108 Email: rines001@umn.edu

Advances in genomic analysis and application of marker-assisted selection to oat genetic improvement is currently limited by a lack of genomic information and molecular genetic tools, particularly user-friendly molecular markers adapted to high-throughput technology. Identification of such markers in large numbers would allow oat breeders and geneticists to take advantage of the services of recently established regional marker labs, thus enabling much more ready trait marker association identification and application of marker-assisted selection. Single-sequence repeat (SSR) markers are marker-of-choice for many situations because they are often co-dominant and multi-allelic. However, they are arduous and expensive to develop. Only a limited number of genomic SSRs have been reported to date for oat and the amount of polymorphism detected among cultivars has been disappointingly low (Jannink and Gardner 2005). Identification of SSR sequences in expressed sequence tag (EST) sequences in GenBank and other data bases have been a less expensive source of these markers, but only a few thousand ESTs have been reported in oat limiting the number of oat EST-SSRs identified (Brautigam et al. 2005). Genome sequence similarities among grasses allow some cross-detection of markers across species, particularly for EST-SSR markers (Varshney et al. 2005), providing opportunities for identification of markers from wheat, barley, lolium, fescue, and other grasses that are useful in oat. Communication and coordination among researchers are needed to make screening markers from other species on oat more efficient. Other type markers (e.g., RFLPs, AFLPs) found associated with genes or QTLs of interest, or even candidate genes, have been converted to PCR-based markers to increase their efficiency, but again in limited numbers (Rines et al. 2006). Several new technologies for identification and scoring of SNPs and other markers have arisen. A most promising technology, Display Array Technology (<http://www.diversityarrays.com/applicationsdart.html>), which could provide genome-wide finger-printing for several hundred markers rapidly and at a low per-marker cost, currently is being pursued by an international consortium of oat researchers. This presentation is intended to promote a discussion of how oat workers can best coordinate their efforts to improve opportunities for marker development and use in oat improvement.

- Brautigam M., A. Lindhof, S. Zakhrebekova, G. Gharti-Chhetri, B. Olsson, and O. Olsson. 2005. Generation and analysis of 9792 EST sequences from cold acclimated oat. *BMC Plant Biology* 5:18
- Jannink J-L, and S.W. Gardner. 2005. Expanding the pool of PCR-based markers for oat. *Crop Sci.* 45:2383-2387
- Rines, H.W., S.J. Molnar, N.A. Tinker, and R.L. Phillips. (2006) Oat. *In: Kole, C. (ed.) Genome mapping and molecular breeding in cereals.* Springer, New York (In press).
- Varshney R.K., A. Graner, and M.E. Sorrells. 2005. Genic microsatellite markers in plants: features and applications. *Trends Biotechnol.* 23:48-55.

Use of Breeding Populations to Detect and Use QTL

Jean-Luc Jannink

Iowa State University, Ames, IA

Moderately high density and throughput markers would allow the oat community to go beyond QTL mapping in experimental populations to estimating QTL effects in breeding populations, making the estimates immediately useful in selection decisions. For this approach to be effective, continued community cooperation in the effort will be essential. This cooperation will allow us to bring together into a single analysis enough lines so as to be able to detect and reliably estimate the effects of QTL useful to marker assisted selection. As a community, we should also devise plans to evaluate the levels of linkage disequilibrium between the markers we are developing, and to determine the level of population structure that exists between our breeding programs. The barley Coordinated Agricultural Project is providing funds to the barley community to initiate such efforts and we should be able to learn from their experience.

Application of molecular marker technologies on cereal crops improvement

Shiaoman Chao

USDA-ARS Biosciences Research Lab, 1605 Albrecht Blvd, Fargo, ND 58105

The use of PCR-based DNA markers has greatly improved the efficiency in mapping agronomic traits. One such DNA marker is SSR or microsatellite. It is multiallelic and capable of detecting higher levels of polymorphism. At the moment, SSR is the most extensively used marker system in both wheat and barley. SNP (single nucleotide polymorphism), a biallelic marker system, is newly emerging and will become the next generation of marker in cereal crops. SNPs are numerous in plant genomes and development of SNP markers is currently underway in both wheat and barley. The development of a high-throughput analytical platform and the potential for multiplexing analysis have further increased the efficiency and effectiveness of using PCR-based markers for both genetic studies and breeding practice. High throughput genotyping will facilitate the mapping of agronomic traits through the use of association mapping strategies, which can complement the traditional linkage mapping analysis. Identification of robust markers linked to important agronomic traits is critical for marker-assisted breeding practice. In addition to the availability of robust markers, high throughput genotyping cost and breeding strategies, such as population size, number of traits/markers screened, and selection strategies, should also be taken into consideration in order to efficiently implement marker-assisted selection in the practical cereals breeding programs.

Oat Kernel Density and the Physical Basis of Test Weight

Douglas C. Doehlert¹ and Michael S. McMullen²

¹USDA-ARS Wheat Quality Laboratory, Fargo, ND USA, ²Plant Sciences Department, North Dakota State University, Fargo, ND, USA.

Test weight or bulk density of oats (*Avena sativa* L.) has a major influence on the value of oat grain yet little is known about the physical basis for test weight in oats. Test weight can be attributed to a combination of kernel density and packing efficiency. We have measured oat kernel volume and density by a sand displacement method, and thus derived the packing factor for six oat cultivars grown in three environments. Kernel volumes ranged from 31 to 38 mm³, were highly correlated with kernel mass. Kernel densities ranged from 0.96 to 1.03 g/cm³. Packing efficiency, which is defined as the percentage of the volume of a container occupied by the grain, ranged from 53 to 55%. Both values exhibited genotypic and environmental variation. Regression analysis suggested that 78% of the variation in test weight could be attributed to kernel density and most of the remaining variation could be attributed to the packing efficiency. Size fractionation of grain by sieving and size analysis by digital image analysis indicated that smaller kernels packed more efficiently than larger kernels within an oat sample, and larger kernels in a sample were less dense than the smaller kernels. Analysis of oat kernel components indicated groat densities were about 1.3 g/cm³ and hull densities were about 0.7 g/cm³, with very little genotypic variation in these traits. However, the sum of groat and hull volumes were consistently less than that of whole kernels, suggesting the presence of empty space within the hulls, which could profoundly affect test weight. The difference in densities of groat and hull provide the physical basis for the recognized relationship between groat percentage and test weight.

Enhancing Oat End Product Quality

Dr. Nancy Ames

Agriculture and Agri-Food Canada, 195 Dafoe Road, R3T 2M9
Winnipeg, Manitoba, Canada. names@agr.gc.ca

Development of oat cultivars using specific end product characteristics as part of the screening criteria is in its early stages, relative to other crops such as wheat and corn that have long been a staple in the human diet. Traditionally, oat improvement programs have focused on agronomic characteristics first, testing a limited scope of quality characteristics once the breeding material is at an advanced stage of development. With the increase in human oat consumption in recent years, quality aspects of oat products are becoming more clearly defined. Oat mills that supply the food industry with oat flakes, flour and oat fractions, are close to consumers in the value chain and have gained an understanding of consumer preferences for oat products through customer feedback and sensory evaluation. Information defining oat end product quality will be valuable to breeders, but it is just the first step towards going beyond traditional oat breeding priorities. If end-product quality is to become a true breeding priority it needs to start in early generations. Traditionally, breeders select for agronomic suitability early on, waiting several generations before selecting for quality attributes even if a quality based trait such as β -glucan is a major objective. This reduces the numbers advanced but means poor quality lines are carried forward unnecessarily. Greater improvements in quality could be made if end product quality could be tested earlier.

Understanding oat end product quality from both a sensory and nutritional perspective is a major focus of the cereal chemistry research at the AAFC, Cereal Research Centre. Efforts have been made to bridge gaps between new germplasm development and consumer benefits by developing small scale processing equipment and rapid screening methodologies for streamlining the evaluation of oat breeding lines for end product quality throughout the breeding process. Some aspects of food quality are already being considered by breeders but techniques often need to be reassessed in order to ensure that the accuracy and volume capacity are sufficient to make progress. For example, an ELISA method for measuring β -glucan has recently been developed at the Cereal Research Centre. Implementing this technique into breeding programs would increase the number of samples that could be tested and reduce the sample requirement, which is ideal for early generation selection. The research work presented here will focus on methodologies to test the small quantity of seed available at the early generation stages of plant breeding with emphasis on methods that measure key oat milling and end-product characteristics as well as nutritional quality.

References:

- Ames, N. and Rhymer, C. 2003. Development of a Laboratory-Scale Flaking Machine for Oat End Product Testing. *Cereal Chem.* 80(6):699-702.
- Rampitsch, C., Ames, N., Storsley, J., and Marien, L. 2003. Development of a monoclonal antibody-based enzyme-linked immunosorbent assay to quantify soluble β -glucans in oats and barley. *J. Americ. Food Chem.* 51:5882-5887.
- Rampitsch, C., Bizimungu, B., Ames, N. and Rothwell, L. 2006 Early generation β -glucan selection in oat using a mono-clonal antibody-based enzyme-linked immunosorbent assay. *Cereal Chemistry* (Accepted).
- Rhymer, C., Ames, N., Malcolmson, L., Brown, D. and Duguid, S. 2005. Effects of genotype and environment on the starch properties and end-product quality of oats. *Cereal Chem.* 82:197-203.

Avenanthramides in Oat (*Avena sativa*), a Value Added Phytonutrient

Mitchell L. Wise

USDA, ARS, Cereal Crops Research, Madison WI 53726. E-mail: mlwise@wisc.edu.

Avenanthramides are polyphenolic alkaloids produced uniquely in oat. These metabolites stem from the phenylpropanoid and anthranilic acid biosynthetic pathways. Although numerous avenanthramides have been described, the three principal forms found in oat are conjugates of 5-hydroxy anthranilic acid and either *p*-coumaric, ferulic or caffeic acid (termed avenanthramide A, B and C respectively)¹. Recent studies have shown that these phytonutrients can reduce exercise induced muscle inflammation in rats². Detailed analysis using cellular model systems have also demonstrated potent anti-atherosclerotic properties as well^{3, 4}. Thus, there are likely health benefits from consuming oat with high avenanthramide content. In plants the avenanthramides are found primarily in leaf tissue, in response to fungal infection by the crown rust organism *Puccinia coronata*, and in the grain. In most oat cultivars all three avenanthramides are found in the grain; however the proportions and absolute quantities are highly variable depending on cultivar and growth environment^{5, 6}. To investigate the signaling mechanisms eliciting their biosynthesis and the metabolic flux in this novel biosynthetic pathway we have developed a cell suspension system responsive to chitin elicitation; that system will be described.

References

1. Collins, F. W. 1989. Journal of Agriculture and Food Chemistry 37: 60.
2. Ji, L. L., Lay, D., Chung, E., Fu, Y., and Peterson, D. M. 2003. Nutrition Research 23: 1579.
3. Nie, L., Wise, M. L., Peterson, D., and Meydani, M. 2006. Free Radical Biology & Medicine, in press.
4. Nie, L., Wise, M. L., Peterson, D. M., and Meydani, M. 2006 Atherosclerosis, In Press.
5. Dimberg, L. H., Molteberg, E. L., Solheim, R., and Frolich, W. 1996 Journal of Cereal Science 24: 263.
6. Emmons, C. L. and Peterson, D. M. 2001. Crop Science 41: 1676.

Key Words: Avenanthramides, atherosclerosis, biosynthesis, oat suspension culture,

β -Glucan Content and Variance in Crosses Between High β -Glucan and Elite Agronomic Lines

Alona Chernyshova

Iowa State Univ., Ames IA

β -Glucan in oat (*Avena sativa* L.) grain is primarily responsible for the beneficial effect of oat fiber on lowering blood serum cholesterol levels in humans. The objectives of this study were to estimate the genetic components of variance in β -glucan concentration and viscosity in high β -glucan lines, elite agronomic lines, and variance in their crosses. The second objective was to evaluate the differences between elite agronomic lines and high β -glucan lines for β -glucan and viscosity. The third objective was to use a more powerful mating design to detect epistatic interaction among parents. A North Carolina Design II was used for the experiment to cross twelve inbred lines of high β -glucan concentration with twelve inbred lines with good agronomic performance. The $F_{3:4}$ generation was evaluated in a field experiment in 2005 at two Iowa locations and oat grain was analyzed in the laboratory for the β -glucan traits.

