



American Oat Workers Conference

July 21-24, 2024
Saskatoon, Saskatchewan, Canada



ORAL PRESENTATION ABSTRACTS

Thirty years of oat genomics: Out of the woods and into the field

Nick Tinker¹, Rick Jellen², Catherine Howarth³, Charlene Wight¹

¹Agriculture and Agri Food Canada, Ottawa, ON, Canada

²Brigham Young University, Provo, UT, USA

³IBERS, Aberystwyth, Ceredigion, UK

It has been just over 30 years since the first molecular marker maps were published in diploid oat, and not much longer since the first molecular tools were introduced to oat research. Today we have access to fully sequenced and annotated hexaploid oat genomes and a forthcoming pan genome. We are poised on the edge of thrilling possibilities in gene discovery, gene editing, pathway analysis, and many associated applications in oat improvement. For those at the beginning of their careers, 30 years may seem like a long, slow road to where we are now. For those whose careers have spanned this period, it was three decades filled with challenging puzzles and interesting discoveries. But we all might ask “why didn’t we just do something else for 30 years while we waited for the technology to assemble whole oat chromosomes without a map”. There are several parts to the answer: (1) no-one knew how long this road would be, or whether it even led to this place; (2) we did accomplish useful outcomes along the way; (3) the accumulated germplasm, populations, maps, phenotypes, QTLs, and cytogenetic knowledge were, and still are, essential for discovering and validating the causes of traits, and deploying that knowledge in oat improvement. In this talk, we will take a short trip down the memory-lane of oat research: the early breakthroughs in cytogenetics; the first Quaker-sponsored initiatives in oat mapping; the days of RFLPs, RAPDs, and DARts; the Collaborative Oat Research Enterprise (CORE); the SNP maps and diversity analyses; and finally, the complete genome sequences. We will discuss some of the triumphs, the failures, the surprises, the motivators, and the people. We will also acknowledge that we already stood on the shoulders of giants from the more distant past: the oat breeders, geneticists, cytogeneticists, physiologists, pathologists, and others who recognized the importance of patient observation, of adopting new tools, and of mentoring and encouraging our generation. We hope this perspective will be both interesting as well as informative for those who will carry the torch into the next 30 years.

The international oat pan-genome project (PanOat): Unveiling the genetic diversity and structural variants in hexaploid oat genomes

Nadia Kamal, Martin Mascher, Raz Avni, Manuel Spannagl, Wubishet Bekele, Thomas Lux

Technical University of Munich, School of Life Sciences, Computational Plant Biology, Freising, Germany

The International Oat Pan-Genome Project (PanOat) has developed high-quality, chromosome-scale assemblies for 32 oat genomes, encompassing both cultivated hexaploid oats and their wild relatives. These pangenomic resources highlight the genetic diversity of allohexaploid *Avena sativa* (haploid genome size approximately 10.9 Gb) and reveal the complex genomic architecture of oats. Comparative genomics provide insights into core and dispensable gene sets, as well as variations in gene presence, absence, and copy number. The genomes were annotated using long-read and short-read transcriptome data from 24 diverse accessions, derived from replicated tissue samples, including embryos, roots, leaves, stems, panicles, and caryopses, ensuring high-quality genome annotations. Additionally, a diverse panel of 295 spring oat varieties was skim-sequenced and complemented by replicated phenotypic data (CORE). This combination has enhanced high-resolution association genetics and facilitated the discovery and genotyping of structural variants. Specifically, a large inversion on chromosome 7D was found to be associated with earlier heading time in non-inverted genotypes. None of the three available Australian genome assemblies show this inversion, which may indicate adaptation to hot and dry conditions during maturation. Our comprehensive gene expression atlas elucidates gene expression dynamics within the oat pan-genome, revealing stable and dynamic expression patterns, as well as compensatory expression patterns of homoeologous genes in this polyploid plant. This thorough analysis deepens our understanding of the prevalence and impact of structural variants, thereby bolstering future gene isolation strategies and advancing population genomic studies in oats. The project not only sheds light on the complex genetic architecture of oats but also sets a precedent for genomic studies in polyploid crops.

Challenges and opportunities of oat genetic resources maintained at the Canadian national gene bank, Plant Gene Resources of Canada

Axel Diederichsen, Travis Sander, Colleen Nielson

Plant Gene Resources of Canada, Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, Saskatoon, SK, Canada

Plant Gene Resources of Canada (PGRC) maintains the largest collection of oat genetic resources world-wide. The collection contains 29 *Avena* species comprising nearly 28 thousand accessions, 55% of which are crop wild relatives. In 1977, PGRC accepted the role from the International Board for Plant Genetic Resources (IBPGR, today: Alliance Bioversity & CIAT) to preserve the “World Base Collection of Oat Germplasm”. All oat germplasm is integrated in the active PGRC collections and available for research, breeding and education. Back-logs in regeneration of the wild *Avena* species exist and pose a permanent challenge given that PGRC maintains all together germplasm of nearly 1000 botanical species of cultivated plants and their crop wild relatives. The PGRC website (www.agr.gc.ca/pgrc-rpc) is used to provide access to detailed information about the PGRC germplasm holdings. Active utilization of the PGRC oat collection occurs nationally and internationally. From 2005 to 2023 PGRC distributed 24,459 seed samples of all 29 *Avena* species to genebank clients in 28 countries. Canadian scientists have been very active in collecting and utilizing wild oat germplasm on breeding for resistance to crown rust and stripe rust diseases, and for breeding of hull-less oat. In recent years wild oat germplasm collections conducted by the Global Crop Diversity Trust and the Millenium Seed Bank of Kew Gardens were added to the active PGRC genebank collection. Deposits of recently released Canadian oat cultivars at PGRC have slowed down because additional seed storage capacities are needed at PGRC and breeders became more hesitant about depositing germplasm in public genebanks. The concept of global “Base Collections” has been given up. The usage of the PGRC genebank switched in recent years from plant breeders and associated research to molecular research in oat diversity. However, recent disease resistance screenings conducted at the University of Saskatchewan have also been supported by PGRC germplasm.

