American Oat Workers Conference

April 18 – April 21, 2010
Baton Rouge, Louisiana

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American Oat Workers Meeting
Core / AFRI Workshop Sponsors

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AOW Conference Program
April 18 – April 21, 2010. Baton Rouge, LA
http://www.aow.lsu.edu/aow.htm

Saturday, April 17 CORE Workshop (Eric Jackson).

"The CORE workshop will be formatted to give briefings to participating members and stakeholders on the current progress and to allow discussions and assessments by the group. The workshop is open to those currently not participating in the CORE, but who have interest in the program and discussion."

9:00 AM: **Travel to Ben Hur Farm**

9:30 AM: **CORE Material Evaluations**
*Field books will be made available
*Short description will be give by submitting researchers

11:30 AM: **Lunch Cajun style at the farm (Shrimp and Catfish)**

1:00 PM: **Travel back to Hotel**

1:30 PM: **Introduction: From BASS to the AFRI to the CORE**. Eric Jackson. USDA-ARS

Phenotyping: The Foundation of the CORE

1:50 PM: **Experimental Design: The Nuts and Bolts (agriBase).** Don Obert. USDA-ARS

2:10 PM: **Group Discussion and Assessment. (coffee and snacks available)**

3:20 PM: **Data Curation: From Submission to Utilization.** Gerard Lazo. USDA-ARS

4:40 PM: **Group discussion and assessment (coffee and snacks available)**

5:00 PM: **Roundtable Discussion with Stakeholders.** Moderator – Eric Jackson, USDA-ARS
Panel Members: Jane Demarchi, North American Millers Association.
Joe Lutz/Mark Ramsland/John Wiebold, General Mills, Inc
Bruce Roskens, Pepsi Co/Quaker
Bill Bonner, 21st Century Grain
Rick Schwein, Grain Millers, Inc
Jack Dawes, Prairie Oat Growers Association

7:00 PM: Dinner with Roundtable Group (attendees) - Transportation provided

SUNDAY, APRIL 18 CORE Workshop cont.

Genotyping: the supporting structure of the CORE

8:00 AM: **cDNA and ESTs Briefing.** Marc Rubenfield. Beckman/Coulter Genomics

8:25 AM: **OOPA LUMPA: SNPs/SNPs/SNPs.** Shiaoman Chao. USDA-ARS

8:50 AM: **DArTing the CORE.** Nick Tinker. Diversity Array Technology

9:05 AM: **Data Curation: From Submission to Utilization.** Gerard Lazo. USDA-ARS

9:30 AM: **Group Discussion and Assessment** **(working coffee break – available around 10:00 AM)**

CORE Business

11:00 AM: **Funding: How Does It Work and What Does It Mean?** Glenda Rutger. USDA-ARS

11:30 AM: **Publication to Infinity and Beyond.** Eric Jackson. USDA-ARS

12:00 PM: Lunch on your own

Sunday, April 18.
American Oat Workers' Conference

1:00 PM: Welcome. Steve Harrison and John Russin. Louisiana State University Agricultural Center.

Session One: Oat Molecular Genetics (Eric Jackson and Mark Sorrels)

1:10 PM: **Introduction.** Eric Jackson. USDA-ARS

1:15 PM: **A New Frontier: cDNA and ESTs for Oat.** Marc Rubenfield. Beckman/Coulter Genomics Beverly, MA

1:40 PM: **SNPs Mining: from ESTs and DArTs.** Nick Tinker. AAFC Ottawa, Canada

2:05 PM: **Mapping the Oat Genome.** Rebekah Oliver, et al. USDA-AR

2:20 PM: **Molecular Breeding in Oat; Technology Development and Applications in Novel Food and Feed.** Bräutigam, M.[1] , Chawade, A.[2], Sikora, P.,[2] Viveknande, V.[2], Olsson, O[2] [1]CropTailor AB, Erik Dahlbergsgatan 11A, SE-411 26 Göteborg, Sweden and [2]Department of Plant and Environmental Sciences, Carl Skottsbergs gata 22B, Gothenburg University, SE40530 Göteborg, Sweden

2:45 PM: **Gene Mining from Related Species.** Catherine Howarth*, Tim Langdon, Sandy Cowan, Irene Griffiths, Athole Marshall and Wayne Powell IBERS, Aberystwyth University, Gogerddan, Aberystywth

3:05pm: **Mapping Genetic Diversity of Naked Oats with AFLP Markers.** Zongwen Zhang, Wei Xu, Bin Wu Institute of Crop Science of Chinese Academy of Agricultural Sciences, China

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3:30 PM: **Coffee Break**

Session Two: Oat Quality, Processing and Nutritional Benefits. (Mitchell Wise for Nancy Ames)

3:50 PM: **Oat Milling Industry Concerns – Keeping Mycotoxins Out of the Food Supply** Kelly Henderson. Viterra Food Processing - Oat and Specialty Grain Milling, Portage La Prairie, MB, Canada

4:10 PM: **Bioactive Fiber and Protein in Cereal Grains.** Wally Yokoyama. USDA-ARS

4:30 PM: **Effect of Feeding Enzyme Deactivated Oats Using a Rat Model**. Xinzhong Hu*, Hongmin Zhen, Peipei Zhang, Chao Xu, Guangzhong Luan. College of Food Science & Engineering, Northwest A&F University, Yangling, Shaanxi, China

4:50 PM: **Better Oat Fat.** R. Dhanda.*[1], B.G. Rossnagel.[1], A. Diederichsen.[2] and A.D. Beattie.[1] [1]Crop Development Centre, University of Saskatchewan; [2]Plant Gene Resources of Canada, Agriculture and Agri-Food Canada Research Center

Supper on your own.

Monday, April 19 American Oat Workers' Conference

6:30 – 8:00 AM: Sponsored Continental Breakfast

8:10 AM: Call to Order and Announcements

Session Three: Oat Processing and Chemistry (Mitchell Wise)

8:20 AM: **Avenanthramides in Oats: A New Method of Producing Whole Oats and Oat Ingredients with Greatly Elevated Avenanthramide Levels.** F. William Collins. Agriculture and Agri-Food Canada, Eastern Cereal and Oilseed Research Centre, Ottawa, Canada

8:40 AM: **The Effect of Chemical Systemic Acquired Resistance Elicitors on Oat Avenanthramide Biosynthesis.** Mitchell L. Wise. USDA-ARS, Cereal Crops Research Unit.

9:00 AM: **Therapeutic Bioactive Molecules from Oats (Avena sativa L.) for Use in Cosmetic and Personal Care Products.** Paul Moquin*, David Fielder. Ceapro Inc., Edmonton, Alberta, Canada

9:20 AM: **Impact of Molecular Weight of Oat Beta-glucan on Potential Health Effects.** Hyun Jung Kim, Pamela J. White. Iowa State University, Ames, IA

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9:40 AM: **Predictive Ability of Genomic Selection for Beta-glucan in Oats.** Franco Asoro*[1], Mark Newell[1], William Beavis[1], Adrienne Lauter[2] and Jean-Luc Jannink[3] [1]Iowa State University; [2]USDA-ARS; [3]USDA-ARS, New York and Cornell University.

10:00 AM: Coffee Break

10:20 AM: AOW Business Meeting

- Outstanding Service Awards.
- 2012 International Oat Conference Invitation.
- 2014 American Oat Workers Conference Site Selection.
- Officer Election.
- Annual Oat Newsletter Discussion.
- Oat Germplasm Committee and germplasm priorities Discussion

12:00 – 1:30 PM: Sponsored Lunch

2:00 PM: Field Trip to Nurseries. Casual dress.

6:00 – 8:00 PM: Supper at Mike Anderson's Seafood

- **load bus / vans at 6:00 PM**
- **paid by AOW registration fees**
- **spouses / family welcome (no charge).**

Tuesday, April 20 American Oat Workers' Conference

6:30 – 8:00 AM: Sponsored Continental Breakfast

Session Four: Pathology (Mike Bonman)

8:00 AM: **Mapping of Pc91 and its Postulation with Markers.** C.A. McCartney*, R.G. Stonehouse, B.G. Rossnagel, P.E. Eckstein, G.J. Scoles, T. Zatorski, and J. Chong University of Saskatchewan, Cereal Research Centre, Agriculture and Agri-Food Canada

8:20 AM: **Durable Resistance to Crown Rust: Can We Get There From Here?** Marty Carson. USDA Cereal Disease Laboratory, St. Paul, MN

8:40 AM: **Characterization of the Transcriptome in a Susceptible Reaction to BYDV-PAV.** Joseph M. Anderson. USDA-ARS Crop Production and Pest Control Research Unit

9:00 AM: **RT-PCR to Evaluate Selected Oat Lines for Differences in Relative Susceptibility to Fusarium Graminearum or F. Poae.** W. Yajima*[1], X.M. Zhang[1], T.S. Grewal[2], W. Yan[3], A. Beattie[1], G.J. Scoles[1], and B. Rossnagel[1]. [1]University of Saskatchewan, [2]Saskatchewan Research Council, [3]Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada

9:40 AM: **New Crown Rust Resistance Genes from Diploid Avena Strigosa and Tetraploid A. Barbata and Their Transfer into A. Sativa.** Howard W. Rines* and Marty L. Carson. University of Minnesota, USDA Cereal Disease Laboratory

10:00 AM: **SNPs linked to Crown Rust Resistance in MN841801, Ogle, and TAM-301.** M. Acevedo[*1], E. W. Jackson[1], R. E. Oliver1, G. R. Lazo[2], J. Chong[3], H. W. Rines[4], J. Lutz[5], S.A. Harrison[6], and J. M. Bonman[1].

10:20 AM: Coffee Break

Session Five: Pasture, Dual Purpose, and Food plots (Paul Murphy)

10:40 AM: **Double Cropping Breeding of Oats in China**. Ren Changzhong[*1,2], Laichun Guo [2,] Chunlong Wang [2.] . [1.] China Agriculture University, Beijing, China; [2.] Baicheng Academy of Agricultural Sciences of Jilin Province of China, Baicheng, Jilin, China, 137000

11:00 AM: **Food Plot Research and Development for White-Tailed Deer: 30 Years of Experience.** James C. Kroll and Ben H. Koerth. Institute for White-tailed Deer

Management & Research, Arthur Temple College of Forestry & Agriculture, Stephen F. Austin State University, Nacogdoches, TX 75962

11:20 AM: **Surviving Winter: How do They do it?** David Livingston[1], Tan Tuong[2], Cynthia Henson[3]. [1]USDA-ARS and North Carolina State University, Raleigh, NC; [2]USDA-ARS, Raleigh, NC; [3]Department of Agronomy, University of Wisconsin-Madison, USDA-ARS, Cereal Crops Res. Unit, Madison, WI,

11:40 AM: **Breeding Oats for Forage.** Saha M.C., J. Baker, H.S. Bhandari and J.H. Bouton. Forage Improvement Division, The Samuel Roberts Noble Foundation, Ardmore, OK

12:00 AM: **Effect of fertilizers application on yield and quality of oats in Qinghai-Tibetan Plateau.** Gensheng Bao*, Qingping Zhou, Zhilin Han, Hongbo Yan. Qinghai Academy of Animal and Veterinary Science, Xining, Qinghai, 810016

12:20 AM: Sponsored Lunch

Session Six: Breeding and Genetics (Fred Kolb and Mike McMullen)

1:30 PM: **Oat breeding in Brazil, Argentina, and Uruguay.** Luiz Federizzi. Universidad Federal Rio Grande de Sol, Brazil

1:50 PM: **Extent of Linkage Disequilibrium in Oat.** Mark Newell*[1], Jean-Luc Jannink[2], Nickolas Tinker[3],Franco Asoro[1], Diane Cook[4], and William Beavis[1]. [1] Dept. of Agronomy, Iowa State University, Ames, IA; [2] USDA-ARS, Ithaca, New York and Cornell University; [3] Eastern Cereal and Oilseed Research Center, Canada; [4] Dept. of Statistics, Iowa State University, Ames, IA

2:10 PM: **Breeding and Selection for Resistance to Black Spot (Pyrenophora) in Oats.** Marcello Pacheco. Universidad Federal Rio Grande de Sol, Brazil.