**Organic Market Opportunities:
Value-added Marketing for High Beta-glucan Oat Varieties**

Kathryn Begeal and Brittin Eustis

Ceres Organic Harvest, Inc., Organic Grain and Milling, Inc.
Clyde, ND

Organic Grain and Milling, Inc. (OGM) is a North Dakota owned elevator based out of Clyde, ND that handles grain procurement for Ceres Organic Harvest, Inc., its parent company. OGM has an exclusive license from the NDSU Research Foundation for organic production, processing and marketing of the oat cultivar, HiFi. Since 1992, Ceres has specialized in developing strategic relationships between growers and manufacturers and has pioneered the organic semolina market with several North Dakota mills. Ceres Organic and OGM also work with organic spring wheat, barley and oats. Both OGM and Ceres value the sustainability in organic agriculture and work hard to cultivate fair relationships with growers and other business partners.

OGM will market the HiFi oat as a “value-added” premium organic oat to both manufacturers and processors of organic oat products. OGM will take a branded approach to market the variety and focus on the variety’s higher beta-glucan content of 6.0%. OGM will publicize the well-known cholesterol reducing benefits of beta-glucan and highlight the polymer’s role as an immune system stimulant and glycemic level regulator. The organic market is a prime place to introduce high beta-glucan oats to the consumer and high beta-glucan oats can give manufacturers a credible competitive advantage to differentiate their products.

Feeding Value of Oats in Livestock Diets

Greg Lardy

Animal and Range Sciences Department, North Dakota State University, Fargo, ND 58105;
Phone: 701.231.7660; Fax: 701.231.7590; E-mail: glardy@ndsuext.nodak.edu

Oats are a commonly used feed for many classes of livestock. Oats contains approximately 13% CP and 78% TDN. Oats is lower in energy than other common cereal grains due to the presence of the hull, which typically remains attached to the kernel during threshing. The hull of the oat kernel makes up 24 to 30% of the weight. For livestock feeding, quality is generally determined by bushel weight, with heavier oats have greater levels of energy. Test weight is dependent on size of the groat (whole seed minus the hull) and kernel plumpness. Oats are a useful feed grain in many livestock feeding applications. Oats is a preferred feed among horse enthusiasts and heavy test weight oats is commonly marketed as “race horse” oats in many parts of the country. In beef cattle production, oats is used in creep feeds and in receiving diets for beef calves following weaning. Oats are an easy grain to feed due to the high hull and fiber content, which generally limit digestive disturbances, founder, and acidosis in beef and dairy cattle. In recent years, oat breeding programs have developed hull-less oat varieties. The grain from these varieties contains greater levels of nutrients and is higher in digestibility than conventional varieties. In many cases, cost limits inclusion levels of oats in diets for beef and dairy cattle, as well as swine, since the oat market for horses is typically priced at a premium relative to other species.

References

- Johnson, L. and S. Boyles. 1991. Oats as a feed for beef cattle. AS-1020. NDSU Extension Service. <http://www.ext.nodak.edu/extpubs/ansci/beef/as1020w.htm>
- NRC, 1996. Nutrient Requirements of Beef Cattle. Seventh revised edition. National Academy Press, Washington, D.C.
- Zinn, R. A. 1993. Influence of processing on the feeding value of oats for feedlot cattle. *J. Anim. Sci.* 71:2303-2309.

Key Words: Cattle, Energy, Horses, Livestock, Oats, Protein

Bayesian Modeling Of Heterogeneous Error and Genotype by Environment Interaction Variances: Model Assessment

Massiel Orellana

Iowa State Univ., Ames IA

Identifying plant varieties that provide superior performance for growers across a wide range of growing conditions is a very important and expensive task. Varieties must be evaluated in many environments and performance data summarized in order to identify not only the best varieties, but also those with the most stable performance. Edwards and Jannink, in a previous work, used a Bayesian approach to estimating heterogeneous error and genotype by environment interaction variances applied to yield data from the Iowa State University Oat Variety Trial for the years 1997 to 2003. The objectives were i.) to take advantage of technological advantages in statistics and computing in order to provide more precise rankings of experimental varieties, and ii.) to provide a more precise method for identifying varieties that provide stable performance across varying environmental conditions. In this work we perform a model assessment, i.e., we test whether or not the heterogeneous variance model really provides better predictors of cultivar performance. We used two approaches: Cross-Validation and Posterior Predictive Checking. The first one is a widely used method for estimating prediction error. We set aside a validation set and use it to assess the performance of our prediction model. The second method is a Bayesian approach, where simulated values are drawn from the posterior predictive distribution of replicated data and then compared to the observed data. The dataset has a total of 34 environments and 80 total genotypes, with 40 tested in each year; some genotypes were tested in all years.

Towards a global strategy for the *ex situ* conservation of oat genetic resources

Christoph U. Germeier¹, Lothar Frese¹ and Brigitte Laliberte²

¹ Federal Centre of Breeding Research on Cultivated Plants, Bundesallee 50, 38116 Braunschweig, Germany, Email: c.germeier@bafz.de, l.frese@bafz.de.

² Global Crop Diversity Trust, c/o International Plant Genetic Resources Institute, Via dei Tre Denari 472/a, 00057 Maccarese, Rome, Italy, Email: b.laliberte@cgiar.org

About 220,000 accessions of oats in *ex situ* collections have been estimated in the state of the world's plant genetic resources report (FAO 1996). Large collections are held by the USDA (ca. 20,000 accessions), the PGRC (ca. 30,000 accessions) and within the European ECP/GR framework (more than 34,000 accessions). For those about 90,000 accessions documentation is easily accessible in the internet. Further large collections have been mentioned in Kenya (13,000 accessions), Israel (7,500 accessions) and Australia. Though the East Asian sub-region is known as a diversity center for the interesting naked forms, only 1,500 oat accessions are mentioned for China in the World report. More recent sources mention 3,171 accessions in China (Xu, 2002) and 1,336 in Mongolia (Altansukh 2002).

The Global Crop Diversity Trust is supporting through a series of consultations and studies the development of a set of conservation strategies that will guide the allocation of resources to the most important and needy crop diversity collections. One of the strategies being initiated is a global strategy for the *ex situ* conservation of oat genetic resources. The objective is to develop and implement the most cost efficient and effective ways for ensuring the long-term conservation and availability of oats germplasm. This process is largely driven by experts and holders of genetic resources of oats and began with a preliminary period of research into the state of diversity in the collections of that crop by an expert consultant, with assistance from IPGRI and FAO. To get an updated and more differentiated information basis, the extent, status and development potential of the world's oat collections will be surveyed by questionnaires. Results will be presented. An important issue within global conservation strategies is improving effectiveness of conservation and use by building networks of international cooperation. A precondition is easy access to integrated information systems. The European *Avena* Database (<http://eadb.bafz.de>) will be presented as an example. Reference to other integrated information systems on oat genetic resources, e.g. Pedigree of Oat Lines (<http://avena.agr.gc.ca/OGIS>), provided by the Eastern Cereal and Oilseed Research Centre, Canada, GrainGenes (<http://wheat.pw.usda.gov/GG2>) of the USDA Agricultural Research Service and other molecular databases will be given and suggestions for an integration of oat genetic resources information will be made.

Altansukh N. (2002): Plant genetic resources status and progress of activities in Mongolia. In: Zhang Z., Zhou M. and V. Ramanantha Rao (Eds.). Plant genetic resources network in East Asia. Proceedings of the meeting for the regional network for conservation and use of plant genetic resources in East Asia. 13-16 August 2001. Ulaanbataar, Mongolia. IPGRI Office for East Asia, Beijing, China.

FAO (1996): The state of the world's plant genetic resources for food and agriculture. Background documentation prepared for the International Technical Conference on Plant Genetic Resources Leipzig, Germany 17-23 June, 1996

Xu L. (2002): The status and progress on plant genetic resources in China. In: Zhang Z., Zhou M. and V. Ramanantha Rao (Eds.). Plant genetic resources network in East Asia. Proceedings of the meeting for the regional network for conservation and use of plant genetic resources in East Asia. 13-16 August 2001. Ulaanbataar, Mongolia. IPGRI Office for East Asia, Beijing, China.

Results of a Phenotypic Characterization of a Large *Avena sativa* Germplasm Collection

Axel Diederichsen

Plant Gene Resources of Canada (PGRC), Agriculture and Agri-Food Canada, 107 Science
Place, Saskatoon, Saskatchewan, S7N 0X2, Canada
e-mail: diederichsena@agr.gc.ca

Plant Gene Resources of Canada (PGRC) maintains more than 11,000 accessions of hexaploid cultivated oat, *Avena sativa* L. s.l., which includes common oat, hull-less oat and red oat. This study quantifies the genetic diversity in the PGRC *A. sativa* collection by measuring the *richness*, i.e. the number of distinct morphological groups, and the *evenness*, i.e. the frequency of representation of morphological groups of *A. sativa* in the PGRC oat collection. Qualitative morphological characteristics indicating genetic differences were used as descriptors in *A. sativa* during field regeneration at Saskatoon, Saskatchewan, Canada, in 1999-2004. Each of 10,105 accessions with complete characterization data for eight characters were assigned to one morphological group based on the combination of character expressions observed in the respective accession. The 10,105 accessions included 8754 accessions of common hulled oat, 183 accessions of hull-less oat and 1168 accessions of red oat. They represented 113 different morphological groups which are also genetically different. The number of accessions in each group ranged from 4820 accessions in the most frequent morphological group to one accession in the groups number 84-113. In other words, the distribution was very uneven as the most frequent morphological group included 48% of the accessions, and the 13 most frequent morphological groups cover already 90% of the accessions. The characterized germplasm included 126 Canadian oat cultivars released since 1866 which represented 10 different morphological groups and included 112 hulled and 14 hull-less cultivars. When considering separately Canadian cultivars released within each of the past eleven decades, there was no change in relative number of morphological groups over time visible, however, a strong correlation of the number of cultivars released within a decade and the number of morphological groups represented in each decade ($r=0.86$) was found. Thus, the morphological diversity in Canadian oat cultivars has not decreased over time. The grouping is useful for collection management regarding acquisition of new germplasm, identification of rare germplasm or gaps in the collection, and for establishment of a core collection. All characterization data is available via the Internet (<http://www.agr.gc.ca/pgrc-rpc>).

AFLP Variation in Cultivated Oat Germplasm Collection

Yong-Bi Fu

Plant Gene Resources of Canada, Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada, Phone: 306-956-7642, Email: fuy@agr.gc.ca

An attempt was made to characterize a structured sample representing a world collection of 11622 cultivated hexaploid oat accessions with the hope to understand the genetic structure of the world collection. AFLP technique was applied to screen 670 accessions representing 79 countries and one group of uncertain origin. Analyses of the AFLP data showed the effectiveness of the stratified sampling applied in capturing country-wise AFLP variation. The majority (89.9%) of the AFLP variation resided within accessions of each country, and only 6.2% AFLP difference existed among accessions of major geographic regions. Accessions from the Mediterranean region were the most distinct and from Russia and USA were the most diverse. Two distinct groups observed were separated largely by common oat and red oat. Red oat was genetically more diverse than common and hull-less oats, and hull-less oat was more related to common oat than red oat. Landrace and non-landrace accessions displayed similar AFLP variation. These patterns are significant for understanding the domestication of cultivated oat and are useful in classifying intraspecific diversity of oat germplasm, developing specific core subsets of the oat collection, and exploring new sources of genes for oat improvement.

References

Fu, Y.B., Peterson, G.W., Williams, D., Richards, K.W., and Mitchell Fetch, J. 2005. Patterns of AFLP variation in a core subset of cultivated hexaploid oat germplasm. *Theoretical and Applied Genetics* 111: 530-539

Key Words: Cultivated oat, core collection, AFLP, oat domestication

A Graphical Web-Based Database of Oat Molecular Markers

Diane Bergeron, Charlene Wight, Hai Pham, Nick Tinker
ECORC, AAFC, 960 Carling Ave. Ottawa ON K1A-0C6 Canada.