2:30 PM: **Introgression of Yellow Dwarf Disease Resistance from Avena Strigosa into A. Sativa.** Herb Ohm* and Joseph Anderson. Purdue University, West Lafayette, IN

2:50 PM: **Oat Crown and Stem Rust Resistance Breeding In North Dakota.** Mike McMullen. Department of Plant Sciences, North Dakota State University

3:10 PM: Coffee Break

3:30 PM: **The Quaker International Oat nursery.** R. D. Barnett*, S. A. Harrison, D. D. Stuthman, & L. C. Federizzi. University of Florida, Louisiana State University Agricultural Center, University of Minnesota, University Federal Rio Grande de Sol, Brazil

3:50 PM: **Development of Oat SNP Markers Based on 454 Genomic Sequences from Tetraploid Avena magna.** Rachel Redman*, Maughan, Eric Jackson, Jackson, Oliver, and Rick Jellen. Brigham Young University

Sponsored Banquet 6:00 – 8:00

Outstanding Service Awards:
James Chong
Grant Morrison
Howard Rines
Gregory E. Shaner
Deon D. Stuthman

Wednesday, April 21. American Oat Workers' Conference:

Sponsored Continental Breakfast

American Oat Workers Officers

Chairman	Steve Harrison
Chair-Elect	Brian Rossnagel
Past Chairman	Paul Murphy
Secretary	Michael Bonman
Ed. Oat Newsletter	Jean-Luc Jannink
Northeast USA	Mark Sorrells
North Central USA	Deon Stuthman
Western USA	Donald Obert
Southern	Ben Edge
USDA-ARS	Kay Simmons
East Canada	Art McElroy
Western Canada	James Chong
AAgri-Food Canada	Jeff Stewart
Mexico	Jose Salmeron
Member-at large	Steve Shirtliffe
Member-at large	Dave Marshall
Member-at large	Trevor Pizzey
Industry	Bruce Roskens

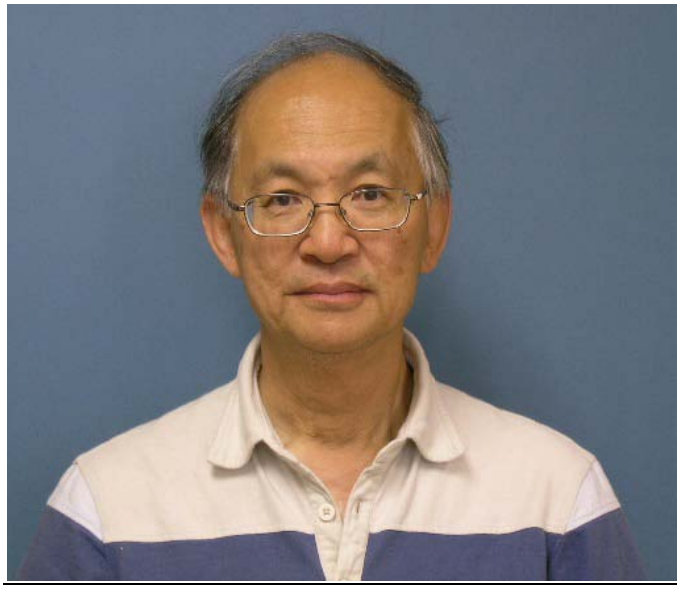
Awards and Recognition Committee:

Jennifer Mitchell Fetch
Paul Murphy
Mike McMullen

Program Committee:
Steve Harrison
Eric Jackson
Mark Sorrels
Mitchell Wise
Nancy Ames
Mike Bonman
Paul Murphy
Fred Kolb
Mike McMullen

Fundraising
Steve Harrison
Eric Jackson
Jennifer-Mitchell Fetch

Program Editor: Tom Barnett, LSU AgCenter



James Chong

Dr. James Chong obtained his Bachelor Degree and Master Degree from Carleton University, Ottawa, in 1969 and 1973. Dr. Chong joined Agriculture & Agri-Food Canada in Ottawa in 1972 and moved to Winnipeg in 1973, after a promotion, to work at the Cereal Research Centre. While working full time, he started his PhD study with the University of Manitoba in 1978. After obtaining his PhD degree in 1981, Dr. Chong was promoted to Research Scientist with responsibility for the oat crown rust program at CRC.

During the early part of his career, Dr. Chong's work on ultrastructure and cytochemistry of the structural components at the cereal host-rust fungal parasite interface earned him the Gordon J. Green Award for Outstanding Achievement of a Young Scientist from the Canadian Phytopathological Society in 1985. His work in monitoring virulence shifts and race patterns of *Puccinia coronata* f. sp. *avenae* in the eastern prairie region has shown the rust fungus is extremely diverse due to the importance of the sexual state in North America, particularly in the mid-western regions of the United States and in the eastern prairie region of Canada. Resistance of major seedling resistance genes, e.g., *Pc48*, *Pc68*, recently deployed in commercial oat cultivars, was overcome by the highly variable pathogen within several years. Additionally, recent virulence data showed that the *Puccinia coronata* f. sp. *avenae* sexual population is

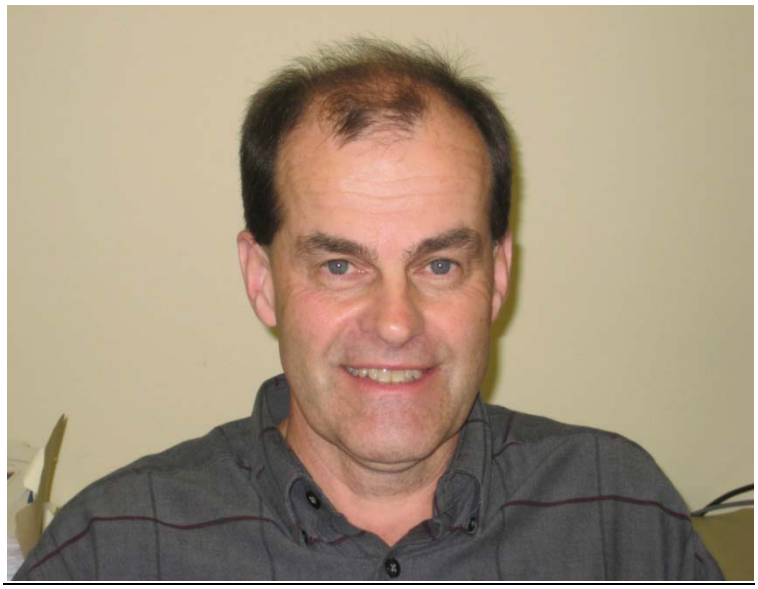
endemic in the eastern prairie region, and is playing a major role in initiating early crown rust epidemics for this region. His screening of exotic *Avena* species has provided much needed, new effective sources of resistance, which he characterized genetically and introgressed into suitable background for use in breeding programs.

Dr. Chong's collaborative work USDA scientists has led to a better understanding on the genetics of adult-plant/partial resistance, a form of resistance which is considered to be more durable than major seedling resistance. His collaborative work with molecular biologists at CRC, University of Saskatoon, and at ECORC, Ottawa, and with USDA molecular biologists at the University of Minnesota and at National Small Grains Research at Aberdeen, Idaho, led to development of various types of molecular markers (Avenin, RFLP, PCR, SCAR, or SNP) for numerous crown and stem rust resistance genes, including crown rust resistance genes *Pc38, Pc39, Pc48, Pc68, Pc91, Pc94,* and *PcX,* and stem rust resistance genes, *Pg1*, *Pg2*, *Pg4*, *Pg8,* and *Pg13*. Dr. Chong has contributed to the development of over 18 oat cultivars in his collaborative work with oat breeders in three AAFC Centres.

To date, Dr. Chong has authored or coauthored 97 peer-reviewed scientific papers, six book chapters, 79 Proceedings and Abstracts, and 115 technology transfer articles.

Dr. Chong was the Study Leader of the Oat Program at CRC (1995 – 2001).
Disease Coordinator, Western Cooperative Oat Test (1983-2007).
Member, Barley & Oat Disease Subcommittee, PRRCG. (1983-2010).
Member, International Oat Committee.
Western Canada Representative, American Oat Workers Conference.
Editor of the Oat Newsletter 1997-2000.
Adjunct Professor, University of Manitoba. (1983-2005).

At various times, Dr. Chong has received research funds from:
- Quaker Oats (6 years),
- North American Millers Association (3 years),
- Can-Oat (1 year),
- ARDI (Agricultural Research Development Initiative) – 3 years,
- AAFC Matching Investment Initiative (5 years).
- Dr. Chong was also a co-applicant of the research project, led by Dr. Curt McCartney, and funded by Agriculture Development Fund, SK. (5 years).



Grant Morrison

Grant Morrison has over 33 years experience with The Quaker Oats Company (a division of PepsiCo since 2001). Grant began his career with Quaker Oats as a Research Technician in Quaker's Canadian R&D organization after completing a graduate degree in Chemistry. His Quaker career has included work in the operations, R&D, and quality assurance departments, as well as the most recent work in the Regulatory and Government Affairs for PepsiCo. He has been a recipient of the Quaker Chairman's Award for Excellence. Besides his years of work with food, grains, and milling (and particularly oats), he was highly instrumental in setting up Quaker's allergen management program in the mid 1990's, for which Quaker was awarded Anaphylaxis Canada's "Susan Daglish Award for leadership and commitment to anaphylaxis safety" in 2001. Grant also led in the development of a confident and expanded Food Safety program necessary to enable launch of "peanut free" Quaker Chewy Bars, until recently PepsiCo's only 'allergen free' label claim.

For many years, Grant has been the primary Quaker/Pepsi-QTG point of contact with governmental agencies and departments regarding Policy Development and Crisis Management. Along with these duties, Grant has been the primary contact in Canada for much of Quaker's Oats varietal research programs during the past 10 or more years. His hard work, leadership, insights, and dedication to the advancement of oats breeding in Canada has been highly instrumental in the development and release of quality enhanced oats varieties in both eastern and western Canada. His critical eye to detail and quality has been an asset to not only oats breeders, researchers, and to Quaker, but also the Canadian seed industry. For the past several years, Grant has been the secretary and a leader for the Oats Quality committee of the Prairie Regional Recommending Committee for Grains (now the PGDC) in western Canada.