Our laboratory has conducted a survey of RFLP loci on a panel of oat mapping parents and other diverse oat germplasm. These data provide a useful resource for planning or interpreting new experiments that are based on these RFLP markers. Unfortunately, these data are sometimes difficult to interpret because the images have not been annotated extensively enough to show the relationships between the graphical electrophoretic patterns and the numerical scores that have been derived from these patterns. The segregation patterns of many RFLPs reveal several loci, often with overlapping migration distances, and interpretation can be confusing. Part of the problem is that we are dealing with two very different types of data: numerical allele scores and bit-mapped images. What is needed is a consistent link between interpreted allele scores and the objects in the images that have been interpreted. We have taken a novel approach to solving this problem using a new software package called GELATO (Diane Bergeron, thesis in preparation). Instead of storing graphical images, GELATO stores the interpreted data in a way that enables virtual reconstruction of the original electrophoresis patterns. Furthermore, these “virtual gels” can be reconstructed to show segregation patterns of any subset of varieties in any order – as long as records of the varieties are present in the database. This feature is convenient because it facilitates side-by-side comparison of two varieties even if they originally appeared on two separate gels. Here we present a set of data from an RFLP survey in oat that has been recorded using GELATO. Data from this survey are available at “<http://avena.agr.gc.ca/GELATO/>”, and demonstrate the ability of GELATO to provide a useful, on-line data repository that can be queried by any user through a simple web-based interface. This resource may be expanded in future to provide access to additional molecular marker data from oat. Details of the GELATO software and use of GELATO to construct a new database will be presented elsewhere at a later date.

Evaluation of Oats for Reaction to Fusarium Head Blight

W. Cao, G. Fedak, A. Xue and M. Savard

ECORC, Agriculture and Agri-Food Canada
960 Carling Ave. Ottawa, ON Canada K1A 0C6

Fusarium head blight affects (FHB) wheat and barley production by reducing grain yield and quality and contaminates grains with deoxynivalenol (DON). The disease has been observed attacking oat in several cases in eastern Canada, producing up to 15 ppm of DON in the harvested grains. The objective of this study was to evaluate oat cultivars for Fusarium head blight resistance in an FHB nursery. One hundred oat cultivars or advanced lines were collected from University of Saskatchewan, ECORC and oat breeding programs in United States. The experiment was conducted with a randomized complete block design with two replications. A single row plot with one meter length and 30 cm spacing was used. Plots were inoculated at booting stage with infected corn and barley grains and irrigated twice for 30 minutes each day (morning and afternoon). FHB incidence was rated at 21 days after flowering. Plots were trimmed before harvesting. A half meter of the plots was harvested for yield and DON analysis. A correlation analysis indicated that FHB incidence had a negative correlation with plant height with a coefficient -0.45, but it was not correlated with grain yield. It appears that the level of FHB development this year was not severe enough to affect yield of oat. Probably this was caused by the late application of inoculum. Therefore, this experiment needs to be repeated next summer with some modifications: 1) Inoculation will be applied at tiller stage; 2) FHB symptom will be rated at 14 days after flowering instead of 21 days.

Key Words: Oats, Fusarium head blight, deoxynivalenol

Virulence in US crown rust populations from 2001-2005

M. L. Carson and G. E. Ochocki
USDA-ARS Cereal Disease Lab, St. Paul, MN 55108

A total of 680 single uredinial isolates of oat crown rust, *Puccinia coronata*, were collected from cultivated and wild oat (*Avena sativa* and *A. fatua*, respectively) in the major oat production areas of the United States from 2001 through 2005. They were tested for virulence on seedlings of differential oat lines in the greenhouse. A total of 171 races were found among the 357 isolates from the winter oat region of the US, whereas 212 distinct races were found among 323 isolates from the spring oat region. The crown rust population derived from winter oat in the southern US was significantly differentiated from the spring oat population in the upper Midwest. Although there was no virulence unique to either population, only 45 of the 338 races found in this time period were found in both regions. Virulence to *Pc48* and *Pc52* increased significantly in both regions during the 2001-2005 time period. Virulence to *Pc59* increased and virulence to *Pc53* decreased in the winter oat region during the same period. Most of the virulence associations reported by Leonard et al (2005) in the US oat crown rust population in the early 1990's were also found in this survey. The virulence of crown rust isolates in the U.S. increased significantly from 2001 to 2005, indicating that virulence to *Pc* genes derived from *A. sterilis* appears to be accumulating in the crown rust population much as what previously happened to *Pc* genes from *A. sativa*. Much of the virulence diversity in the oat crown rust population in the United States can be related to the deployment of resistance genes in commercial oat cultivars and virulence associations existing in the oat crown rust population.

Molecular Mapping of the *Dw6* Dwarfing Locus

Julie Chapados¹, Solomon Kibite², Bonnie Bancroft¹, and Stephen J. Molnar¹

¹Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, Central Experimental Farm, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada.

²Lacombe Research Centre, Agriculture and Agri-Food Canada, 6000 C & E Trail, Lacombe, AB T4L 1W1, Canada. (in memorium)

In crosses involving multiple height modifying genes, deducing the genotype of intermediate height plants can be a challenge. Molecular markers linked to each locus could be used diagnostically in such situations. In this study, a set of seven pairs of Near Isogenic Lines (NILs) (Kibite 2001) contrasting for the *Dw6* dwarfing gene were investigated. Random genotyping of these NILs with Amplified Fragment Length Polymorphism (AFLP) markers demonstrated that on average there remained approximately 5% residual heterozygosity between the tall and short lines constituting a NIL pair, much higher than the 0.4% expected from classical theory. However, very few of the heterozygous regions would be expected to be common to all seven NIL pairs, except for the region flanking the *Dw6* locus. Therefore the NILs were used to test for correlation between tall/dwarf phenotype and polymorphic genotype using Restriction Fragment Length Polymorphism (RFLP) and other markers selected from candidate regions of the Kanota x Ogle map (Wight et al 2003). Additional candidate markers were identified by comparative mapping with the Terra x Marion map (De Koeber et al 2004). This strategy located *Dw6* to a small chromosomal region on Kanota x Ogle linkage group 33, near RFLP loci *cdo1428b*, *bcd421b* and *aco227di*. These and other tightly linked markers have potential for marker assisted breeding.

De Koeber et al (2004) A molecular linkage map with associated QTLs from a hulless x covered spring oat population. *Theoretical and Applied Genetics* 108: 1285-1298.

Kibite (2001) Registration of seven pairs of oat near-isogenic lines, dwarf vs tall. *Crop Sci.*41: 277-278.

Wight et al (2003) A molecular marker map in Kanota x Ogle hexaploid oat (*Avena* spp.) enhanced by additional markers and a robust framework. *Genome* 46: 28-47.

Pedigrees of Oat Lines (POOL): Updates and Usage

Jitka Deyl and Nick Tinker

Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada,
Central Experimental Farm, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada.

We recently described a resource called “Pedigrees of Oat Lines” (POOL; Tinker and Deyl, *Crop Sci.* 45: 2269–2272), which can be accessed at <http://avena.agr.gc.ca/>. This Internet resource is intended to document the ancestry, origin, and characteristics of cultivated and historical varieties of oat. Although POOL contains information about uncultivated germplasm and wild oat relatives, this is included primarily to document the breeding history of cultivated oat. Thus, this database complements the databases provided by many oat germplasm banks, which contain rich documentation of available germplasm, but sparse information about breeding history of modern cultivated varieties. An important feature of POOL is an extensive thesaurus of names, synonyms, and numeric identifiers, each attached to a unique identifier for a unit of germplasm. Alternate identifiers include foreign names, abbreviations, pre-registration identifiers, and gene bank identifiers. Another important feature is an extensive documentation of reference material used in the assembly of the database.

Curation of this database is an ongoing project. It includes the addition of new oat varieties as well as further research to document older varieties and reconcile inconsistency and redundancy. Data is gathered from new and old publications as well as online resources, personal communications, and gene banks. POOL presently contains 42,316 names and synonyms for 17,431 unique entries. Although the database was originally developed for AAFC use, the content of POOL is increasingly international in scope. Recent improvements to the web interface enable access to references and comments that were not previously accessible. The database now resides on a high-performance server that accelerates the execution of queries returning large pedigrees. Usage of POOL has increased dramatically since publication. Typically there are 248 new visitors per month and 141 repeat visitors; an average visit lasts 8 minutes. Thus, POOL has become a popular Internet resource, which we attribute to its uniqueness, global relevance, easy access, and user-friendliness.

Molecular markers for the oat stem rust resistance gene *Pg16*

P. Eckstein¹, T. Fetch², D. Hay¹, T. Zatorski¹, B. Rossnagel¹, G. Scoles¹

¹Department of Plant Sciences/Crop Development Centre, University of Saskatchewan
Saskatoon, SK, CANADA, S7N 5A8, e-mail: graham.scoles@usask.ca. ²Cereal Research
Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB, CANADA, R3T
2M9, e-mail: tfetch@AGR.GC.CA.

The oat stem rust resistance gene *Pg16* is effective against many races of *Puccinia graminis* f. sp. *avenae*, including race NA67. This gene was stably introgressed into hexaploid oat from *Avena barbata* Pott. collection D203 by Brown et al (1986), and is the same source of *Pg16* resistance used in current breeding germplasm. We have identified tightly linked molecular markers for *Pg16* through bulked-segregant RAPD analysis of 100 F₄ derived F₅ RILs from the cross W99162 (resistant) x Ronald. Five 10-mer primers (OPB20, UBC110, UBC172, UBC297, UBC331) produced six polymorphic fragments which co-segregated with the resistance. The polymorphic fragments were amplified from DNA of the resistant parent, failed to amplify from the susceptible parent, and were 100% linked with the disease reaction of lines homozygous for resistance/susceptibility. All six fragments were isolated from the resistant parent and sequenced. The 1100bp fragment produced by primer OPB20 was chosen for conversion to a PCR-based MMAS friendly marker. Primers complementary to the ends of the fragment produce a robust single band from DNA of resistant genotypes, while failing to amplify any fragments from susceptible genotypes. Linkage between the marker and the resistance gene was identical to that of the RAPD fragments. Attempts to locate the gene to an oat genetic map have failed since the fragment is not produced in either the Kanota/Ogle or the Marion/Terra mapping populations. This, combined with the 100% co-segregation, suggests that the polymorphic fragments are being generated from a piece of unique DNA originating from *A. barbata*. The marker is being tested on additional lines from the same cross, and an additional cross (OT399 x OT2030), to confirm linkage estimates.

References

Brown, P.D., Forsberg, R.A., McKenzie, R.I.H., and Martens, J.W. 1986. The use of disomic alien addition lines in the transfer of oat stem rust resistance to hexaploid oats. In: Lawes, D.A. and Thomas, H. (eds.). Proc. 2nd Int. Oat Conf., Dordrecht, Netherlands. pp16-20.

Key Words: oat, stem rust resistance, NA67, molecular marker

**Enlargement of PCR-based marker resources in oat by surveying
genomic-derived SSRs from barley and wheat**

Gongshe Hu, Robert Campbell, Eric Jackson, and J. Michael Bonman

USDA-ARS, Small Grains and Potato Germplasm Research Unit, 1691 South 2700 West,
Aberdeen, Idaho 83210

Simple sequence repeats (SSRs), a relatively new generation of DNA markers, are developing rapidly in most crop species. SSR's are advantageous because they are present in large numbers, are evenly dispersed, and are highly polymorphic. Oat lacks of SSR markers due limited investment in developing genomic and genetic resources in *Avena*. To search for an alternative means to enlarge the SSRs pool in oat, we surveyed 356 genomic derived SSR markers from wheat and barley chosen to based on even dispersal across different chromosomes. These were tested for amplification and polymorphisms in parental lines of the main mapping populations of oat; TAM O-301, Ogle1040, Kanota156, and Ogle157. Eighty-nine of 210 wheat SSRs (42%) and fifty six of 156 barley SSRs (38%) successfully amplified in oat. At least 60 markers (39% of the amplified markers and 18% of total markers) showed polymorphism between the parental lines of at least one mapping population. The percentage of polymorphic SSRs among the amplified primers is comparable to that for oat-derived SSRs in published data. Work is underway to determine if the polymorphic SSRs from the Ogle X TAM O-301 population can be mapped. The survey results indicate that genomic SSRs from wheat and barley may be good sources of SSR markers for oat genetics research. The genomic relationships regarding DNA marker amplification provides clues for adapting of other types of DNA markers, such as SNPs, from barley and wheat to oat in the future.