Grant has also been an active member of numerous industry scientific organizations, as well as representing Pepsi-QTG in leadership positions on a number of other trade and agricultural associations, scientific groups and committees. He has truly been a leader in the oats industry not only in Canada, but worldwide. Grant is well deserving of being recognized with a "Distinguished Service Award" from the American Oat Workers.

Howard Rines

Award for Distinguished Service to Oat Improvement

Dr. Rines grew up on a general crops/livestock farm in Indiana and received his BS (Agricultural Science) and MS (Genetics) degrees from Purdue University and PhD (Genetics) from Yale University. Following 2 years of military service and 5 years as an Assistant Professor in the Department of Botany at the University of Georgia, Athens, he joined ARS in 1976 as a Research Geneticist in the Plant Science Research Unit, St. Paul, with an adjunct appointment in the Department of Agronomy and Plant Genetics, University of Minnesota. He was promoted to GS-15 rank in ARS in 2000 and to Adjunct Full Professor in the University of Minnesota in 1989.

Dr. Rines' research in his ARS career has focused on oat genetics with emphasis on cellular and molecular approaches to oat improvement. Highlights of this research include recovery of the first haploid oat plant from another culture, participation in development of molecular marker maps in oat and mapping of oat genes for disease resistance and grain quality traits, production of partial hybrids of oat and corn, and sexual transfer of disease resistance genes from related wild species into cultivated oat. During his career he has authored or co-authored more than 90 journal articles and book chapters, advised or co-advised 17 MS or PhD students and 11 post doctorates, and served as co-Principal Investigator with University and other ARS colleagues on grants from Federal Agencies and Industry totaling more than $7,000,000. He has served as coordinator of the regional Uniform Early and Midseason Uniform Oat Performance Nurseries his entire ARS career. He also served as an associate editor for Crop Science, a Division 7 chair of the Crop Science Society of America, and secretary of the American Oat Workers Conference. He is a Fellow of the Crop Science Society of America and the American Society of Agronomy.

During his career, Dr. Rines provided an important connection between cellular- molecular research and applied cultivar development. His expertise and understanding of germplasm evaluation in the field coupled with molecular biology expertise enabled identification of research areas that would benefit applied breeding and provided important input that drew

applied and basic research closer together. He provided extremely valuable service in his careful coordination and reporting of the Uniform Early and Midseason Oat Performance Nurseries. He was familiar with germplasm lines in the Uniform Nurseries and could discuss the pertinent agronomic characteristics of the lines while readily recognizing traits of genetic interest for further study. After his retirement, Dr. Rines is again contributing beyond normal duty and continues to coordinate the Uniform Nurseries while remaining familiar with nursery entries. In addition to an extensive list of publications, he developed useful germplasm including crown rust resistance sources that he generously shared with breeding programs. These will continue to benefit oat improvement long into the future.

Dr. Howard Rines was outstanding in his advocacy for workplace and work assignment adjustments regarding the progressive disability of Richard Halstead, the technician who worked on his research project. Dr. Rines established a flexible workplace agreement which allowed Richard to work from home as necessary and remain productive in the oat research community. Dr. Rines' sensitivity and awareness made it possible for Richard to continue to be productive until his retirement. Dr. Rines received the USDA-ARS Midwest Area Equal Opportunity Award for his exemplary efforts on behalf of disabled.

Dr. Gregory E. Shaner – Purdue University

Dr. Greg Shaner grew up in Portland, Oregon and completed his B.S. in 1964 and his Ph.D. in 1968 at Oregon State University. During his college days, Shaner spent several summers working for the U.S. Forest Service, providing fire suppression, disposal services and campground maintenance. Being a true Oregonian, he is an outdoor enthusiast. He is currently involved locally with "Trees Lafayette" and enjoys sailing and woodworking and spending time with his family.

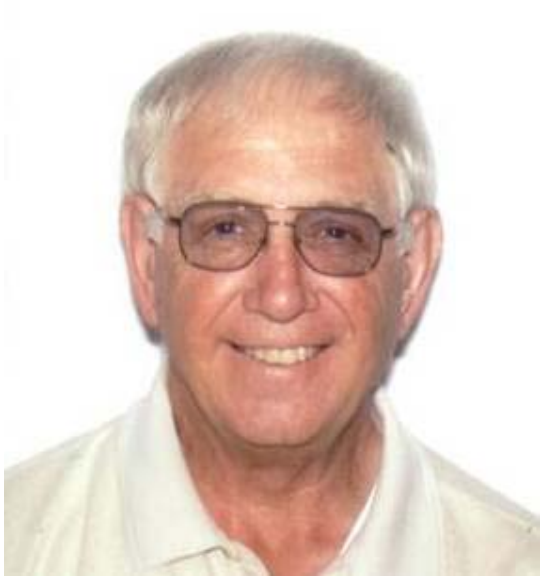
Greg Shaner came to Purdue University in 1968 as an assistant professor of plant pathology. For 40 years he was an imaginative and highly productive plant scientist who devoted his research efforts to host plant resistance, plant genetics, plant breeding, crop protection, and disease epidemiology related to the improvement of soft red winter wheat and spring oat. He was a member of a research group that included other plant pathologists, agronomists, and entomologists who focused basic and mission-oriented developmental research to answer basic questions related to the development of improved germplasm useful in the improvement of cultivars. Shaner was directly involved in the development of 15 cultivars and 4 germplasm lines of soft red winter wheat, and 4 cultivars of spring oat. Several of these have become leading cultivars in the eastern United States, as well as important sources of germplasm for other cereal breeding programs throughout the world. The importance of these cultivars is that they combine superior agronomic traits, grain quality, and resistance to a broad spectrum of diseases.

During his career, Dr. Shaner was one of only a few cereal pathologists who bridged the spectrum from molecular bases to field expression to actual breeding for disease resistance. His contributions to the development and release of multiple soft wheat and spring oat cultivars earned him the highest acknowledgement of being named a "Fellow" by both the Crop Science Society of America and the American Phytopathological Society.
Dr. Shaner brought very effective leadership to state, regional, and national agricultural groups and committees including the American Oat Workers Committee, the Oat Crop Advisory Committee, the Indiana Crop Improvement Association Board of Directors, and regional

committees NCR-15, and NCAC-14. He served as vice-chairman of the Agricultural Chemicals Study Committee, Indiana Institute of Agriculture, Food and Nutrition. In his multiple roles during his career, Dr. Shaner has helped define oat research priorities and scientific manpower needs during times of budget reductions, or shifts from an applied to a basic emphasis within ARS/USDA, and of increased interest and opportunities in oat research due to health and nutritional attributes.

Shaner's research program constituted only one aspect of his wide ranging professional activities, which also included teaching, administration and service. For many years he taught a successful, well-received graduate-level course in plant disease resistance. Shaner was one of the department's most dedicated, consistent and conscientious teachers. He excelled as an educator, mentor, and friend to numerous undergraduate and graduate students over the past 40 years. He served as a major professor for 18 Ph.D. and M.S. students and on the advisory committees on more than 100 other graduate students at Purdue University.

Shaner received numerous invitations to lecture, both nationally and internationally. He served as head of the Department of Botany and Plant Pathology from 1982-1987, supervising a large and diverse group in research ranging from cell physiology through weed science and plant pathology. His involvement in field research over the past 40 years and in extension for the last 15 years gave him a thorough understanding of crop disease encountered in the field and the technical skills and information needed to solve problems. He is well respected throughout the State of Indiana, nationally, and internationally for his presentation skills, knowledge, and professionalism. He is an educator at many levels.



Deon D. Stuthman

Award for Distinguished Service to Oat Improvement

Dr. Deon Stuthman grew up on a farm and received his early education in eastern Nebraska. During his sophomore year in high school, he set a goal of earning a Ph.D. in either plant genetics or soil chemistry. Fortunately for the oat improvement community, plant genetics was his chosen area of interest. In pursuit of this interest, he entered the University of Nebraska and worked three summers in the Winter Wheat/Small Grain Breeding Project with notable plant scientists such as V.A. Johnson and J.W. Schmidt. After completing his B.S. in Technical Agronomy in 1962 he proceeded to Purdue University where he received his M.S in 1964 and Ph.D. in 1967 in Plant Breeding and Genetics. Dr. Stuthman joined the faculty of the University of Minnesota Department of Agronomy and Plant Genetics in1966 working in the area of Oat Breeding and Genetics. He retired officially in June 2009, but remains active in oat research as Professor Emeritus.

During his 43 years at the University of Minnesota, Dr. Stuthman advised more than 50 graduate students for 1 or 2 degrees and remains an important mentor for former students. He has become a mentor to oat scientists around the world through his activities in international agriculture. He made his first trip to Mexico as a consultant for oat improvement programs and continued annually until 1994 when he began travelling to oat research programs in the southern cone of South America as a consultant with the Quaker Oat Improvement Program in South America. As a mentor to these programs, he contributed to the development of more than 25 oat cultivars in Mexico as well as approximately 20 cultivars in Brazil, Argentina, and Chile.

Dr. Stuthman's breeding program released 19 successful cultivars in Minnesota beginning with 'Otter' in 1970 and most recently 'Winona' in 2005. His program continues to produce superior lines that will be the foundation of further Minnesota cultivar releases. His research program demonstrated the effectiveness of recurrent selection for improvement of traits as diverse as grain yield and crown rust resistance. He and his long time colleague in Plant Pathology, Matt Moore, were early proponents of durable nonspecific crown rust resistance to protect the oat crop

and he developed germplasm with nonspecific resistance that provides a genetic basis for oat cultivars with durable resistance to crown rust. He collaborated with grain quality scientists to provide fundamental information on oat milling quality. Dr. Stuthman provided research leadership for sustainable agriculture groups and is a strong advocate for sustainable agriculture practices.

Dr. Stuthman received many awards during his career which include selection as a fellow of the American Society of Agronomy (1987), Crop Science Society of America (1987) and American Society for the Advancement of Science (2009). He served as president of the Council of Agricultural Science and Technology (CAST), President of Minnesota-Uruguay Partners of America, a member of the Organizing Committee for the National Plant Breeding Workshop Planning Committee. He served as chair of many important University committees including one of his other passions, the University of Minnesota Athletic Committee.

He is an active participant in national and international oat organizations. He is an effective advocate for increased oat research funding and is a charter member of Oat Research Lobby Group working in conjunction with American Oat Association/North American Millers Association. In this capacity he traveled to Washington, DC annually since 1981 to explain the importance of oat research to members of congress. He has serve on nearly all committees involved with oat improvement in North America, was Chair of the Local Host Committee for the 8th International Oat Conference held in Minneapolis in 2008, hosted an American Oat Workers Conference in St. Paul, and is the current Chair of the International Oat Committee through 2012. Deon Stuthman's service to local, national and international oat improvement is ongoing and he is a friend and mentor to all in the oat community.