Stabilizing naked oats with infrared roasting and the effects on groat quality

Hu, Xin-Zhong¹, J. Frégeau Reid² and V. Burrows²

¹College of Food Science & Engineering, Northwest A & F University, Yangling, Shaanxi, P R China, 712100 email: hxinzhong@yahoo.com. ²Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-food Canada, KW Neatby Building, 960 Carling Avenue, Ottawa, Ontario K1A 0C6 Canada. Correspondance email: fregeauja@agr.gc.ca

Naked oats are the preferred oats in China for food applications but there are still limited choices of products. The usual treatment for stabilizing groat is with steam. Another treatment that could be used is infrared roasting also named micronizing where tempered groats are exposed for a short period to very high temperatures, effectively vaporizing water to steam within the grain and inactivating the enzymes. The objectives of this research were 1) to compare different deactivation methods including steaming, autoclaving, dry heat roasting and infrared micronizing and 2) to micronize several naked oat lines and study the effects of the treatment on the quality of grains. The results showed that lipase and peroxidase activities of raw oats were removed following treatment by steaming, autoclaving and micronizing. Dry heat roasting treatment can not deactivate these enzymes. Size of kernels can influence the treatment protocol required to stabilize groats; small kernels have higher levels of lipase and peroxidase activities than larger kernels and longer times were needed to obtain deactivation. Steaming and autoclaving stabilized groats in 20 min and 10min respectively. Micronizing can achieved the same effect with 15 sec of applied infrared heat followed by a resting period in a holding insulated tank. One of the advantages of micronizing is the potential of improving the flavor of groats which could be used in developing new food products.

Key Words: naked oat, stabilizing, infrared roasting, micronizing

A detached leaf method for cereal rust disease studies.

E. W. Jackson¹, J. Chong², J. B. Avant¹, and J. M. Bonman¹.

¹USDA-ARS, Small Grains and Potato Germplasm Research Unit, 1691 S. 2700 W., Aberdeen ID 83210; ²Cereal Research Centre, Agriculture & Agri-Food Canada, Winnipeg, MB, Canada R3T 2M9

Cereal rust pathogens have complex race structures and are obligate biotrophs with wind disseminated propagules. These characteristics make propagation of single-race cultures difficult in environments where multiple races are present. In this study an isolated propagation system using detached leaves was developed with the oat crown rust pathosystem. The utility of the system for propagating other cereal rust pathogens and studying crown rust resistance was also examined. Oat leaves were cut into 10-cm sections, disinfested with 0.5% NaOCl for 5 min, and rinsed in sterile ddH₂O. Leaf sections were then suspended in plastic boxes by enclosing 3.5 cm of each leaf section end between 4% agar blocks amended with various chemical constituents. The exposed 3-cm portions were inoculated in an aseptic hood with *Puccinia coronata* urediniospores suspended in water. Boxes were sealed and incubated in a lighted growth cabinet at 21°C until sporulation. Experiments testing agar amendments indicated that 100 mg L⁻¹ 6-benzylaminopurine (BAP) and 10 mg L⁻¹ Chlorothalonil maintained green leaves longer, resulting in more viable spores. Initial results with *P. graminis* f. sp. *avenae*, and *P. triticina* indicate viable urediniospores can also be produced on detached leaves of the respective host. Using the detached leaf method, 16 differential oat cultivars inoculated with two isolates showed the same reactions as whole plants screened under standard conditions in a growth chamber. The detached leaf system will improve propagation of single-race cultures and should be useful in developing an *in vitro* system for identifying and studying resistance to cereal rust pathogens.

Oat Information in GrainGenes

Gerard R. Lazo¹, David E. Matthews^{1,2}, Victoria Carollo^{1,3}, and Olin D. Anderson¹

¹ USDA-ARS, Western Regional Research Center, Albany, CA 94710-1105 USA

² USDA-ARS, Dept. of Plant Breeding, Cornell University, Ithaca, NY 14853 USA

³ Plant Science & Plant Pathology, Montana State University, Bozeman, MT 59717 USA

The GrainGenes database and website (<http://wheat.pw.usda.gov>) exist to serve the small grains community including oat. In recent years the database has seen a rapid increase in genome data for the cereals. Much of this information, regardless of the plant origin, is of general utility in research on oat, Triticeae, and related grass species. Recent changes in the GrainGenes database structure and software have expanded its capacity to display genome map, molecular marker, QTL, and phenotype data. Features such as the CMAP display can aid in building consensus maps for the linkage groups of oat. Recently added oat data includes the "AM" SSR markers, 1000 oat EST sequences, the MN841801-1 x Noble-2 map, and results from oat performance nurseries. GrainGenes also provides links to resources like Howard Rines' inventory of oat markers, and a site for the online Oat Newsletter. The "oatmail" mailgroup, maintained by Nick Tinker, provides a forum for discussions and announcements of community interest; see <http://greengenes.cit.cornell.edu/oatmail.html> for information. The GrainGenes website also maintains pages for developing "Quick Queries" or "Advanced Queries" for the database. Feedback from the users of GrainGenes helps to guide the type of information maintained and the building of services needed to supply information to the community.

QTLs Affecting Heading Date in Oat Under Short Day Conditions.

Ana Locatelli¹, Luiz C. Federizzi², Sandra C. K. Milach¹, Charlene P. Wight³, Stephen J. Molnar³, Julie T. Chapados³, Nicholas A. Tinker³.

¹Pioneer Sementes Ltda., Paissandú 582, P.O.Box 72, Passo Fundo, 99.010-100, Brazil. ²Federal University of Rio Grande do Sul, Caixa postal 776, CEP 91.501-970, Porto Alegre, RS, Brazil.

³AAFC, CEF, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada.

Time to heading (flowering) is an important characteristic in crop plants that affects adaptation to cropping cycles and growing seasons. The objectives of this study were to identify molecular markers associated with heading date in three oat populations developed from Brazilian oat varieties and to compare their map locations with those of other loci that may influence time to flowering. Heading date was studied in recombinant inbred lines (RILs) from the hexaploid oat populations UFRGS 8 x Pc68/5*Starter, UFRGS 881971 x Pc68/5*Starter, and UFRGS 8 x UFRGS 930605. Bulked segregant analysis using AFLP was followed by selective mapping in each population and in a reference population, 'Kanota' x 'Ogle' (KxO). One QTL with major effects on heading date was identified in each cross. Comparative mapping showed that a major QTL with earliness alleles originating from UFRGS 8 and UFRGS 881971 is in a region with close homology to KxO group 17 and to a locus reported previously that confers daylength insensitivity in oat (*Dil*). This is the first report that identifies the map location of the *Dil* locus, and putatively confirms the presence of *Dil* alleles in new germplasm. Further comparative mapping and alignment of mapped oat markers with the sequenced rice genome suggest that this QTL and/or *Dil* may be orthologous to the *Hdl* locus in rice and the *CONSTANS (CO)* gene in Arabidopsis and other species. A different QTL with major effects segregated in the cross UFRGS 8 x UFRGS 930605, where the early allele from *Dil* was probably fixed. Two additional QTLs with smaller effects were identified in the UFRGS 8 x Pc68/5*Starter population. These results suggest that the Brazilian oat line UFRGS 8 contains an optimal set of alleles conditioning earliness under the short-day conditions of the Brazilian winter growing season, and that molecular selection could be used to introgress these alleles into other breeding material.

**Managing wild oat in tame oat through the seeding date
and seeding rate of tame oat**

May, W.E., Shirliffe, S.J. Lafond, G.P and McAndrew, D.

AAFC, Indian Head Research Farm, Box 760, Indian Head, SK, S0G 2K0

Traditionally farmers have managed their wild oat by using tillage and delayed seeding to control wild oat populations. However, yield and quality decline as planting is delayed especially after the middle of May (May et al. 2004). Many producers have now moved towards reduced- or no-till management strategies, reducing the effectiveness of delayed seeding. To make these decisions farmers need agronomic and economic information that is not currently available. Therefore a study was initiated to investigate the ability of early seeded oat to compete with wild oat using high seeding rates. Four seeding dates, early May, mid-May early June and mid-June and four tame oat seeding rates, 150, 250, 350 and 450 viable seeds m⁻² were used in the presence and absence of wild oats. The study was conducted in 2002, 2003 and 2004 at the Indian Head and Saskatoon, SK, and at Winnipeg in 2002 and Morden in 2003 and 2004. Wild oat panicle density decreased as the seeding rate increased at all locations except Saskatoon in 2003. The seed date with the highest wild oat panicle density was early or mid-May depending on the site and year. The grain yield increased as the seeding rate increased except at Saskatoon in 2003. Seed yield tended to decrease as seeding was delayed. The results from this study indicate that high seeding rates of tame oat are required to manage wild oats when seeding tame oat early in order to maximize yield and quality.

May, W.E., Mohr, R.M., Lafond, G.P., Johnston, A.M. and Stevenson, F.C. 2004. Early seeding dates improve oat yield and quality in the eastern prairies. *Can. J. Plant Sci.* 84:431-442.

Key Words: *Avena sativa*, *Avena fatua*, seeding date, seeding rate, test weight, yield

Altering the competitiveness of tame oat verses wild oat with phosphorous and seeding rate

May, W.E., and Lafond, G.P.

AAFC, Indian Head Research Farm, Box 760, Indian Head, SK, S0G 2K0

Traditionally, tillage in combination with delayed seeding has been used to control wild oat in tame oat. Recent research in oat has shown the importance of early seeding to optimise yield and quality (May et al. 2004). However, early seeding requires that any flush of wild oat emerging as the tame oat emerge must be controlled using agronomic practices since no incrop herbicide is registered to control wild oat in tame oat. High seeding rates are important for controlling wild oat in tame oat (May 2001). Phosphorous banded near the seed has promoted the early season growth in cereals (Grant 2001). The yield response of oat to phosphorous has always been tested in a weed free environment. Therefore, phosphorous fertilizer by increasing early season growth may make the oat crop more competitive resulting in higher yield and quality. Since seeding rates increase the competitiveness of oat, the effect of phosphorous needs to be measure across a range of seeding rates. The objective of this research was to determine if phosphorous place near the seed would increase the competitive ability, quality and yield of tame oat in the presence of wild oat in the field. Three rates of phosphorous 0, 15, and 30 kg ha⁻¹ and four tame oat seeding rates , 150, 250, 350 and 450 viable seeds m⁻² were used in the presence and absence of wild oats. The study was conducted in 2003, 2004 and 2005 at the Indian Head, SK on plot land that had low levels of available phosphorous in the soil. Wild oat panicles m⁻² averaged 59 in 2003, 53 in 2004 and 74 in 2005. In all three years the rate of phosphorous did not change the density of wild oat panicles. In 2004 and 2005, increasing the tame oat seeding rate decreased the density of wild oat panicles. In 2003 very little moisture was received during the growing season. In 2003, when little precipitation occurred during the growing season, the addition of phosphorous increased the grain yield of tame oat, however, there was no yield response to phosphorous in 2004 and 2005. Increasing the seeding rate of tame oat increased grain yield of the tame oat in all three years. These results indicate that seeding rate is more important than the addition of phosphorous when using agronomic practices to control wild oats in a crop of tame oat.

Grant, C.C., D.N. Flaten, D.J. Tomasiewicz, and S.C. Sheppard. 2001. The importance of early season phosphorous nutrition. *Can. J. Plant Sci.* 81:211-224.

May, W.E., Mohr, R.M., Lafond, G.P., Johnston, A.M. and Stevenson, F.C. 2004. Early seeding dates improve oat yield and quality in the eastern prairies. *Can. J. Plant Sci.* 84:431-442.

May, W.E. 2001. Oat Agronomy: Optimizing Economic Returns to Oat Producers. Final report to Saskatchewan Agriculture and Food's Agricultural Development Fund.

Key Words: *Avena sativa*, *Avena fatua*, phosphorous, seeding rate, test weight, yield

Oats with Maize Chromosome and Chromosome Segment Additions

Matthew D. Walch¹, Howard W. Rines^{1,2}, Ronald L. Phillips¹, Richard V. Kowles³, Adrian O. Stec¹, Ralf G. Kynast¹, Ron J. Okagaki¹, Morrison Jacobs¹, Mark W. Galatowitsch¹, Christina M. Schmidt¹, Paul A. Huettl¹

¹Department of Agronomy and Plant Genetics, University of Minnesota, and ¹USDA-ARS, 1991 Upper Buford Circle, St. Paul, MN 55108, ³St. Mary's University, Winona, MN. Email: rines001@umn.edu

Oat (*Avena sativa* L., $2n = 6x = 42$) plants crossed with maize (*Zea mays* L., $2n = 2x = 20$) yields both haploid oat plants and plants with one or more maize chromosomes added to a haploid oat genome. Recovery of plants requires embryo rescue following partial or full elimination of the maize chromosomes during embryo development. Doubled haploid plants may be produced either as a result of unreduced gamete formation (Rines and Dahleen, 1990) or through colchicine doubling (Davies et al., 2006). Self-fertile single maize chromosome additions to oat ($2n = 42 + 2$) have been recovered for each of the ten maize chromosomes (Kynast et al., 2004). Many of these exhibit novel phenotypes resulting from expression of maize genes present. Enzymes associated with C4 photosynthesis have been shown present in addition lines with maize chromosomes carrying genes for these enzymes, phosphoenolpyruvate carboxylase (PEPC) in a maize chromosome 9 addition and pyruvate orthophosphate kinase (PPDK) in a chromosome 6 addition (Kowles et al., 2005). Plants with both maize chromosomes 6 and 9 present are being made to test possible effects on CO₂ compensation points. No instances of enhanced resistance to oat crown rust were found in seedling tests of the set of addition lines. Expression and possible effects of maize systemic resistance genes currently are being studied in these materials. Treatment of these addition lines with gamma irradiation has allowed recovery of "radiation hybrids" with only segments of individual maize chromosome present. The maize chromosome and chromosome segment additions to oat have been distributed to more than 40 labs as valuable tools for physical mapping of maize genes and for other maize genomic studies, as well as being a possible new source of genes for oat improvement.

Kowles, R.V., J.M. Minnerath, R.L. Phillips, and H.W. Rines. 2005. Expression of C4 photosynthetic characteristics in oat-maize addition lines. 47th Maize Genetics Conf. Abstr. p.21.

Kynast, R.G., R.J. Okagaki, M.W. Galatowitsch, M.S. Jacobs, A.O. Stec, H.W. Rines, and R.L. Phillips. 2004. Dissecting the maize genome by using chromosome addition and radiation hybrid lines. Proc Natl. Acad. Sci. USA 101:9921-9926.

Rines H.W., and L.S. Dahleen. 1990. Haploid oat plants produced by application of maize pollen to emasculated oat florets. Crop Sci. 30:1073-1078.

Sidhu, P.K., N.K. Howes, T. Aung, P.K. Zwer, and P.A. Davies. 2006. Factors affecting oat haploid production following oat x maize hybridization. Plant Breed. (In press)

Key Words: Oat-maize addition lines, C4 photosynthesis

Identification of Molecular Markers for Aluminium Tolerance in Diploid Oat Through Comparative Mapping and QTL Analysis

Charlene P. Wight¹, Solomon Kibite², Nicholas A. Tinker¹, and Stephen J. Molnar¹

¹Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, Central Experimental Farm, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada.

²Lacombe Research Centre, Agriculture and Agri-Food Canada, 6000 C & E Trail, Lacombe, AB T4L 1W1, Canada. (in memorium)

The Food and Agriculture Organization of the United Nations (FAO) lists aluminium toxicity as affecting 14% of all soils worldwide. In Canada, it is a problem for cereal production in the acidic soils of Alberta. The degree of natural aluminium tolerance varies widely across cereal species, with oats (*Avena* spp.) being among the most tolerant. The objective of this study was to identify molecular markers linked to aluminium tolerance in the diploid oat *A. strigosa* which could be used for breeding hexaploid cultivated oats with enhanced aluminum tolerance. Published information on aluminium tolerance loci in wheat, rice, and other cereals was used as a guide. Restriction fragment length polymorphism (RFLP) markers were tested in genomic regions where comparative mapping with other grass species indicated the potential for orthologous quantitative trait loci (QTLs). Amplified fragment length polymorphism (AFLP) and sequence characterized amplified region (SCAR) markers were used to provide additional coverage of the genome. Four QTLs were identified. The largest QTL explained 39% of the variation and is possibly orthologous to the major gene found in the *Triticeae* as well as *Alm1* in maize and a minor gene in rice. A second QTL may be orthologous to the *Alm2* gene in maize. Two other QTLs were associated with anonymous markers. Together, these four QTLs accounted for 55% of the variation in aluminium tolerance segregating in this population. A SCAR marker linked to the major QTL identified in this study could be used to introgress the aluminium tolerance trait from *A. strigosa* into cultivated oat germplasm.

Wight, Kibite, Tinker and Molnar (2006) Theoretical and Applied Genetics 112: 222-231

Release of a High Yielding Forage Oat for Subtropical Australia

B. Winter¹, L. Song² and R. Uebergang¹

¹) Leslie Research Centre, PO Box 2282, Toowoomba, Queensland, 4350, Australia
Email: bruce.winter@dpi.qld.gov.au

²) Heritage Seeds, 22 Suscatand St, Rocklea, Queensland, 4106, Australia

Forage varieties of cultivated oat (*Avena sativa* L.) are widely grown in Australia during the winter months, providing high quality forage for cattle and sheep when native and improved pastures are dormant (Platz et al. 1992). Crown rust (*Puccinia coronata*) is a serious limitation to forage yield and quality, particularly in sub-tropical areas (Park 2000). The Queensland Department of Primary Industries and Fisheries initiated a breeding program in 1994 to develop high yielding, locally-adapted commercial varieties of forage oat with durable resistance to crown rust. Two approaches have been taken to disease resistance: 1) pyramiding of two or more genes conferring resistance to crown rust (Rooney et al. 1994; Adhikari et al. 2001), resulting in the release of 'Volta' in 2003; and 2) the use of partial resistance to crown rust (Brake et al 1992), resulting in the recent release of a new variety coded 'QA2'. QA2 is moderately susceptible to crown rust at the seedling stage, but develops moderate to high levels of resistance at the adult plant stage. Under high levels of crown rust infection, QA2 has lower infection frequency, smaller uredia and reduced sporulation in comparison with susceptible varieties. In addition, QA2 has also produced 16 – 28% more forage yield than comparable commercial cultivars in replicated multi-cut trials at two sites over two years. This high yielding, late maturity variety with partial resistance to crown rust will be available to farmers in Australia in 2007.

References

- Adhikari, K. N. and R. A. McIntosh. 2001. Identification of stem rust and leaf rust resistance genes in Amagalon oats. *Australian Journal of Agricultural Research* 52: 1011-1016
- Brake, V. M. and J. A. G. Irwin. 1992. Partial resistance of oats to *P. coronata* f sp. *avenae*. *Australian Journal of Agricultural Research* 43: 1217-1227.
- Park, R. F. 2000. Occurrence and pathogenic specialisation of *Puccinia coronata* in Australasia - 1999-2000. *Oat Newsletter*. 46.
- Platz, G. J., D. R. Woodruff, et al. 1992. Phenology of rust-resistant forage oats in sub-tropical Australia. Fourth International Oat Conference, Adelaide, Australia, International Oat Conference Committee.
- Rooney, W. L., H. W. Rines, et al. 1994. Identification of RFLP markers linked to crown rust resistance genes *Pc91* and *Pc92* in oat. *Crop Science* 34: 940-944.

Poster 17

Oatlink - progress in molecular marker identification at IGER

Tim Langdon¹, Joana Dulawa², Robert Hasterok², Sandy Cowan¹,
John Valentine¹, Catherine Howarth¹

¹Institute of Grassland & Environmental Research, Plas Gogerddan, Aberystwyth SY23 4UJ, UK

²Faculty of Biology and Environmental Protection, University of Silesia, Jagiellonska 28, 40-032
Katowice, Poland

Abstract not available

Quantitative trait loci for winter hardiness component traits in oat

David R. Wooten Jr., David P. Livingston, III, H. Jeanette Lysterly, and J. Paul Murphy

Department of Crop Science, North Carolina State University, Raleigh NC 27695
drwooten@ncsu.edu

Winter hardiness is an important limitation to winter oat (*Avena byzantina* and *A. sativa*) production in much of North America, but field evaluation of winter hardiness is difficult. The discovery of quantitative trait loci for winter hardiness should allow marker assisted selection for winter hardiness. A population of 135 recombinant inbred lines (RIL) derived from a cross between winter hardy 'Norline' and winter tender 'Fulghum' were evaluated for the winter hardiness component traits field survival, freeze tolerance, maturity, vernalization and photoperiod response. The RIL were screened with RFLP markers in regions of suspected QTL. QTL were identified with single factor analysis and multiple interval mapping using QTL cartographer. QTL for field survival, freeze tolerance, and vernalization were found on chromosomes 17 and 7C. Breeders could utilize these QTL to improve oat winter hardiness through marker assisted selection.

Key Words: Winter Hardiness QTL Freeze Tolerance Vernalization

Development of a Rapid Detection Method for Yellow Dwarf Viruses.

Mahua Deb¹ and Joseph M. Anderson²

Agronomy¹ Department and USDA-ARS², Purdue University, West Lafayette, IN 47907

Barley and Cereal yellow dwarf viruses (B/CYDVs), constitute the most economically important group of oat viruses. A multiplex reverse transcription polymerase chain reaction method was developed for the simultaneous detection and discrimination of five B/CYDVs viruses. The protocol uses specific primers sets for each virus producing five distinct fragments 294 bp, 179 bp, 238 bp, 397 bp and 331 bp, indicating the presence of all three strains of BYDVs, -PAV, -MAV, -SGV and two strains of CYDVs, -RPV and -RMV respectively. The amplification specificity of these primers was tested against wide range of field samples from different parts of United States. Another version of the protocol utilizes fluorescently tagged primers which streamlines the detection of each virus through fluorescent capillary electrophoresis. This method fulfills the need for a fast and specific method to detect any of these five viruses. This method will be an important diagnostic tool and will also be very useful in examining the epidemiology of these viral diseases.

The Susceptibility Response to BYDV in *Avena sativa*: Using the Wheat Gene Microarray as a Tool for Measuring Gene Expression in Oat in Response to BYDV Infection.

Joseph M. Anderson
USDA-ARS, Purdue University, West Lafayette, IN 47907

The development of wheat and barley microarrays for gene expression analyses have opened the ability to identify genes whose expression patterns change relative to some applied treatment. The development of these gene arrays has only been possible because of the large amount of EST sequencing. Because of very limited resources a relatively low level of sequencing has been done in oat. In this study, the wheat microarray was examined as a potential tool for examining global gene expression in oat. The wheat microarray was chosen because it has approximately 55,000 genes arrayed compared to the 23,000 gene barley array. Anecdotal evidence suggests that oat is inherently more susceptible to BYDV than other cereals such as wheat. My laboratory has preliminary data that suggests that Clintland 64, a variety that is highly susceptible to BYDV-PAV, accumulates more of this virus than comparable susceptible wheat lines and some defense response genes are down-regulated after infection. The aim of this project is to begin examining the susceptible response to infection with BYDV-PAV. RNA isolated from Clintland 64 plants that were untreated, infested with nonviruliferous aphids and infested with aphids viruliferous with BYDV-PAV at ten times points post-infestation were initially examined for virus accumulation. Samples before, during and after maximum virus accumulation were used to hybridize to Affymetrix wheat microarrays. The data from these experiments will determine which percentage of the wheat array will be useful in examining oat gene expression and how the plant is responding to virus infection.

Near-Infrared Reflectance Spectroscopy for the Determination of Fiber and β -glucan in Oats

Ames, N., Rhymer, C. and Mitchell-Fetch, J.

Cereal Research Centre, Agriculture & Agri-Food Canada, 195 Dafoe Rd., Winnipeg, MB,
Canada, R3T 2M9.