Posters

Detection and Quantification of FHB-causing Fusarium spp. in oat using RT-PCR. W. Yajima[1], X.M. Zhang[1], F.L. Dokken-Bouchard[2], A. Tekauz[3], R.A. Martin[4], A. Beattie[1], G.J. Scoles[1], and B. Rossnagel[1].
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New Advances in Marker Assisted Selection for Winter Hardiness in Oats. P. V. Maloney, P. V. Maloney[1], J. H. Lyerly[1], D. R. Wooten[1] , J. M. Anderson [3], D. P. Livingston III[2], G. Brown-Guedira[2], D. Marshall[2], and J. P. Murphy[1]
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Large Scale Microsatellite Development for Oat (Avena sativa) using enriched Libraries. Ziya Dumlupinar[1], Rick Jellen[2], Joe Anderson[3], Mike Bonman[4], Martin Carson[5], Don Obert[4], Eric Jackson[4]
[1]Kahramanmaras Sutcu Imam University, Department of Agronomy, Kahramanmaras, Turkey; [2]Brigham Young University, Department of Plant and Wildlife Science, Provo, UT, USA; [3]USDA-ARS Crop Production and Pest Control, West Layette, IN, USA; [4]USDA-ARS Small Grains and Potato Germplasm Research Unit, Aberdeen, ID, USA; [5]USDA-ARS Cereal Disease Laboratory, St. Paul, MN, USA;

Effect of Feeding Enzyme Deactivated Oats Using a Rat Model
Xinzhong Hu, Hongmin Zhen, Peipei Zhang, Chao Xu, Guangzhong Luan
College of Food Science & Engineering, Northwest A&F University, Yangling, Shaanxi, China

AMERICAN OAT WORKERS CONFERENCE 2010

ABSTRACTS OF SESSION TALKS

DArTing the CORE. Nick Tinker, Andrzej Kilian. AAFC / Diversity Array Technology

The forthcoming oat SNP platform promises to provide an exceptional new genomics resource for use by the oat community. In order to expand this resource, and link it most effectively to past and current work, the CORE project will also enhance and utilize the recent oat DArT genotyping platform. All germplasm and mapping populations in the CORE project will be genotyped using the current version of the DArT genotyping array. This will provide an important link between work based exclusively on the DArT platform, and/or future work that could be based exclusively on the SNP platform. In addition to this, funds are available for one of two options: (1) an expansion of the current DArT genotyping platform, or (2) an implementation of a new sequence-based DArT genotyping approach. DNA sequence data from DArT representations of 8 oat varieties will be presented in order to evaluate the latter option, and a group discussion to plan the next steps in this module will follow.

SNPs mining: from ESTs and DArTs. Nick Tinker. AAFC Ottawa, Canada

The recent sequencing of cDNA libraries from 20 diverse oat varieties has provided an unprecedented library of expressed sequence tags (ESTs) from oat, and an opportunity for detailed analysis of genetic variants in oat DNA. We have also sequenced genomic representations based on Diversity Array Technology (DArT) from the same oat varieties. Together, these two DNA sequence resources have allowed us to custom-design SNPs from both coding and non-coding regions of the oat genome. As we begin to associate these SNPs with the inheritance of desired oat alleles, we will be able to design precise and rapid assays for use in diagnostics and oat breeding. This presentation will summarize what we have learned from detailed analysis of EST and DArT-based DNA sequence assemblies, and will outline some of the challenges that are being overcome in the development and utilization of an oat SNP resource.

Mapping the Oat Genome. Rebekah Oliver[1], Andrzej Kilian[2], Gideon Ladizinsky[3], Abraham Korol[4], Gerard Lazo[5], Rick Jellen[6], Joseph Lutz[7], Nick Tinker[8], Joseph Anderson[9], Ziya Dumlupinar[10], Nicole Wisniewski[1], Robert Campbell[1], Irene Shackelford[1], Jeff Maughan[6], Shiaoman Chao[11], and Eric Jackson[1]

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Development of a genetic linkage map for hexaploid oat (*Avena sativa* L. 2n = 6 x = 42) that defines all 21 chromosomes has been hindered due to the lack of oat-based markers and the size and complexity of the oat genome. Recent efforts in oat DArT, SSR, and SNP marker development should improve map resolution. In addition, development of a complete tetraploid linkage map with DArT, SSR, and SNP markers complementary to a hexaploid map would allow direct alignment and possibly the elucidation of marker positions in the more complex hexaploid genome. The objectives of this work were to: i) develop new oat-based SSR and SNP markers, ii) update the existing Ogle1040/TAM O-301 linkage map with the new markers, iii) physically anchor the new OT map to chromosomes using DArT aneuploid dilution analysis, iv) expand the existing DArT marker array to include representations from *A. maroccana* (2n = 4x =28), and v) construct a tetraploid linkage map with markers complementary to the Ogle1040/TAM O-301 linkage map,. We will present our overall mapping efforts in both hexaploid and tetraploid oat using the MultiPoint map construction approach. In addition, we will report on the first 21-linkage-group map of hexaploid oat partially anchored to chromosomes. We will also report the first complete tetraploid oat map and reveal preliminary alignments between the oat species.

Molecular Breeding in Oat; Technology Development and Applications in Novel Food and Feed. Bräutigam, M.[1] , Chawade, A.[2], Sikora, P.,[2] Viveknande, V.[2], Olsson, O[2] [1]CropTailor AB, Erik Dahlbergsgatan 11A, SE-411 26 Göteborg, Sweden and [2]Department of Plant and Environmental Sciences, Carl Skottsbergs gata 22B, Gothenburg University, SE40530 Göteborg, Sweden

Classical breeding has been very successful over the years but when it comes to efficiently engineer specific biochemical or multigenic pathways, breeding has its limitations. However, recent developments within the field of high frequency mutagenesis in combination with molecular based, high precision selection methods open the door to novel applications [1]. To increase the genetic variation in oat breeding we have produced a TILLING-population of 2,500

lines, each carrying approximately 6,5 million different mutations [2]. We have also sequenced more than 650,000 ESTs from a normalised cDNA library from developing seeds using the 454 FLX titanium platforms. These sequences have been assembled into 13,232 contigs (> 700bp) with an average coverage of 4,9 X. We are now in the process of analysing these sequences using our previously developed annotation pipeline [3]. We have also developed various bioinformatic methods to define which key genes to mutate in order to modify a specific character [4]. Taking advantage of this information we can screen our oat TILLING population for point mutations (SNPs) in specific genes at the genomic level using an optimised MALDI-TOF based method [2]. In addition, by scaling down and optimising biochemical assays for lignin, ß-glucan and sterol quantification and by using these assays in large scale screenings we have identified several promising lines in the TILLING-population that display altered levels of these macromolecules. Eventually, the use of these technologies will lead to the development of oats with a higher value both for farmers and end-users.

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Harnessing New Technologies for Sustainable Oat Production and Utilisation (QUOATS).

Catherine Howarth, Tim Langdon, Sandy Cowan, Irene Griffiths, Athole Marshall and Wayne Powell. IBERS, Aberystwyth University, Gogerddan, Aberystywth SY23 3EB

This newly funded project is developing core underpinning molecular technologies for the identification of specific genes and markers associated with key traits that will increase the use of oats in sustainable production systems. It will validate and apply molecular markers already identified to assist selection in oat breeding. In particular diploid progenitor species are being used as a model for the improvement of cultivated hexaploid oats building on existing extensive phenotypic and genetic analyses of both diploid and cultivated oats. The reduced complexity of working with a single genome and presence of high levels of polymorphism have been used to develop a genetic map at the diploid level between two A-genome parents differing for a range of grain and agronomic characteristics. Genomic resources (EST sequences, BAC libraries) and novel populations are being created and used to elucidate the genetic basis of key traits.

Mapping Genetic Diversity of Naked Oats with AFLP Markers. Zongwen Zhang, Wei Xu, Bin Wu. Institute of Crop Science of Chinese Academy of Agricultural Sciences, China
Email: Zongwenz@163.com

A total of 281 accessions of naked oats were analyzed with 20 AFLP primer combinations. The Amplification created 1137 bands, of which 260 were polymorphic. The diversity index was varied among different geographic groups of naked oats from China. Accessions from Inner Mongolia and Shanxi of China were most diversified. Comparison on genetic variation was made between Chinese accessions with those from other countries.

Oral presentation at Session one: Oats molecular genetics

Bioactive Fiber and Protein in Cereal Grains. Wally Yokoyama. USDA, ARS, Albany,CA,USA

Whole grains are associated with lowering risk factors for cardiovascular disease and diabetes. However, 80% of grains consumed in the U.S. is wheat and the typical consumer in 2003 had only one serving of whole grain/day. There is a need to increase whole grain consumption and oat is a good candidate. Bread made entirely of oat flour was found comparable to whole wheat bread by a consumer sensory panel. The consumer is knowledgeable about the heart healthy claims for oat as shown by the demand for breads containing oat. Oat contains beta-glucan a soluble fiber that lowers plasma cholesterol. In our research we have shown that beta-glucan and some other soluble fibers have a wider health promoting application. Soluble dietary fibers prevent increases in plasma cholesterol, triglycerides, fasting glucose and insulin; blood pressure, abdominal adiposity, insulin resistance and other signs of obesity related metabolic disease. Recently soy and cereal proteins have been shown to contain bioactive peptides that reduce blood pressure, cholesterol and perhaps prevent diabetes. Once the sequence of the bioactive peptides are known, their gene sequence in oat can also be determined. Our research has shown that a factor in barley may also reduce the synthesis of cholesterol in the liver.

Effects of Feeding Enzyme Deactivated Oats Using a Rat Model. Xinzhong Hu*, Hongmin Zhen, Peipei Zhang, Chao Xu, Guangzhong Luan. College of Food Science & Engineering, Northwest A&F University, Yangling, Shaanxi, CHINA 712100, Correspondence E-mail: hxinzhong@yahoo.com

Abstract: In order to keep oat products for a long time, it is necessary to deactivate its enzyme. At present, frying, steaming and Infrared roasting are commonly used to deactivate enzyme, but the influence of inactivation methods on oat nutritional effects is unclear. The objective of this study was to investigate the nutritional effects of oat treated by different enzyme inactivation methods. 50 SD rats (ten per group) were fed for 4 weeks with an oat-free control diet, untreated

oat diet, fried oat diet, steamed oat diet, and Infrared roasting oat diet, which containing 50% different treated oat whole meal.

Rats fed with oats had significant higher final body weight (P<0.05), body weight gain (P<0.05), fecal wet weight (P<0.01), fecal dry weight (P<0.01) and Fecal moisture content (P<0.05). But there is no significant difference in different oat based diet Groups.

Total cholesterol (TC) and total glucose (TG) of Rats in Untreated oat group and IR group decreased significantly (P<0.05) when compared with rats of Control group. Rats consumed oat based diet had significant lower (P<0.05) LDL-C and significant higher (P<0.05) FFA, but there is no significant difference between different oat based diet groups. Fasting blood insulin of rats fed with oat based diets was lower than that in rats of control group, but there is no significant difference.

The total length of small intestine of rats fed with oat based diets increased significantly (P<0.05), pH value of rats fed with fried oat decreased significantly in Cecum (P<0.01) and Colon (P<0.05) when compared with rats in control group. Bifidobacterium and Lactobacillus in colon of rats of Fried group, Steamed group and IR group were significant higher (P<0.05) than rats in control group. But there is no significant difference in different oat based diet Groups.