Email: names@agr.gc.ca

Breeding oat (*Avena sativa*) cultivars high in total dietary fiber (TDF) and β -glucan, has become increasingly important in cultivar improvement programs because of their positive effects on human health. The current procedures recommended for measuring total, soluble and insoluble dietary fiber are enzymatic methods that are extremely time consuming and labor intensive, and thus unsuited for early-generation screening for thousands of plants with low quantities of seed available. Near-infrared reflectance spectroscopy was investigated as a rapid screening tool for evaluation of β -glucan and TDF in oat breeding lines. The Foss NIR Systems 6500 spectrometer was used to obtain spectra on genetically/environmentally diverse, whole and ground groat samples. For TDF n =157 samples in the calibration and n=40 in the validation set ranging from 8.42-19.19% TDF as determined using AACC Method 32-07. For β -glucan in whole oats , n= 258 in the calibration set and n=50 in the validation set; for ground groats, n= 600 in the calibration and n=150 in the validation set with and representing a range of 1.47 to 6.09 % β -glucan in whole oat and 3.47 to 8.37 % β -glucan in ground groats as determined using AACC Method 32-23. NIR reflectance spectroscopy (1104-2494nm) of ground groat samples for β -glucan resulted in a model with RSQval= 0.88 and RSQcal= 0.89 compared to RSQval=0.75; RSQcal=0.82 for whole oat. The precision in prediction of TDF was significantly lower with RSQval= 0.50. The results of this study suggest large numbers of progeny in oat breeding programs can be screened for β -glucan using the NIR reflectance model developed for ground groats. The low precision and accuracy associated with the TDF model suggests further development is necessary before this technique could be used in selection of high TDF cultivars.

Key Words: Oat, NIR, TDF, β -glucan, fiber

Genotype and Environment Effects on Oat β -glucan, Total Dietary Fiber and Antioxidant Activity

Ames, N.¹, Rhymer, C.¹ and Rossnagel, B.²

¹Cereal Research Centre, Agriculture & Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB, Canada, R3T 2M9. ²University of Saskatchewan, Crop Development Centre, Saskatoon, SK, Canada. Email: names@agr.gc.ca

Availability of oat cultivars with high levels of β -glucan and total dietary fiber (TDF) is essential for oat millers and food processors to meet health claims and improve consumer nutrition. Plant breeding programs have responded to this market need by selecting for higher levels of β -glucan and lower oil but further improvement in these traits and other nutritional characteristics may be made by identifying specific genotype and environment effects. Canadian oat genotypes were grown at several sites across western Canada to assess the effects of genotype, environment and interactions on oat fiber composition and antioxidant activity. Significant differences in β -glucan content existed among genotypes, showing a range of 3.9 to 7.4 % as measured using standard, AACC approved enzymatic method 32-23. While location effects were observed for β -glucan content, there were no interactions and rank order of genotypes was stable across environments. The correlation between sites for β -glucan content was 0.95. For several genotypes tested, β -glucan levels were consistently higher at one of the environments tested, suggesting that for some genotypes, specific growing locations may be used to further improve β -glucan content. Genotype variation was also observed for TDF with a range of 11.98 to 17.5% as measured using the AACC approved method 32-07. For TDF the correlation between sites was 0.72 and interactions were observed for some cultivars. Despite large genotype effects for TDF, variation due to the analytical method contributed significantly to the error making it difficult to draw conclusions regarding environmental effects for this variable. Further GXE studies for TDF are currently underway to try to control this confounding factor. Antioxidant activity was also measured to assess genotype differences in adapted germplasm and test a simple method of analysis which could be used to screen breeding samples. Antioxidant activity, measured in Trolox Equivalents, ranged from 1300 to 1700 TE/100g and was not consistent across locations.

Development of a microsatellite library for *Puccinia coronata*

Hattie Dambroski and Martin Carson

USDA-ARS-Cereal Disease Laboratory, St. Paul, MN, USA

Puccinia coronata or oat crown rust has no microsatellite (simple sequence repeats, SSR) markers available for use in population studies. Microsatellites found in *P. graminis*, wheat stem rust, and *P. triticina*, wheat leaf rust, were not useful in *P. coronata* studies. A CA repeat SSR library was enriched with Dynabeads M-280 Streptavidin. This library had a success rate of only two polymorphic markers out of 192 sequenced clones. Three more libraries were constructed with enrichment of repeats AAT, AAC and CA. An additional selection of hybridization with biotin-labeled probes was used on these libraries to reduce the number of false positives. No markers were found in the AAT (0/56) or AAC (0/65) libraries, but three more markers were found from 45 sequenced clones in the second CA library.

**2006 American Oat Workers Conference,
Distinguished Service to Oat Improvement Awards**

Dr. Stephen (Steve) James Molnar



It is a privilege to honour Steve Molnar as a distinguished contributor to oat research. Steve will modestly confess that oat has only occupied the latest chapter of his career, that he has no rural roots, and that he has never occupied the hallowed rank of “oat breeder” or “agronomist”. But the diverse background, fresh ideas, and critical thinking that Steve brings to oat research are precisely why we wish to honour him.

Steve obtained his B.Sc. at the University of Toronto (his home town) in 1971. He specialized in geophysics and theoretical physics, but was enticed toward biology through courses in Medical Biophysics. His M.Sc. and Ph.D. (1978) were at the Ontario Cancer Institute at the University of Toronto, where he studied somatic cell genetics of Chinese hamster ovaries. Frustrated that whole organisms could not be regenerated from stabilized mutant cultures, Steve turned to plants. From 1978 to 1980 he worked on the isolation of amino acid metabolism mutants from plant suspension cultures, and on the development of regenerable corn tissue cultures. This work was conducted at Pfizer Pharmaceuticals in Connecticut, with a cross appointment in the Department of Crop and Soil Sciences, Michigan State University.

In 1980, Steve was recruited as a Research Scientist to join a new Biotechnology Group being established at Agriculture and Agri-Food Canada in Ottawa. He first focused on the isolation of amino acid analog resistant mutants in tissue cultures of corn, *Brassica*, and bromegrass. Then, in 1988, he changed research direction in response to emerging molecular marker technologies, and initiated work on “structural genomics” in barley. Soon afterward, he extended this work to oat, and then added soybean in 1995.

In 1989, Steve was invited by Dr. Fran Webster of The Quaker Oats Company to develop a proposal for recombination mapping and molecular marker development in oats. An exciting series of collaborations followed, involving groups from Minnesota, Cornell, Iowa State, Saskatoon, Winnipeg, and Lacombe. Fostered by continued guidance and support from Quaker,

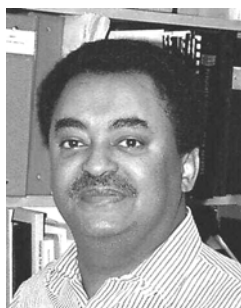
these collaborations evolved toward marker applications in molecular breeding and genomic discovery. As a collective, these collaborations and other extended interactions are responsible for much of the “oat genomic toolbox” that we now take for granted. Specifically, Steve has been instrumental in developing hexaploid oat maps, in the discovery of markers linked to agronomic traits, and in the development of simple PCR-based markers for application in breeding. Throughout, Steve has been an eager and reliable collaborator. To the oat team at Ottawa, he has been a thoughtful and careful leader, as well as a wise and willing mentor.

Steve’s research in oat is nicely complemented by his ongoing work in structural genomics of barley and soybean. He has held various roles as Study Leader and Research Team Leader at AAFC Ottawa. He has willingly carried out duties as Professional Advisor and Student Supervisor, as well as Editor, Director, and Secretary of societies and committees. Steve’s contributions are recognized in five book chapters (three on oat), 31 refereed articles (13 on oat), and numerous other scientific communications.

For his solid and ongoing leadership and productivity in oat research, Dr Steve Molnar is a most deserving recipient of this award.

**2006 American Oat Workers Conference,
Distinguished Service to Oat Improvement Awards**

Dr. Solomon Kibite



It is with great respect and honor that we honor the late Dr. Solomon Kibite, former AAFC oat Breeder and researcher at Lacombe, Alberta, Canada, with the 2006 Distinguished Service to Oats Improvement Award from the American Oat Workers. Dr. Kibite has been a student colleague, a professional colleague and collaborator, and as friend to many of us for the more than 30 years that he provided his outstanding service to the Canadian and international oat community.

Solomon, oat breeder and researcher at the Agriculture and Agri-Food Canada Lacombe Research Centre in Alberta, Canada passed away suddenly at age 54 on August 20, 2003. Solomon was born in Addis Ababa, Ethiopia and grew up there during very turbulent times. He completed his B.Sc. degree in Plant Sciences at Alemaya College in Ethiopia in 1973 and then came to Canada where he earned his M. Sc. and Ph.D. in plant breeding from the Plant Sciences Dept., University of Manitoba.

In 1980 he moved to the University of Alberta where he taught and conducted research on wheat and barley until 1984 when he joined AAFC as cereal breeder at Lacombe. While initially responsible for wheat, barley and oat R&D, shortly after arriving at Lacombe Solomon's responsibilities became 100% oat and he excelled in his activity as an oat researcher for nearly 20 years. During his all too short career he released 13 oat, barley and wheat varieties. His most recent oat release, AC Morgan, is an outstanding variety for the non-rust areas of western Canada with high grain yield potential, very good straw strength and good milling quality. Not only is it a widely grown variety; it will undoubtedly survive in the pedigree of many future western Canadian varieties.

Solomon's breeding materials have also found their way in numerous breeding programs around the world. He developed important germplasm with acid tolerance, herbicide tolerance, early maturity (the variety Lu), hullless types (the variety Boudrias), forage types (the variety Murphy) and with high levels of antioxidants, beta glucan, protein and fat. This material will be important in future Canadian and international oat varieties. He also developed techniques to more efficiently measure important quality traits.

Solomon was internationally respected as a Canadian member of the Executive Committee of the International Oat Conference, original Chair of the 2006 American Oat Workers Conference, and as an Assoc. Editor of the Canadian Journal of Plant Science. He served on the executive of the Western Expert Committee on Grain Breeding, the Prairie Region Recommending Committee for Grain, and many other regional and provincial committees.

In recognition of his outstanding contribution to western Canadian oat R&D Solomon was recognized by the oat producers of the area as the first recipient of the Kirylchuk Award for Outstanding Contribution to the Oat Industry from the Oat Producer's Association of Alberta (now the Prairie Oat Grower's Association) in 1998.

Solomon was known as a real gentleman by the Canadian and International oat community. Colleagues from around the world have spoken fondly of their social interaction with Solomon who often enjoyed pleasant visits with many colleagues and their families. Solomon had the ability to foster much collaboration with scientists around the world that turned into friendships beyond the work.

We miss our respected colleague, his quiet efficiency and his great eye for oat. Solomon was a great colleague and, for many members of the oat community, a special friend.

**2006 American Oat Workers Conference,
Distinguished Service to Oat Improvement Awards**

Dr. David M. Peterson



We present Dr. David M. Peterson the 2006 Distinguished Service to Oat Improvement Award. Dr. Peterson has been a central figure in the oat improvement research community for over three decades as a highly respected colleague and recognized authority in oat grain composition, oat plant and grain development, nutritional value in human diets and animal feed, and genetic and environmental influences on it.

David Peterson began his career in oat research in 1971 as a USDA-ARS Plant Physiologist with the Oat Quality Laboratory, which had been established through a cooperative agreement with the Agronomy Department of the University of Wisconsin, Madison, in 1970. Prior to that appointment he had worked a short while in the agro-chemical industry after receiving a B.S. degree at the University of California, Davis, an M.S. at the University of Illinois and his Ph.D. at Harvard University. Dr. Peterson's assignment in the Oat Quality Laboratory was to do research to improve the quality of oats for human consumption, initially with an emphasis on protein quality and quantity.

Dr. Peterson was widely recognized for his early research which first demonstrated the similarity in structure between oat storage proteins and those of legume seeds. He showed that this unique aspect of oat storage protein was responsible for the superior amino acid balance of oats. He then led a team that found cholesterol inhibitors in barley that were identified as tocotrienols, which were also present in oats and other cereals. The mechanism of inhibition was different than that of the soluble fiber, beta-glucan, which is prominent in oat bran. Dr. Peterson's more recent research was to characterize the antioxidant compounds that are present in oats. He showed that a unique class of compounds called avenanthramides shows antioxidant activity by in vitro tests and also investigated, with a collaborator in Sweden, the possible role of avenanthramides in the resistance of oat to fungal diseases.

Many oat workers know Dr. Peterson well through his work in cooperatively conducting and supporting oat quality genetic improvement efforts. Publications either by Dr. Peterson or with colleagues described the roles of genotype, environment, and genotype-by-environment interactions on oat grain protein, oil, beta-glucan, and antioxidant component levels. In addition his lab provided assays for entries from the National Oat Collection, the regional Uniform Early and Midseason Oat Nurseries, and various breeders' materials to identify germplasm elite in content for grain quality components.