The oat have the positive significant effects on the body control, blood glucose, total length of small intestine, Bifidobacterium and Lactobacillus numbers in colon of rats.

Key words: oat, enzyme deactivation, blood biochemical parameters, intestinal environment

Better Oat Fat. R. Dhanda.[1], B.G. Rossnagel.[1], A. Diederichsen.[2] and A.D. Beattie.[1] [1]Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8; [2]Plant Gene Resources of Canada, Agriculture and Agri-Food Canada Research Center, 107 Science Place, Saskatoon, SK, Canada, S7N 0X2

Oat is a very important crop for livestock feed and human nutrition. Increased interest in the health promoting properties of oat has led to the exploration of oat germplasm for improved nutritional quality. A study was conducted to evaluate the fatty acid profile of diverse accessions from the world oat collection preserved in the Canadian national seed gene bank, Plant Gene Resources of Canada (PGRC), at the Agriculture and Agri-Food Canada Research Centre, Saskatoon, Saskatchewan, Canada and from the Crop Development Centre, University of Saskatchewan oat breeding program. Accessions included a wide range of *Avena sativa* L. and other selected species from the genus *Avena* L. (*A. byzantina* K. Koch, *A. sterilis* L., *A. fatua* L. and *A. strigosa* Schreb.). The fatty acid profile of 650 oat accessions was analyzed using gas chromatography, revealing significant variability for the three major fatty acids in oat oil,

palmitic, oleic and linoleic acid. Some *A. sativa* accessions had higher oleic and lower palmitic acid levels. Some hexaploid wild oat accessions (*A. sterilis*) showed very high oleic and lower palmitic and linoleic acid versus the *A. sativa* average. Based on initial results, selected accessions were grown in 2009 in replicated field trials and evaluated again to determine the influence of the growing environment on fatty acid composition. The results suggest the possibility of improving the fatty acid profile of future oat cultivars for food and feed.

Avenanthramides in Oats: A New Method of Producing Whole Oats and Oat Ingredients with Greatly Elevated Avenanthramide Levels. F. William Collins. Agriculture and Agri-Food Canada, Eastern Cereal and Oilseed Research Centre (ECORC), KW Neatby Bldg., 960 Carling Ave., Ottawa, ON, Canada, K1A 0C6

Avenanthramides, of which over 35 distinct components have been found to date, represent the major readily-bioavailable, soluble phenolics present in the oat kernel These hydroxycinnamoyl alkaloids are found only in oats and have been shown to not only act as antioxidants but also to inhibit the pro-inflammatory processes associated with atherosclerotic disease progression. Based on recent *in vivo* pharmacokinetic results in humans and *in vitro* human vascular cell culture models, effective concentrations of avenanthramides required to influence vascular antioxidant status and the inflammatory response can be provisionally projected. Threshold response levels (approximately 30 to 60mg from a dietary source delivery system such as a 50g serving of oat bran) would require an oat product with at least 600 to 1,200 ppm total avenanthramides. This is a significantly higher concentration range than those currently recorded for existing oat varieties or existing whole grain oat products. Recently a process has been found that significantly increases the levels of avenanthramides in native oat kernels. Levels ranging from about 900 to 2,000 ppm in the whole groat, representing an enrichment factor of about 25- to 40-fold have been achieved by this process, without significantly altering the milling quality of the product. The process involves the concept of “false malting” wherein selected or pre-treated grain is conventionally malted but does not germinate. The selected oats refer to “dormant oat” varieties, i.e. varieties exhibiting secondary dormancy and preferably hulless, while non-dormant varieties can be made dormant using a simple dry heat process. In-depth HPLC analyses of avenanthramides from oats treated by this patent-pending process show little if any qualitative differences relative to untreated oats. Abrasion bran fractions show levels as high as 3,500 ppm total avenanthramides.

The Effect of Chemical Systemic Acquired Resistance Elicitors on Oat Avenanthramide Biosynthesis. Mitchell L. Wise. USDA, ARS, Cereal Crops Research, Madison, WI

Abstract. Oats produce a group of phenolic antioxidants termed "avenanthramides". These metabolites are, among food crops, unique to oats. They are potent antioxidants in vitro and have shown certain desirable nutritional characteristics such as inhibiting atherosclerotic plaque formation and reducing exercised induced inflammation in experimental systems. Although produced constitutively in the oat grain, the levels of avenanthramides tend to be highly variable in the oat crop and the levels are strongly influenced by environment, genotype and genotype × environment interactions. Recent work in my laboratory has shown that avenanthramide levels in vegetative tissue, and to some extent in the grain, can be enhanced by treatment with agrochemicals formulated to elicit systemic acquired resistance (SAR). Specifically these compounds are benzothiadiazoles (BTH) and isonicotinic acid (INA). Treatment of the plants by soaking the roots with BTH or INA or spraying the leaf tissue produced a strong up-regulation of avenanthramide biosynthesis within 48 hours. This response tends to be fairly long lasting (days to weeks). Treatment protocols and the dynamics of avenanthramide biosynthesis in various tissues of oat plants will be described in detail.

Therapeutic Bioactive Molecules from Oats (*Avena sativa L.*) for Use in Cosmetic, Personal Care Products. Paul Moquin*, David Fielder. Ceapro Inc., Edmonton, Alberta, Canada

Oatmeal has been used for centuries to provide relief from itching and irritated skin associated with a variety of dermatoses and colloidal oatmeal is recognized by the US Food and Drug Administration as a Type I skin protectant.

Over the past ten years, scientists have been identifying the active molecules from oats that provide therapeutic benefits and have generated conclusive clinical data. The therapeutic benefits of purified active oat ingredients has resulted in commercially available products using innovative processing technologies for cosmeceutical as well as a number of nutraceutical and medical applications.

While the market is modest in size at this time, new therapeutic ingredients from oats has provided greater profit margin to farmers and contract growers than typical commodity oat. Upon reviewing the innovative oat products currently available and the potential products that could have applications in future non-traditional markets, it is clear that the demand for higher margin specialty oats and oat actives will increase significantly over the next decade.

* Oral presentation presenter.

Impact of Molecular Weight of Oat Beta-glucan on Potential Health Effects. Hyun Jung Kim and Pamela J. White. Iowa State University

Beta-glucans from oats are valuable as dietary fiber in human diets. The molecular weight (MW) of the beta-glucan impacts viscosity of oat mixtures, as a predictor of the health benefits and sensory qualities of foods. Beta-glucan was extracted from oat flour and treated to yield high, medium, and low MW. The low MW beta-glucan (with low viscosity) bound more bile-acid than did high MW, indicating a greater cholesterol-lowering effect, and produced more short-chain fatty acids, providing an improved biological environment in the colon that reduces tumor formation. Thus, beta-glucan MW is an important consideration in developing nutritious and healthful oat-containing foods.

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Predictive Ability of Genomic Selection for Beta-glucan in Oats. Franco Asoro[1] , Mark Newell[1], William Beavis[1], Adrienne Lauter[2] and Jean-Luc Jannink[3]. [1] Dept. of Agronomy, Iowa State University, Ames, IA, [2] USDA-ARS, Ames, IA; [3] USDA-ARS, Ithaca, New York and Cornell University

Genomic selection (GS) strategies rely on densely positioned markers across the genome that can predict the total genetic value of an individual. Several simulation and empirical studies on the accuracy of GS in plants and animals have been encouraging. These technologies can hasten the improvement process of nutritional traits in plants like beta-glucan amount in oats. The objectives of this study are to explore the predictive ability of GS for beta-glucan using empirical data set and propose a recurrent selection scheme. Beta-glucan and DArT marker data of 446 elite oats from different oat breeding institutions in North America were used in various cross validation designs. Two models were used to estimate the marker effects while genomic estimated breeding values (GEBV) of each line was the summation of marker effects across loci. Predictive ability was computed as correlation between observed phenotype and GEBV in validation set. Results showed that factors that increase predictive ability are the number of individuals in training population, marker density, and genetic relationship between lines in training and validation data. The usefulness of genomic selection will be evaluated in a practical breeding program with a one-year breeding cycle time.

Mapping of Pc91 and its Postulation with Markers. C.A. McCartney, R.G. Stonehouse, B.G. Rossnagel, P.E. Eckstein, G.J. Scoles, T. Zatorski, and J. Chong. Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; (J.C.) Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada

Crown rust, caused by *Puccinia coronata* Corda f. sp. *avenae* Eriks., is one of the most important diseases of oat in North America. Crown rust resistant oat varieties are an efficient and effective control measure for managing crown rust. *Pc91* is a seedling crown rust resistance gene that is highly effective against the current *P. coronata* population in North America. The objective of this study was to develop DNA markers for *Pc91* for purposes of marker-assisted selection in oat breeding programs and resistance gene postulation. The *Pc91* locus was mapped using a population of one hundred F_7-derived recombinant inbred lines (RILs) developed from the cross CDC Sol-Fi/HiFi by single-seed descent from the F_4 generation. The RILs were evaluated for reaction to *P. coronata* in field nurseries in 2008 and 2009. The population was assessed with Diversity Array Technology (DArT) markers, which yielded 408 DArT markers suitable for linkage analysis. *Pc91* mapped to a linkage group consisting of 44 DArT markers. DArT markers were successfully converted to sequence characterized amplified region (SCAR) markers. Nine *Pc91*-linked SCARs mapped identically with the Diversity Array Technology (DArT) clones from which they were designed. Both the susceptible and resistant products of a tenth co-dominant SCAR were cloned and sequenced. A co-dominant Taqman SNP assay was developed based on a 3 base pair insertion-deletion (indel), and a co-dominant SCAR was developed for electrophoresis on DNA sequencer. A panel of 24 oat lines was screened with the SCAR and the Taqman markers to assess their utility for resistance gene postulation and marker-assisted selection in North American oat germplasm.

Durable Resistance to Oat Crown Rust: Can We Get There From Here? Marty Carson. USDA-ARS Cereal Disease Lab, St. Paul, MN 55108

Crown rust (*Puccinia coronata* f. sp. *avenae*) is considered the most damaging disease of oat and the use of race-specific seedling (*Pc*) genes for resistance has been the primary means of control. As these resistance genes from *Avena sativa* and *A. sterilis* were deployed in oat cultivars, corresponding virulence in the U. S. crown rust population increased rapidly, such that the effective lifespan of a resistant cultivar in the U.S. is now five years or less. Efforts are now turning to introgression of resistance from diploid and tetraploid *Avena* species, despite difficulties due to differences in ploidy levels and the lack of pairing of homeologous chromosomes between species.However, there is no evidence to suggest that this resistance is any more durable than previously deployed *Pc* genes. Strategies to enhance the durability of race-specific seedling genes include gene pyramiding, multilines and varietal mixtures, and regional gene deployment. Gene pyramiding, whether practiced consciencely or not by the breeder, has not led to an increase in durability, as the pathogen continues to increase in

virulence complexity. The use of multilines or varietal mixtures does appear to reduce crown rust development, but the level of control is inadequate to mitigate losses. Evidence suggests that such methods may actually increase the level of virulence complexity in the rust population. Although race surveys show some divergence in virulence frequencies between the winter and spring oat regions of the U.S., virulence to any *Pc* gene is not exclusive to either region, suggesting that regional deployment is not a viable strategy to enhance durability.

Race non-specific, or so-called 'partial' or 'slow-rusting' resistance to oat crown rust has been known for quite some time, but with a few exceptions, little progress has been made and oat cultivars with effective levels of partial resistance have not been released. The reasons for this vary from program to program but a few common themes emerge: it's easier to use the latest single race-specific gene (besides, when that gene loses its effectiveness, demand is automatically created for the newest release; it's called job security); it's hard to select for given the highly variable pathogen population (is it truly partial resistance or is it race-specific resistance with low corresponding virulence in the pathogen?); and the poor agronomics of the better sources of partial resistance (why should I add any more 'trash' to my program?) among others. Recent developments in methods in identification and phenotyping partial resistance along with marker technologies should reduce or eliminate some of the barriers. However, we should be under no illusion that improving the level of partial resistance in U.S. oat cultivars will be easy or quick. A significant long-term investment and coordinated effort in germplasm enhancement (or 'pre-breeding'), efficient phenotyping, and moving from QTL mapping to practical MAS for partial resistance QTL will be required. The relatively small size of the oat community in North America presents many challenges, but also opportunities for better coordination of research efforts. Increasing the level of durable, partial resistance in our cultivars represents one such opportunity.

Characterization of the Transcriptome in a Susceptible Reaction to BYDV-PAV Infection.
Joseph M. Anderson. USDA-ARS Crop Production and Pest Control Research Unit, Purdue University, West Lafayette, IN 47907

Understanding how a susceptible oat line responds to infection by BYDV-PAV has the potential to identify gene targets that can be manipulated to increase resistance to BYDV and CYDV viruses. Our primary approach has been to identify genes whose activity is either changed by the virus as it tries to reprogram the plant to make it a more conducive host for virus replication and systemic infection or changed by the plant to defend against the viral infection. 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. We have previously attempted to characterize these gene activity changes using the wheat Affymetrix gene array but with limited success. In these experiments only 9% of the genes (~6,000 out of

55,000 arrayed) contained on the array were able to be detected using oat cRNA as a probe. The genes detected represent a small fraction of the oat gene space and very few showed changes in their abundance. It is clear, therefore, that this approach was not very informative for identifying candidate response genes. Recent advances in high throughput sequencing have dramatically changed our ability to examine the oat transcriptome during virus infection, replication and systemic movement. Furthermore, this approach is unbiased because, unlike microarrays, we are not limited to a set of genes present on an array but what can be sequenced from total polyA+ RNA. We have used Clintland 64 for these experiments because it is highly susceptible to BYDV-PAV. RNA isolated from Clintland 64 plants that were untreated (Control) 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 construct cDNA which was sequenced using Roche 454 Genome Sequencer FLX System, with long-read GS FLX Titanium chemistry. Data from these experiments will identify genes whose expression has changed (induction and repression) as a consequence of virus treatment.

RT-PCR to Evaluate Selected Oat Lines for Differences in Relative Susceptibility to *Fusarium graminearum* or *F. poae.* W. Yajima[1], X.M. Zhang[1], T.S. Grewal[2], W. Yan[3], A. Beattie[1], G.J. Scoles[1], and B. Rossnagel[1]. [1]Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8. [2]Saskatchewan Research Council, 125-15 Innovation Boulevard, Saskatoon, SK, Canada, S7N 2X8. [3]Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6

Fusarium head blight (FHB) may be caused by a number of different species including *F. graminearum* and *F. poae*. *F. graminearum* is typically associated with deoxynivalenol (DON) production while *F. poae* can produce the more toxic T-2 and HT-2 toxins. For food or feed use, the presence of mycotoxins is ultimately a concern for oat producers. As part of our oat-FHB research program at the Crop Development Centre, University of Saskatchewan (funded in part by the Western Grains Research Foundation), we are screening various oat lines for differences in susceptibility to *F. graminearum* and *F. poae* using an RT-PCR based assay as well as toxin analysis in order to identify possible sources of resistance or tolerance. Here we report the standardization of a TaqMan-based real-time PCR (RT-PCR) assay to identify and quantify *F. graminearum* or *F. poae* on oat plants. Subsequent mycotoxin analysis revealed a strong positive correlation between DON concentration and *F. graminearum* DNA abundance from an oat field nursery (r=0.65) and a controlled environment growth chamber (r=0.75). Furthermore, there are obvious differences between varieties tested in terms of *Fusarium* DNA and mycotoxin abundance, indicating variability in susceptibility to FHB.

New Crown Rust Resistance Genes from Diploid *Avena strigosa* and Tetraploid *A. barbata* and their Transfer into *A. sativa.* Howard W. Rines, University of Minnesota, St. Paul, MN
Marty L. Carson, USDA Cereal Disease Laboratory, St. Paul, MN

Resistance to oat crown rust (*Puccinia coronata* f. s. *avenae*) was transferred from two accessions of the diploid oat species *Avena strigosa* into hexaploid cultivated oat *A. sativa* and is being transferred from several accessions of the tetraploid oat *A. barbata* into *A. sativa*. The initial transfer of a resistance gene (presumably *Pc94*) from *A. strigosa* CI6954SP (2*x* = 14) by a cross to 'Black Mesdag' (6*x* = 42), colchicine doubling of the 4*x* F_1 plant to produce 8x seed, followed by multiple backcrosses to 'Ogle' (6*x*) to produce 6*x* derivatives with rust resistance has been described (Rines et al., Euphytica 158: 67-79, 2007). Subsequent analysis of derived lines revealed two groups with the resistance gene stably introduced into independent, segregating sites. Ogle backcross 5 derived lines MN07BT306 and MN07BT333, with *Pc94* present at different sites, are available for use as crossing parents; however, virulence to *Pc94* has recently been identified.

Crown rust resistance from a second *A. strigosa* accession, PI258731, was transferred by a cross to 'Ogle,' followed by embryo rescue, colchicine doubling, and three backcrosses to IL02-8658. Derived lines with this stably inherited introgressed gene display a moderately susceptible reaction on very young tissue, but quickly become resistant in older tissues. No virulence has yet to be observed in field testing of adult plants in the St. Paul buckthorn rust nursery.

Transfer of resistance from several accessions of *A. barbata* indentified by Carson (Plant Disease 93: 363-366, 2009) into *A. sativa* has been initiated. One of these accessions, PI287203, like *A. strigosa* PI258731, shows a pattern of tissue development-age resistance. Whether this type of resistance, when introgressed into cultivated oats, might prove more durable than more-conventional full resistance is unknown.

Double Cropping Breeding of Oats in China. Changzhong Ren 1, 2 , Laichun Guo 2, Chunlong Wang 2. 1. China Agriculture University, Beijing, China; 2. Baicheng Academy of Agricultural Sciences of Jilin Province of China, Baicheng, Jilin, China, 137000. Correspondence E-mail:renchangzhong@163.com

Abstract:
The increased land degradation problem and shortage of forage reserve for over-wintering in diary production in northern China has accentuated the need for seeking alternative cropping systems. Thermal deficiency and low temperature are major limitations to cereal production in regions of 45° N, north-eastern China, and crop varieties with short growing season and tolerant to low temperature may extend cropping period. Three new oat varieties, Baiyan 8, Baiyan 9 and Baiyan 10, were bred in Baicheng Academy of Agricultural Sciences of Jilin Province of China .

These new oat varieties can be sown both in the spring and summer and thus it is possible to harvest two crops a year in the short growing season. The oat produced 2.4 Tones ha^{-1} and 1,6 Tones ha^{-1} grain when sown in spring and summer, everagly. In addition, 4.0 Tones ha^{-1} of oat straw are valuable forage for animal industry as fodder is great demand for over-wintering since the adoption of new policy to convert marginal cropland into grassland and forest and all animals must be fed in feedlots. The new varieties could be used to extend cropping system from one crop to two crops a year and to integrate forage crop into the farming strategy of food crop plus cash crop in this region.

Key words: Naked oats (avena nuda), Breeding, double cropping

Food Plot Research and Development for White-Tailed Deer: 30 Years of Experience. James C. Kroll and Ben H. Koerth, Institute for White-tailed Deer Management & Research, Arthur Temple College of Forestry & Agriculture, Stephen F. Austin State University, Nacogdoches, TX 75962

Abstract- Food plots for white-tailed deer (*Odocoileus virginianus*) have become increasingly popular Among landowners, hunting clubs and professional wildlife managers, for increasing antler quality, recruitment and harvest. Over the last three decades, we have conducted continuous research and development on several species and varieties of forage crops. This research begins with selection of potentially useful plants, selective breeding and field evaluation of performance, nutrition and deer preference in various geographic locations. In 1987, we began a significant program in cereal grain research, focused primarily on oat varieties. This work involves a cooperative effort with Louisiana State University. The work recently led to release of a new variety, LA-99017, which will be available in 2011 for deer food plot management. Work also continues on use of herbicides in weed control and management of oats when planted in combination with chicory, clover and forage peas. The presentation also will discuss use of electric fencing in establishing food plots, and controlling timing and intensity of grazing.

Surviving Winter: How do they do it? David Livingston[1], Tan Tuong[2], Cynthia Henson[3]. (1)USDA-ARS and North Carolina State University, Raleigh, NC, (2) USDA-ARS, Raleigh, NC, (3)Department of Agronomy, University of Wisconsin-Madison, USDA-ARS, Cereal Crops Res. Unit, Madison, WI

Freezing tolerance in plants is usually studied by analyzing metabolism and genetics *prior* to freezing, during cold- and freeze-acclimation. How the metabolism of a plant changes during recovery from freezing is generally overlooked. We have been using a variety of techniques to study oats during this period when the plant either dies, or produces new tissue and survives. We froze the winter hardy cultivar Wintok at -12C and after thawing, transplanted it under

controlled conditions. At 0, 1, 3 7, 14, and 21 days after transplanting we harvested crown tissue and produced over 100 serial sections of the bottom 4mm of each plant. A staining procedure was developed which allowed us to identify freeze-damaged tissue. Photographs of each section were processed to produce a 3D image of the crown. Using this approach we identified a region of the crown that forms a barrier around dead tissue and apparently prevents the expansion of damage into meristematic regions. Color recognition software was used to precisely quantify the volume of the barrier in each crown; this volume increased over time during recovery from freezing. Several metabolites from a metabolomic analysis were correlated with the increase in the barrier during recovery and they will be discussed. We also froze the non-hardy cultivar Fulhum at -8C and performed a histological analysis 7d after freezing. We will discuss similarities and differences to its hardy cousin Wintok in its response to freezing.