In 1983 Dr. Peterson was appointed Research Leader of the USDA-ARS Cereal Crops Research Unit at Madison, whose function includes evaluating and improving malting quality in barley, as well as oat quality research. Under his leadership the unit expanded from four to eight scientists, and the Federal budget support more than tripled. In 2003 and 2004, Dr. Peterson and his staff worked with architectural firms to plan a new 34,000 square foot laboratory and office facility on the Madison campus. Since his retirement in 2004 Dr. Peterson has remained active as an ARS Collaborator and Emeritus Professor at the University of Wisconsin and is enjoying the satisfaction of seeing the construction of this new Cereal Crops Laboratory near completion.

During his career Dr. Peterson successfully directed seven M.S. and three Ph.D. students, who have gone on to careers in academia and industry. He authored 88 research publications including several book chapters and served on the editorial board of several professional journals. He was elected a Fellow of AAAS in 1986. His numerous contributions to science and particularly to oat research make Dr. Peterson a most worthy recipient of this award for distinguished service to oat improvement.

**2006 American Oat Workers Conference,
Distinguished Service to Oat Improvement Awards**

Dr. David Lee Hoffman (deceased)



David Hoffman was born Aug. 9, 1955 in Moscow Idaho and grew up on a family farm in the Thorn Creek area near Moscow. Dave's early experience working on his father's farm influenced his career as a scientist as he sought to produce research of practical benefit to growers. As many people would attest, Dave had a real passion for genetic research, especially oat, and enjoyed discussing his work with both colleagues and laymen.

Dr. Hoffman graduated from the University of Idaho with honors in plant science in 1977. His master's degree in agronomy and plant breeding was from New Mexico State University where he was involved in alfalfa breeding and genetics. He received a Ph.D. in plant breeding from Washington State University in 1985 where he worked on lentil. He began his work on oat when he joined the USDA Agricultural Research Service (ARS) Small Grains and Potato Germplasm Unit in Aberdeen, ID in 1986.

While with the ARS Dave's work focused on developing genetic maps for oat and barley. He co-developed the Ogle X TAM-O-301 mapping population, which is now being used to map disease resistance and other traits in oat. In addition, Dr. Hoffman assisted in the improvement of the original Kanota x Ogle (K x O) hexaploid oat map. Dave authored or co-authored more than 30 peer-reviewed scientific publications during his career, the last being accepted for

publication in April 2006. In spite of a physically debilitating illness, Dave worked nearly every day until a few weeks before his death in January of 2006.

**2006 American Oat Workers Conference,
Distinguished Service to Oat Improvement Awards**

Dr. Ronald (Ron) D. Barnett



Dr. Ron Barnett was born and raised in Bradley, Arkansas. He received a B.S. degree from the University of Arkansas in Agronomy in 1965. After completing his undergraduate degree Ron worked as a graduate assistant at the University of Arkansas and completed a M.S. in Plant Breeding in 1968. Ron then accepted an appointment as a graduate research instructor at Purdue University where he worked under Dr. Fred Patterson. Following the completion of his Ph.D. in 1970, Ron joined the University of Florida as an Assistant Professor and Small Grains Breeder at the North Florida Research Station in Quincy. He was promoted to Associate professor in 1975 and to Professor in 1983.

During his 36 years at Quincy Ron has conducted a diverse and productive small grain breeding program. He has been very successful in developing improved varieties and germplasm of oats, wheat, rye, and triticale. He has released five oat varieties: Florida 502, Chapman, Horizon 314, Horizon 474, and Horizon 321, and co-released two additional oats: Terral Trophy & Vigro Caballo. Ron also released five rye varieties and five triticale varieties. He has released or co-released 20 wheat varieties, including Florida 302, which was the dominant wheat variety across the southern US in the late 1980's.

Ron is creative and opportunistic in his approach to plant breeding. He has always looked for unique niches and needs that he can address, including areas such as hull-less oats, bread quality triticale, and dual purpose or forage oats.

In recognition of his many contributions Ron was named a Fellow of the American Society of Agronomy and the Crop Science Society of America. He was also named by Progressive Farmer Magazine as "Man of the Year in Service to Southeastern Agriculture" in 1990. Ron was also honored by the Southern Small Grain Workers at their meeting in 2005. He

has served in leadership positions in many state, regional, national, and international organizations.

Dr. Barnett has provided effective leadership to the Quaker International Oat Improvement Program for many years and currently coordinates the Quaker International Oat Nursery. This assignment entails worldwide collecting of unique oat germplasm, making crosses and beginning early generation development of their progeny and distribution of all of these materials to oat breeders around the world. Ron travels each year to South America as part of the Quaker International Oat Improvement Program and visits with oat scientists to foster exchange of germplasm and relevant scientific knowledge.

Ron has been active in transferring his plant breeding knowledge and acquired skills to others as well. Ron has served as advisor for several graduate students and was supervisor and mentor for Ann Blount, who currently serves as associate professor and forage breeder at the University of Florida in Quincy. Ron has always generously shared his germplasm with other breeding programs and contributed to formation of the SUNGRAINS breeding cooperative among southeastern universities.

Dr. Barnett is married to Pam and they have 3 children and 5 grandchildren. Barnett lives on Millstone Farms near Quincy and stays busy on weekends and evenings breeding beef cattle and helping Pam run a Bed & Breakfast operation on their farm.

**2006 American Oat Workers Conference,
Distinguished Service to Oat Improvement Awards**

Dr. Art McElroy



It is with great respect and honor that we award Dr. Art McElroy the 2006 Distinguished Service to Oat Improvement Award. Art has made a significant impact on numerous tasks and disciplines that he has managed over a relatively short but productive academic career.

Art was born and grew up in Lachute, Quebec. After completing a BSc.(Agr) at McGill University and M.Sc. at Université Laval he served as a regional crop specialist for south-western Québec. He joined the Research Branch of Agriculture Canada in 1978 when he was sent to the Brandon Research Centre to manage the corn and soybean physiology program while Bob Hamilton was seconded to the Dryland Project in India.

In 1979 he was transferred to the Ottawa Research Station to assume the forage grass breeding program with the retirement of Walter Childers. About this same time he initiated studies toward a Ph.D. degree at the University of Guelph; which he completed in 1983. His plant breeding accomplishments during this time resulted in the licensing of two orchardgrass varieties, one tall fescue variety plus two germplasm releases of Timothy that eventually became licensed as varieties. Another significant research activity during this interval was the design of a novel *in vitro* digestibility system for measuring the fibre digestibility, which is currently being marketed commercially by a US firm. The forage quality work led to the routine evaluation of forage cultivars, and Ontario became the first province or state in North America to include quality parameters as criteria for recommending forage varieties. Another project innovation was the development of a protocol for the production of hybrid alfalfa based on the application of somatic embryogenesis for generating sufficient numbers of parental clones for commercial production fields.

In 1996, Art was transferred to the oat breeding program that had been conducted by Vern Burrows. In the space of eight years, Art was involved in the release of ten oat cultivars. These varieties all had their own particular attributes. However the variety Goslin was especially noteworthy for its unique combination of groat and hull characteristics that contributed to an enhanced mill yield. This variety set the standards for milling yield for the Quaker list of

preferred oat varieties for Eastern Canada. In addition to the breeding activities, Art chaired the Quaker-ECORC oat research team for three years. In this capacity he was involved in the application of molecular markers to the breeding program; developed and implemented a strategy for deployment of crown rust resistance genes and initiated a universally available oat pedigree database. This system, which was re-designed and significantly enhanced by Dr. Nick Tinker, and now known as Pedigree of Oat Lines, has been especially useful to the oat genetics-breeding community. The above were innovative technologies and have contributed to oat improvement efforts in significant ways, but Art's most significant contribution to oat breeding enabling technologies was the novel NIR approach for assessing oat quality. He developed sets of prediction equations for determining the oil content and groat percentages without the need for dehulling the samples.

From an extension perspective, he was a strong supporter and driving force behind the formation of the Oat and Barley Council of Ontario. In this context he spearheaded an initiative for exploiting the value-added components of oats and barley by organizing a very successful Oat and Barley Forum in October 2005.

In addition to all of the above activities, he initiated in 1996, as a sideline, a private R&D company, PhytoGene Resources Inc. One of the main initiatives was the development of industrial hemp varieties, the first of which, ESTA-1, was released in 2004.

Art resigned from the research branch in 2004 to devote full time to his private company. In addition to the industrial hemp initiative he launched a private oat breeding program and has developed several collaborations with seed companies.

Meeting Participants

Nancy Ames
Research Scientist
Department of Ag and Agri Food Canada
195 Dafoe Road
Winnipeg, Manitoba R3T 2M9
Canada
Phone: 204 983 1461
Email: names@agr.gc.ca

Joseph M. Anderson
Research Molecular Biologist
USDA-ARS at Purdue University
Crop Production and Pest Control Research Unit,
915 W. State St.
Agronomy Dept., Purdue U.
West Lafayette, IN 47907
Phone: 765 494 5565
Email: janderson@purdue.edu

Keith Armstrong
Plant Breeder (oat forage & grain)
71 Roberta Drive
Barrington, Christchurch 8024
New Zealand
Phone: 61 3 3373 676
Email: armstrongk@crop.cri.nz

Ron Barnett
Professor of Agronomy
University of Florida
155 Research Rd.
Quincy, FL 32351
Phone: 850 875 7118
Email: rdbarnet@ufl.edu

Robert Baumann
Ag Research Technician
NDSU
1357 N. Univ.
Fargo, ND 58102
Phone: 701 232 8062
Email: robert.baumann@ndsu.edu

Kathryn Begeal
Grower Outreach & Grain Buyer
Organic Grain & Milling and Ceres Organic
2121 30th St.
Boulder, CO 80301
Phone: 303 845 1932
Email: Kathryn@ceresorganic.com

Harold Bockelman
Agronomist
USDA-ARS
1691 S. 2700 W.
Aberdeen, ID 83210
Phone: 208 397 4162 ext 112
Email: hbockelman@ars-grin.gov

J. Michael Bonman
Research Leader
Small Grain & Potato Germplasm Research Unit
USDA/ARS
1691 South 2700 West
Aberdeen, ID 83210
Phone: 208 397 4162 ext 108
Email: mbonman@uidaho.edu

William A. Bonner
Director Research and Development
ConAgra Foods
11 ConAgra Dr.
Omaha, NE 68102
Phone: 402 595 4585
Email: bill.bonner@conagrafoods.com

Jay Brandau
Sr. Vice President
Grain Millers, Inc.
Cabriole Center
Suite 400, 9531 W 78th St.
Eden Prairie, MN 55344
Phone:
Email: jay.brandau@grainmillers.com

Patrick M. Carr
North Dakota State University
Dickinson Research Extension Center
1133 State Ave.
Dickinson, ND 58601
Phone:
Email: pcarr@ndsuxext.nodak.edu

Martin Carson
Research Leader
USDA/ARS/CDL
1551 Lindig St.
St. Paul, MN 55108
Phone: 612 624 4155
Email: mcarson@umn.edu

Roger Caspers
Research Coordinator
University of Minnesota
411 Borlaugh Hall
1991 Buford Circle
St. Paul, MN 55108
Phone: 612 625 1994
Email: caspe005@umn.edu

Shiaoman Chao
USDA-ARS
Biosciences Research Lab
1605 Albrecht Blvd.
Fargo, ND 58105
Phone: 701 239 1462
Email: chaos@fargo.ars.usda.gov

Alona Chernyshov
Student
Iowa State University
Department of Agronomy
1301 Agronomy Hall
Ames, IA 50011-1010
Phone: 515 294 8690
Email: acherry@iastate.edu

James Chong
Dr/Research Scientist
Agriculture & Agri-food Canada
195 Dafoe Road
Winnipeg, MB R3T 2M9
Canada
Phone: 204 983 0932
Email: jchong@agr.gc.ca

Chris Coleman
Research Engineer
Quaker Oats
617 W Main St
Barrington, IL 60010
Phone: 847 304 2317
Email: chris_coleman@quakeroats.com

Hattie Dambroski
Research Geneticist
USDA ARS Cereal Disease Lab
1151 Lindig St.
St. Paul, MN 55108
Phone: 612 625 3156
Email: dambr005@umn.edu

Jack Dawes
Executive Director
Saskatchewan Oat Development Commission
Box 158
Saltcoats, SK S0A 3R0
Canada
Phone: 306 744 2775
Email: poga@imagewireless.ca