Breeding Oats for Forage. Saha M.C., J. Baker, H.S. Bhandari and J.H. Bouton. Forage Improvement Division, The Samuel Roberts Noble Foundation, 2510 Sam Noble Parkway, Ardmore, OK 73401

Ranchers and livestock producers in the southern Great Plains have used small grains for high protein pasture. Small grains are important component to the agricultural income in this region. Oats provide high-quality forage for cattle and sheep all over the world. The Noble Foundation initiated a breeding program to develop high-yielding, locally adapted commercial varieties of forage oat with emphasis to fall forage. Single, double, and three-way crosses were made among the parents selected from local cultivars and PI collections. Early generation evaluations were performed on Noble Foundation farms. Advanced lines were tested in multi-location trials alongside standard check cultivars. Seeds were planted between mid-to-late September and forage clippings started between late November and early December. Forage yield data were collected from clipped plots. Prior to jointing, clipping was suspended and the plants were allowed to produce seed. NF27, a facultative winter-type oat, has been developed which has prolific growth habit and excellent total, but especially high fall forage yield when compared to 'Dallas' and 'Harrison.' During six years (2002-2008) of testing, the average forage yield of NF27 was 5,112 lb ac^{-1}, of which 2,008 lb ac^{-1} (39%) was produced during early fall-winter. NF27 is recommended only as a graze-out cultivar. In a sheep grazing trial in 2008-09, an average 193 lb gain ac^{-1} was recorded which is the highest among the small grains (rye, wheat and triticale) tested. The average seed yield was 64.1 bu ac^{-1} with an average test weight of 36.5 lb bu^{-1}. NF27 showed better freezing tolerance than most of the cultivars developed for the southern United States. We are in the process of releasing NF27 for commercial production. A Foundation seed block has been planted in the 2009-10 season.

Effect of Fertilizers Application on Yield and Quality of Oats in Qinghai-Tibetan Plateau. Gensheng Bao, Qingping Zhou, Zhilin Han, Hongbo Yan. (Qinghai academy of animal and veterinary science, Xining, Qinghai, 810016)

Abstract: Effect of N and K fertilizers at various ratios on seed and straw yield, and seed quality of Baiyan No. 7 have been investigated in this study. The results showed that both seed and straw yield were affected by both N and K fertilizers ($P<0.05$), and they increased with increasing of fertilizer application until $N_{75}K_{105}$. Maximum seed and straw yield were $4.90*10^3 kg/hm^2$ and $9.86*10^3 kg/hm^2$ at $N_{75}K_{105}$. Variations of crude protein, crude fiber and crude fat were dependent on amount and ratios of fertilizer. Significant linear relations between the yield and fertilizer was found ($R^2=0.862$, $P<0.05$; $R^2=0.838$, $P<0.05$).

Extent of Linkage Disequilibrium in Oat. Mark Newell[1], Jean-Luc Jannink[2], Nickolas Tinker[3], Franco Asoro[1], Diane Cook[4], and William Beavis[1]. [1] Dept. of Agronomy, Iowa State University, Ames, IA. [2] USDA-ARS, Ithaca, New York and Cornell University. [3] Eastern Cereal and Oilseed Research Center, Canada. [4] Dept. of Statistics, Iowa State University, Ames, IA

The extent of linkage disequilibrium (LD) can have large implications on the power and resolution of genome wide association studies (GWAS) in plants. The objectives of this research were to explore the extent of LD in oat germplasm and define its implications for GWAS in oat. Twelve-hundred-five oat lines consisting of varieties, breeding lines, and landraces were genotyped using Diversity Array Technology (DArT) markers. In total, 400 markers were used in the study, thus 439 linked marker pairs were used to explore the extent of LD. Cluster analysis was implemented and visualization of principal components indicates that oat has weak population structure for the lines included in this study, mainly consisting of spring, hulled types. The extent of LD decayed rapidly with genetic distance; values of LD (measured as r^2) were 0.1 for markers located 2.5 cM apart. There were some minor differences between the extent of LD between clusters, which could have some effects on the design of GWAS in oat. The oat genetic map for the Kanota x Ogle mapping population is about 2000 cM. The results indicate that the minimum marker density required for GWAS in oat would be 1 marker every cM, though resolution could be greatly improved with greater density. It is suggested that marker density be five times this, thus about 10,000 DArT markers would result in high resolution GWAS for oat.

Introgression of Yellow Dwarf Disease Resistance from *Avena strigosa* into *A. sativa*. Herb Ohm[1] and Joseph Anderson[1, 2]. [1]Department of Agronomy, Purdue University, [2]USDA-ARS Crop Production and Pest Control Research Unit, West Lafayette, IN 47907

Yellow dwarf (YD) disease, caused by the luteoviruses BYDV and CYDV, causes significant crop production losses globally in oat. Only moderate resistance has been identified in cultivated oat, *Avena sativa* L., and incorporated in certain cultivars. More effective, although not complete, resistance has been identified in *A. strigosa*, a diploid species with the A genome. We identified two *A. strigosa* accessions, 6688 and 6691 that have more effective resistance than that of A. sativa cvs. Classic and Excel. YD symptom severity (0 = no symptoms to 9 = severe leaf yellowing/reddening and plant stunting) in field tests in which hill plots are infested with viruliferous (BYDV and CYDV) aphids (*Rhopalosiphum padi* L.) for *A. strigosa* lines 6688 and 6691, Clintland 64, Classic and Excel, respectively average 1.5, 1.5, 8, 3, and 3.5. BYDV and CYDV concentrations determined by ELISA, in plant tissue samples two weeks after infestation with viruliferous aphids in controlled tests, consistently average significantly lower for 6688 and 6691 than the *A. sativa* lines in the tests.

Crosses between each of the *A. strigosa* lines 6688 and 6691 were made by Dr. Howard Rines, USDA-ARS, St. Paul, Minnesota, and generously provided the F_1 seeds. At Purdue University, we backcrossed the F_I plants to Clintland 64 and other adapted *A. sativa* cultivars, phenotyping the segregating BC F_1 plants for symptom severity and by ELISA. We have collected root tip tissue from $BC3F_1$ seedlings, and soon will infest the plants with aphids that are viruliferous with BYDV and CYDV, phenotype them with ELISA and transplant the seedlings to the field for YD disease symptoms. Nulcear content will be determined using flow cytometry and chromosome cytology will be determined on selected plants.

Oat Crown and Stem Rust Resistance Breeding In North Dakota. M.S. McMullen. Department of Plant Sciences, North Dakota State University

Oat crown rust (CR) is the most serious oat disease in North Dakota and frequent crown rust infections result in the loss of yield and quality of susceptible cultivars. Stem rust occurs less frequently, but can cause severe losses. Genetic resistance provides the most economical control of these diseases. The North Dakota program utilized the combination of crown rust resistance (CRR) genes *Pc-38* and *Pc-39* that were provided by the Agriculture Agri-Food Canada (AAFC) program at Winnipeg to produce cultivars such as Steele that provided crown rust protection until 1989 when races virulent on the combination developed. Genetic studies of *Pc-38* determined Steele and the AAFC cultivar, Dumont differ by a chromosomal translocation involving the *Pc-38* locus. Progeny of Steele/Dumont crosses produced duplications for the Pc-38 locus resulting in lines with four copies of *Pc-38. Pc 62* and *Pc-63* were reported by AAFC to be effective resistance genes but occurred at the same locus as *Pc-38*, precluding combining them with *Pc-38.* When using lines with Pc38 in the translocated position in attempt to develop

a homozygous *Pc-38 Pc-62* combination, Pc-38 appeared to suppress resistance conferred by *Pc-62* in a dosage dependent manner.

As the *Pc-38,Pc-39* combination became ineffective against prevalent races, we turned to other sources of resistance including amagalon lines from Paul Rothman. After developing RAPD markers for the major CRR gene in Amagalon, *Pc-91*, we found that progeny of one of Rothman's lines possessed CRR genes in addition to *Pc-91*. The additional gene was likely derived from Aojss and conferred resistance to an isolate virulent on *Pc-91*.

For development of stem rust resistance (SRR) we relied again on AAFC to provide *pg-13* and Rothman to provide CI9221 with the *pg-a* complex which together provide broad stem rust resistance. These were combined in ND811386 that was never released in the US, but was released in Australia as the forage cultivar Cleanleaf. ND811386 and similar lines provide the genetic base for stem rust resistance in ND. 'Maida' was released in ND in 2005 with this SRR combination and CRR conferred by *Pc-68*. Soon after the release of Maida, CR races virulent on *Pc-68* appeared.

Progeny of IA B605X exhibited resistance to the new CR virulence and resulted in the release of 'Morton' in 2003. The CRR of Morton is linked in repulsion to SRR conferred by *pg-a* resulting in all SRR progeny from attempts to combine the two are CR susceptible. Subsequently, we developed lines with CRR from Morton closely linked with *pg-a* SRR and now use SRR as a marker for the presence of the Morton CRR gene. Since the combination of *Pc-68* and Morton CRR confer resistance the CR races prevalent in ND, we used Maida as a parent along with parents with the Morton CRR linked to SRR to produce lines currently resistant to races of stem and crown rust in ND.

Stem rust race TJS looms on the horizon as a serious oat disease threat. Australian scientists identified ND lines described as extremely slow rusting when exposed to stem rust. We are using these lines to explore slow rusting to provide stem rust protection.

Quaker International Oat Nursery. R. D. Barnett, S. A. Harrison, D. D. Stuthman, & L. C. Federizzi. University of Florida, Louisiana State University Agricultural Center, University of Minnesota, University Federal Rio Grande de Sol, Brazil.

The success of any plant improvement program is dependent on the availability of genetic diversity. Plant breeders must have genes for the characteristics they need in new varieties available in the germplasm pool they are working with in order to develop improved new varieties that are adapted to specific uses, and environmental conditions that occur in various regions around the world. We coordinate this oat germplasm exchange nursery that contains

about 250 new lines and segregating populations each year and is distributed annually to 20 locations around the world.

The objective of the nursery is to provide new germplasm to oat breeders that will allow them to release improved cultivars that are more productive, have better disease and insect resistance and have improved quality characteristics that serve the oat industry and consumers. A number of oat breeding programs contribute new material to the nursery each year. Entries in the nursery come from the northern spring oat area of the US and Canada, the winter oat production area of the southern US, Australia, New Zealand, Brazil, Argentina, Uruguay, and other oat production areas of the world. The germplasm is handled in accordance with the Oat Workers Code of Ethics and intellectual property protection is afforded to the breeders originating the material in the nursery. There are detailed procedures for releasing varieties developed from pure lines and segregating populations of the QION.

We greatly appreciate the material oat breeders have allowed us to enter in this germplasm exchange nursery. The nursery continues to be a primary source of new germplasm for a number of the breeding programs receiving this nursery. New cultivars are released each year from selections made from this nursery.

This nursery originated in 1974 as part of a project established by Dr. H. L. Shands at the University of Wisconsin with funding provided by a grant from the United States Agency for International Development (USAID). The grant provided funds for the project which was entitled “Breeding Oat Cultivars Suitable for Production in Developing Countries” through 1976. Quaker assumed funding responsibilities for the project after the USAID grant expired and has continued support until the present. So the project currently has a 37 year history.

The focus of the project has been in developing oats for the primary growing areas in South America particularly in Brazil, Argentina, & Chile, but the nursery distribution is worldwide and benefits many programs. The principal activities of the coordinators have centered on developing a germplasm exchange nursery that has made new pure lines and segregating populations available to breeders world-wide. The nursery normally contains about 100 pure lines that represent the very best new germplasm we can gather to make available for crossing purposes by breeders worldwide. Occasional some of the pure lines have been released in a new area with the permission of the owner. One of the most recent examples of this was the release of a New Zealand line by the Carillanca Research Station near Temuco, Chile. When we were in Chile this past December this new variety which was named “SuperNova” was being grown on 10% of the acreage and it was only the second year after its release and it was expected to be grown on at least 20% of the acreage this coming year. Royalties from seed sales of this variety were being returned to the originating breeder.

The nursery also contains 150 or so segregating populations that are in the F2 – F4 generations. We cross pure lines that have excellent crown rust, stem rust, BYDV & other disease resistances coupled with good milling quality, high grain yield, lodging resistance, and other traits of importance. Crosses are normally made between parents of diverse origin and the target

environment for a particular cross is understood based on prior experience and an understanding of the participating programs. We have used various strategies in our crossing program but in recent year we have made a lot of winter X spring crosses with the F1 top-crossed with adapted material from the various countries where the nursery is being sent. We include a lot of diversity in the nursery since it is grown in a wide array of climates. Since some of the countries now have fairly well adapted material we have started making 3-way crosses where we cross an adapted line X 'exotic line' and then back to a different adapted third parent. An example of this type of cross would be the following: UFRGS Guapa/LA99016//BW-33, where the second parent is a 'good Louisiana line and the other two are adapted material from Brazil and Argentina, respectively.

We make use of an off-season nursery location at the USDA facilities in Aberdeen, Idaho so we can get two generations/year and also have very clean disease free seed to ship out in the nursery. We usually make up 25 sets of the nursery to distribute with each envelope containing 6 grams of seed. There are many different requirements for seed treatment, phytosanitary certificates, import permits, and shipping methods used to get the seed to each cooperator.

A second component of the program involves travel to the sites of the various cooperators to assist them with their breeding programs and to collect germplasm to put back into the nursery. The nursery is made of all new entries each year. The nursery has been grown at one time or another in the following countries:

Argentina	Iran	South Africa
Australia	Kazakhstan	Tunisia
Brazil	Mexico	Turkey
Canada	Morocco	United Kingdom
Chile	Nepal	United States
Ecuador	New Zealand	Uruguay

The oat research community has dwindled in number substantially over the past ten years. We believe that it is essential that oat researchers continue to exchange ideas and germplasm, and to share intellectual and other resources if oats are to remain a viable crop worldwide. The Quaker International Oat Nursery is the foremost system of germplasm exchange in oats and serves as a model for other crops.

Development of Oat SNP Markers Based on 454 Genomic Sequences from Tetraploid *Avena magna*. Rachel Redman, Peter J. Maughan, Eric W. Jackson, Rebekah Oliver, and Eric N. Jellen. Brigham Young University and USDA-ARS.

Avena magna (2n=4x=28) is an important tetraploid oat species of rising interest due to its high protein content, large caryopses, and exceptional crown rust resistance. This wild oat species has dramatic implications for gene domestication because it is a possible ancestor of cultivated oat .

Little is known about the molecular nature of A. magna. Here we report the use of genomic reduction and pyrosequencing for rapid marker discovery using two *A. magna* lines, BA 13-13 and Magna 169 , which are the parents of our *A. magna* mapping population. Parent Ba13-13 is a phenotypically uniform and cytogenetically stable line derived from dual-backcross hybridization with hexaploid A. sativa, followed by repeated selfing, to transfer Ladizinsky's domestication syndrome (non-shattering, yellow lemma, glabrous, reduced awns) into A. magna. Following a recently developed genomic reduction approach based on restriction-site conservation using unique multiplex identifier (MID)-barcodes , 454-pyrosequencing contigs were assembled and screened for Single Nucleotide Polymorphisms (SNPs). Putative SNPs are validated by a low-throughput genotyping technique called High Resoultion Melting (HRM), which is capable of detecting polymorphisms, mutations, deletions, insertions or epigenetic differences in double-stranded DNA. As these *A. magna*-based SNPs are validated, they are mapped onto the tetraploid population and also being screened for polymorphism using a panel of hexaploid mapping population parents.

AMERICAN OAT WORKERS CONFERENCE 2010

ABSTRACTS OF POSTERS

Detection and Quantification of FHB-causing *Fusarium* spp. in Oat Using RT-PCR. W. Yajima[1], X.M. Zhang[1], F.L. Dokken-Bouchard[2], A. Tekauz[3], R.A. Martin[4], A. Beattie[1], G.J. Scoles[1], and B. Rossnagel[1]. [1]Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8. [2]Saskatchewan Ministry of Agriculture, 3085 Albert Street, Regina, SK, Canada, S4S 0B1. [3]Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB, Canada, R3T 2M9. [4]Crops and Livestock Research Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PE, Canada, C1A 4N6.

Significant contamination of oat fields with trichothecene mycotoxins resulting from FHB could result in substantial economic losses to oat growers. Because different FHB-causing *Fusarium* species can produce a diverse array of mycotoxins, it is useful to know what species is present in a particular field. With the absence of significant or obvious disease symptoms on oat, diagnosis of FHB typically requires the detection, quantification, and identification of FHB-causing *Fusarium* species and mycotoxins. As part of a Western Grains Research Foundation-funded project, The Crop Development Centre at the University of Saskatchewan has developed an RT-PCR based assay to detect and quantify FHB-causing *Fusarium* species (*F. graminearum*, *F. poae*, *F. sporotrichioides*, *F. culmorum*, and *F. avenaceum*). Appropriate primers and TaqMan (6-FAM/TAMRA) probes were designed based on available sequence information. Here we report the results of a survey of Saskatchewan oat fields conducted in the summer of 2009 to assess the prevalence of *Fusarium* species. The overwhelming majority of tested fields (244 of 259) were contaminated with *F. poae* with *F. avenaceum* (61 fields) and *F. graminearum* (13 fields) being the next most common species. We also report the results of analysis of oat samples from FHB field screening nurseries in Portage La Prairie, MB and Charlottetown, PE to identify and quantify *Fusarium* species.

New Advances in Marker Assisted Selection for Winter Hardiness in Oats. P. V. Maloney[1], J. H. Lyerly[1], D. R. Wooten[1] , J. M. Anderson [3], D. P. Livingston III[2], G. Brown-Guedira[2], D. Marshall[2], and J. P. Murphy[1]. [1]North Carolina State University, [2]USDA-ARS, Raleigh, [3]USDA-ARS, West Lafayette.

Avena sativa, or Common Cultivated Oat, has the poorest winter hardiness Among the small grain cereals. Marker-assisted selection for improved winter survival in oat is difficult, as the number of SSR and other PCR based markers available in this species is limited. The objectives of this research were: 1) to increase the number of SSR markers on the Fulghum x Norline genetic map, and to scan for QTL associated with winter hardiness component traits, including winter field survival, crown freezing tolerance, vernalization response, and heading date, and 2) utilize an association mapping population to validate markers of interest from the Fulghum x Norline population that are most closely linked to the winter hardiness component traits. Phenotypic data for winter hardiness component traits in both the Fulghum x Norline population and the association population were obtained in field and controlled chamber experiments. All previously mapped markers and new SSR markers were evaluated and QTL identified. The Fulghum x Norline map now stands at 101 loci consisting of RFPLs and SSR's from the previous work, along with 60 new SSR markers and four new SNP markers. A subset of the SSR markers from the Fulghum x Norline map was used for an association study to better describe the effect of each allele. The markers that were validated in the association mapping population can be used in MAS for early generation testing of new lines.

Large Scale Microsatellite Development for Oat (*Avena sativa*) using Enriched Libraries. Ziya Dumlupinar[1], Rick Jellen[2], Joe Anderson[3], Mike Bonman[4], Martin Carson[5], Don Obert[4], Eric Jackson[4.] [1]Kahramanmaras Sutcu Imam University, Department of Agronomy, Kahramanmaras, Turkey; [2]Brigham Young University, Department of Plant and Wildlife Science, Provo, UT, USA; [3]USDA-ARS Crop Production and Pest Control, West Layette, IN, USA; [4]USDA-ARS Small Grains and Potato Germplasm Research Unit, Aberdeen, ID, USA; [5]USDA-ARS Cereal Disease Laboratory, St. Paul, MN, USA; E-mail: Eric.Jackson@ars.usda.gov

Microsatellite or simple sequence repeat (SSR) markers are ideal because of good polymorphism levels Among genotypes and even genome distributions. Currently, only 160 genomic-based SSR markers are publicly available for oat. The objectives of this study were to develop additional oat-based SSR markers from newly-enriched libraries. Libraries were enriched for CA, AAT, ATG and CATC SSR motifs using Ogle1040 genomic DNA. Preliminary screening of the libraries indicated good enrichment of the CA (90%) and ATG (79%) libraries, while enrichment of the AAT and CATC libraries was poor (11%). Subsequent sequencing of 1,536 clones from the CA and 1,536 clones from the ATG libraries resulted in 539 and 578 motifs for which primers could be designed, respectively. Of the 1,177 total sequences containing SSR motifs, 98 were redundant. Of the remaining 1,019 SSR markers, 517 produced SSR alleles,

while 243 produced polymorphic alleles across 11 oat lines, 118 of which produced robust assays. Interestingly, 68 primers producing robust assays interrogated alleles at a single locus, 27 interrogated alleles at two loci, and 21 interrogated alleles at three loci. False discovery analysis is currently being done on a subset of these alleles and will be reported. Diversity analysis of all eleven lines resulted in two major clusters. The first cluster included all hexaploid cultivars and the second cluster included the tetraploid species. Divergence between the tetraploid species was expected based on cultivation of the BA 13-13 line. Within the cluster containing the hexaploid lines, two major clusters were found. One sub cluster contained the winter lines TAM O-405 and Kanota while the second cluster contained all spring lines with the exception TAM O-301.

Validation analysis of the SSR primers indicated 146 were polymorphic between Ogle1040 / TAM O-301, 141 between Ogle1040 / Kanota, 136 between MN841801-1 / Noble-2, 131 between Otana / TAM O-405 and 134 between the tetraploid lines A169 / Ba 13-13.

In this study, a remarkable number of SSR markers have been developed for important hexaploid mapping populations segregating for key crown rust resistance genes. In addition, a large number of these SSRs were segregating in the tetraploid oat mapping populations. This will allow the development of markers linked to crown rust resistance to be used in marker-assisted selection. These markers will also enable comparisons between hexaploid and tetraploid genomes.

Effect of Feeding Enzyme Deactivated Oats Using a Rat Model. Xinzhong Hu, Hongmin Zhen, Peipei Zhang, Chao Xu, Guangzhong Luan. College of Food Science & Engineering, Northwest A&F University, Yangling, Shaanxi, China.

Oat (*Avena nuda*) is a minor grain crop and good source of protein, fat, minerals and B-complex vitamins besides heart-healthy soluble fiber β-glucan, used both for human and animal. With its functionality and high nutrition, oat was recognized as a healthy food containing a substance helped heart disease prevention, which became more popular for human diet.

In order to keep oat products for a long time, it is necessary to deactivate enzyme in oat. At present, frying, steaming and Infrared roasting are commonly used to deactivate enzyme, but the influence of different methods on oat nutritional properties is not clear. The objective of this study was to investigate the nutritional effects of oat treated by different methods.