Jitka K. Deyl
Oat Pedigree Database Curator
Research Technician
ECORC, AARC OTTAWA
K.W. Neatby Bldg. #2047
960 Carling Ave.
Ottawa, ON K1A 0C6
Canada
Phone: 613 759 1548
Email: DeylJK@agr.gc.ca

Axel Diederichsen
Dr./Research Scientist, Curator
Plant Gene Resources of Canada - Agriculture & Agri-
Food Canada
107 Science Place
Saskatoon, SK S7N 0X2
Canada
Phone: 306 956 2839
Email: diederichsen@agr.gc.ca

Douglas Doehlert
Research Chemist
USDA-ARS Wheat Quality Research
Harris Hall, NDSU
Fargo, ND 58105
Phone: 701 231 8069
Email: douglas.doehlert@ndsu.edu

Jim Dyck
Senior Research Agronomist/Oat Breeder
Agricore United
710 48th St. E.
Saskatoon, Saskatchewan S7K5B4
Canada
Phone: 306-343-5005
Email: jdyck@agricoreunited.com

Peter E. Eckstein
Research Officer
Univ. of Saskatchewan, Dept. of Plant Sciences
4C25 Agriculture Bldg.
51 Campus Dr.
Saskatoon, SK S7N 5A8
Canada
Phone: 306 966 8476
Email: peter.eckstein@usask.ca

David Fielder
V.P. of Scientific Affairs
Ceapro, Inc.
Suite 1008 Rtf 8308 114 St.
Edmonton, Alberta T6G 2E1
Canada
Phone: 780 917 8381
Email: dfielder@ceapro.com

Yong-Bi Fu
Research Scientist
Plant Gene Resources of Canada
107 Science Place
Saskatoon, SK S7N 0X2
Canada
Phone: 306 956 7642
Email: fuy@agr.gc.ca

Dennis Galbraith
P. Ag.
Can-Oat Milling
#1 Can-Oat Drive
Portage La Prairie, Manitoba R1N 3W1
Canada
Phone: 204 856 5926
Email: dennis.galbraith@can-oat.com

Michael A. Gartner
Owner
Gartner Seed Farm
500 10 Ave NW
Mandan, ND 58554
Phone: 701 663 7731
Email: gartnerseedfarm@westriv.com

Christoph Ulrich Germeier
Scientist
Federal Centre for Breeding Research on Cultivated
Plants
Bundesallee 50
38116 Braunschweig
Germany
Phone: 49 531 5962459
Email: c.germeier@bafz.de

Christopher Green
Managing Director
SW Seed Ltd
49 N. Rd.
Gt. Abington, Cambridge CB16AS
UK
Phone: 044 1223 890777
Email: christopher.green@swseed.com

Stephen Harrison
Professor
Louisiana State University Agricultural Center
LSU Agronomy Dept.
104 Sturgis Hall
Baton Rouge, LA 70803
Phone: 225 578 1308
Email: sharrison@agctr.lsu.edu

Kelly Henderson
Technical Services Manager
Can-Oat Milling
#1 Can-Oat Drive
Portage La Prairie, Manitoba R1N 3W1
Canada
Phone: 204 856 5933
Email: kelly.henderson@can-oat.com

Gongshe Hu
Research Geneticist
USDA-ARS
1691 S 2700 W
Aberdeen, ID 83210
Phone: 208 397 4162 ext 241
Email: gongsheh@uidaho.edu

Xinzhong Hu
Visiting Scientist
Agriculture Canada
960 Carling Ave
Ottawa, ON
Canada
Phone: 613 759 1304
Email: hux@agr.gc.ca

Eric Jackson
Research Plant Pathologist
USDA-ARS
4620 Mountain Park Rd.
Chubbuck, ID 83202
Phone: 208 397 4162 ext 248
Email: ejackson@uidaho.edu

Jean-Luc Jannink
Assistant Professor
Iowa State University
Department of Agronomy
1208 Agronomy Hall
Ames, IA 50011-1010
Phone: 515 294 4153
Email: jjannink@iastate.edu

Alan Koechner
Senior Manager of Milling Research
Quaker Oats Co.
418 2nd St NE
Cedar Rapids, IA 52402
Phone: 319 368 1534
Email: alan_koechner@quakeroats.com

Frederic L. Kolb
Professor of Plant Breeding
University of Illinois
1102 S. Goodwin Ave.
Urbana, IL 61801
Phone: 217 333 9485
Email: f-kolb@uiuc.edu

Tim Langdon
Dr.
The Institute of Grassland and Environmental Research
Plas Gogerddan
Aberystwyth, Ceredigion SY23 3EB
UK
Phone: 44 1970 823111
Email: tim.langdon@bbsrc.ac

Greg Lardy
Animal and Range Sciences Department
North Dakota State University
Fargo, ND 58105
Phone: 701 231 7660
Email: glardy@ndsuxt.nodak.edu

David Livingston
Research Agronomist/Assoc. Prof.
USDA -North Carolina State University
840 Method Rd. Unit 3
Raleigh, NC 27695
Phone: 919 515 4324
Email: dpl@unity.ncsu.edu

Joe Lutz
General Mills Ag Research
1201 N. 5th St.
LeSueur, MN 56058
Email: joe.lutz@genmills.com

David E. Matthews
Grain Genes Curator
USDA-ARS, Cornell University
Dept. Plant Breeding and Genetics
Cornell University
Ithaca, NY 14853
Phone: 607 255 9951
Email: dem3@cornell.edu

Cark Maunsell
Mr
Oat Services Ltd
226 Bassett Avenue
Southampton, SO16 7FU
UK
Phone: 44 2380 767228
Email: cark_maunsell@oat.co.uk

William May
Crop Management Agronomist
Agriculture and AgriFood Canada
Box 760
Indian Head, SK S0G 2K0
Canada
Phone: 306 695 5225
Email: mayb@agr.gc.ca

Art R. McElroy
Research Coordinator
Phytogene Resources Inc.
1855 rue des Arbres
Orleans, ON K1E2T7
Canada
Phone: 613 824 6379
Email: pgr@rogers.com

Michael S. McMullen
Associate Professor
North Dakota State University
Dept. of Plant Sciences
North Dakota State University
Fargo, ND 58105
Phone: 701 231 8165
Email: michael.mcmullen@ndsu.edu

Dwain W. Meyer
Plant Sciences Department
North Dakota State University
Fargo, ND 58105
Phone: 701 231 8154
Email: dwain.meyer@ndsu.edu

Jennifer Mitchell-Fetch
Oat Breeder
AAFC
Cereal Research Center
195 Dafoe Rd.
Winnipeg, R3T 2M9
Canada
Phone: 204 983 1460
Email: jfetch@agr.gc.ca

Stephen J. Molnar
Research Scientist
Agriculture and Agri-Food Canada
960 Carling Ave, CEF
Ottawa, ON K1A 0C6
Canada
Phone: 613 759 1687
Email: molnarsj@agr.gc.ca

Grant Morrison
Director of Quality Assurance
Quaker Oats Canada
14 Hunter St. E.
Peterborough, ON K9J 4B2
Canada
Phone: 705 743 6370
Email: grant.morrison@pepsi-qtg.com

Don Obert
Research Geneticist
USDA-ARS
1691 S 2700 W
Aberdeen, ID 83210
Phone: 208 397 4162 ext 114
Email: dobert@uidaho.edu

Massiel Orellana
Student
Iowa State University
Department of Agronomy
1301 Agronomy Hall
Ames, IA 50011-1010
Phone: 515 294 3440
Email: massiel@iastate.edu

Hedera Porter
Biological Technician
USDA-ARS and Univ. of Minn.
411 Borlaugh Hall
1991 Upper Buford Circle
St. Paul, MN 55108
Phone: 612 625 6223
Email: porte205@umn.edu

Trevor Pizzey
Evp-Operations
Can-Oat Milling
#1 Can-Oat Drive
Portage La Prairie, Manitoba R1N 3W1
Canada
Phone: 204 856 5920
Email: trevor.pizzey@can-oat.com

Dale Reeves
SDSU - retired
3210 Pine Ave
Brookings, SD 57006
Phone: 605 693 2932
Email: dreeves@mchsi.com

Dr. Ginger Rich
Equine Nutritionist
280 Spring Run Lane
Eads, TN 38028
Phone: 901 854 1400
Email: richequine@aol.com

Howard Rines
Research Geneticist
USDA-ARS and Univ. of Minn.
411 Borlaugh Hall
1991 Upper Buford Circle
St. Paul, MN 55108
Phone: 612 625 5220
Email: rines001@umn.edu

Jay Romsa
Research Agronomist
General Mills Operations
1201 N 4th
LeSueur, MN 53058
Phone: 507 380 2586
Email: jay.romsa@genmills.com

A. Bruce Roskens
Sr. Mgr. Ag Research
Pepsi Co. Beverages & Foods
555 W. Monroe
Chicago, IL 60661
Phone: 312 821 2952
Email: bruce_roskens@quakeroats.com

Brian Rossnagel
Professor
University of Saskatchewan
Crop Development Center, Univ. of Sask.
51 Campus Dr.
Saskatoon, Sask. S7N5A8
Canada
Phone: 306 966 4976
Email: brian.rossnagel@usask.ca

Graham Scoles
University of Saskatchewan
College of Agriculture & Bioresources
51 Campus Dr.
Saskatoon, SD S7N 5A8
Canada
Phone: 306 966 4050
Email: graham.scoles@usask.ca

Angela Esther Sebelius
Graduate Research Assistant
NDSU
480B Loftsgard Hall
Fargo, ND 58015
Phone: 701 231 8169
Email: angela.sebelius@ndsu.edu

Steven J. Shirtliffe
Dr.
Department of Plant Sciences
51 Campus Dr.
University of Saskatchewan
Saskatoon, SK S7N 5A8
Canada
Phone: 908 233 7861
Email: shirtliffe@skyway.usask.ca

Dean Stuthman
Professor
University of Minnesota
411 Borlaugh Hall
1991 Buford Circle
St. Paul, MN 55108
Phone: 612 625 3709
Email: stuth001@umn.edu

Nicholas Tinker
Scientist
AAFC
C.E. Farm, Bldg 20
960 Carling Ave.
Ottawa, ON K1A 0C6
Canada
Phone: 613 759 1398
Email: tinkerna@agr.gc.ca

Diego Vilaro
Graduate Student
NDSU
14A University Village
Fargo, ND 58102
Phone: 701 231 7825
Email: diego.vilaro@ndsu.edu

Matthew Walch
Graduate Student
University of Minnesota
411 Borlaugh Hall
1991 Upper Buford Circle
St. Paul, MN 55108
Phone: 612 625 6223
Email: walch023@umn.edu

Samuel H. Weaver III
Retired
Quaker Oats Co.
4 Kirkintilloch Dr.
Bella Vista, AR 72715
Phone: 479 876 6370
Email: shw3@aol.com

Francis Webster
retired
42 Catalina Dr.
Branson, MO 65616
Phone: 417 338 2959
Email: fhwebster@cox.net

Charlene Wight
Molecular Genetics Research Technician
ECORC
K.W. Neatby Bldg.
960 Carling Ave.
Ottawa, ON K1A 0C6
Canada
Phone: 613 759 1671
Email: wightcp@agr.gc.ca

Daniel Winderl
Senior Engineer
General Mills
9000 Plymouth Ave. N
Golden Valley, MN 55427
Phone: 763 764 5742
Email: dan.winderl@genmills.com

Bruce John Winter
Plant Breeder (Oats)
Department of Primary Industries and Fisheries
LRC, PO Box 2282
Toowoomba, 4350
Australia
Phone: 61 7 4639 8849
Email: bruce.winter@dpi.qld.gov.au

Mitchell Wise
Research Chemist
USDA-ARS Cereal Crops Research
501 N Walnut St.
Madison, WI 53726
Phone: 608 262 9242
Email: mlwise@wisc.edu

Weikai Yan
Research Scientist
Agriculture Canada
960 Carling Ave
Ottawa, ON
Canada
Phone: 613 759 1304
Email: yanw@agr.gc.ca

Tom Zutorski
Crop Development Centre - Univ. of Sask.
51 Campus Dr.
Saskatoon, SK S7N 5A8
Canada
Phone: 306 966 8480
Email: tom.zutorski@usask.ca

Notes

Notes

Notes