Towards CRISPR/Cas9-mediated fine-tuning of flowering time in oats: A novel tool for plant breeders

Mehtab-Singh¹, Wubishet A. Bekele², Nathan Liang², Jean-Sebastien Parent², Kirby T. Nilsen³, Nicholas A. Tinker², Jaswinder Singh¹

¹Plant Science Department, McGill University, Montreal, QC, Canada

²Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, Canada

³Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Brandon, MB, Canada

Flowering time is crucial for plant adaptation, impacting yield and other traits within cropping cycles and growing seasons. SQUAMOSA promoter binding-like proteins (SPLs) are plant-specific transcription factors that influence reproductive phase change, spike architecture, and flowering time in plants. SPLs are targeted by miR156 but the SPL/miR156 module is completely unknown in oat. We identified 28 SPL genes (AsSPLs) distributed across all 21 oat chromosomes except for 4C and 6D. A novel oat miR156 (AsmiR156) family with 21 precursors divided into 7 groups was characterized. Intriguingly, AsSPL3s showed high transcript abundance during early inflorescence (GS-54), as compared to the lower abundance of AsmiR156, indicating their role in reproductive development. Recently, our group and others have proposed another candidate gene involved in flowering/maturity, VRN3D located on chromosome 7D. This has been associated with a QTL influencing heading date and yield-related traits. We used CRISPR/Cas9 gene editing to understand its function and dissect its association with the aforementioned traits. We have successfully transformed and edited the oat genotype, Park for the first time with a high editing efficiency of up to 78.5 % in the T1 generation. We are functionally characterizing the gene-edited homozygous mutants at the molecular/ biochemical level to further advance our knowledge about the relationship of VRN3D with flowering time and grain yield.

Hyper-resolution phenomics facilitates the genomic characterization of seedling growth in response to drought in the oat landrace diversity (OLD) panel

Craig H. Carlson¹, Afrina Rahman^{1,2}, Suraj Sapkota³, Kathy Esvelt Klos³, David Evershed⁴, Chuan Lu⁴, Fiona Corke⁴, Gancho Slavov⁴, John Doonan⁴, Kevin Williams⁴, Catherine Howarth⁴

¹Cereal Crops Research, Edward T. Schafer Agricultural Research Center, USDA-ARS, Fargo, ND, USA

²Department of Plant Sciences, North Dakota State University, Fargo, ND, USA

³Small Grains and Potato Germplasm Research, USDA-ARS, Aberdeen, ID, USA

⁴Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Penglais, Aberystwyth, Ceredigion, UK

Greater agricultural productivity and sustainability is critical to meet the global challenges of food security in the presence of climate change. Renewed interest in diversifying our crop resources has developed as the world focuses on food security and the environment. Oat is a globally significant component of temperate cereal cultivation. Requiring fewer inputs than other cereal crops, oat can grow on more marginal land, which expands cropping options for arable production and mixed farming systems. The demand for oat as food has dramatically risen in the past 10 years due to its proven health benefits. This has driven research into understanding yield and quality traits under a wide range of environmental conditions and developing superior germplasm using innovative breeding methods. To successfully develop varieties that can withstand a rapidly changing climate, it is imperative we focus our attention to improving genetic variation in bio-diversity collections and breeding populations, including knowledge of a variety's optimal usage, which depends on a range of environmental aspects. Here, we have developed AI/ML techniques to measure and quantify variation in crop emergence metrics using high-throughput sensor data. As proof-of-concept, a replicated drought stress trial, consisting of an assembly of landrace oat accessions, dubbed the Oat Landrace Diversity (OLD) Panel, was conducted at the National Plant Phenomics Centre (NPPC, Aberystwyth University, UK). Exploiting both high-resolution genotype and phenotype data for GWAS, we discuss new genomic loci of high-effect associated with variation in oat seedling growth at four levels of water availability and response to drought. We expect that this research will have impact in diverse areas, such as enhancing food security in vulnerable regions, contributing to a more sustainable agricultural landscape, and increasing agricultural productivity. This research benefits farmers, the agricultural sector, policy makers, governments, consumers, and the public. Importantly, this technology can be easily transferable to any grass-like crop, enhancing its overall impact.

Physiological response to early-stage drought stress in commercial oat varieties cultivated in Sweden

Radha Sivarajan Sajeevan¹, Maria Vera Jesus Da Costa¹, Erik Alexandersson²

¹Department of Plant Protection Biology, Swedish University of Agricultural Sciences, Lomma, Sweden

²Sweden Department of Plant Breeding, Swedish University of Agricultural Sciences, Lomma, Sweden

Oat (*Avena sativa* L.) ranks seventh in the world's production of cereals. It is an important crop for the Swedish agriculture and food industry and is gaining popularity due to its high nutritional value. Erratic rainfall patterns and rising temperatures due to climate change, which lead to increased occurrences of drought and heat stress, are expected to cause significant declines in both oat production and nutritional quality. Early seedling drought stress poses a significant challenge for oats, hindering the establishment of a robust root system and uniform field growth. However, there has been little effort to identify drought-tolerant oat varieties that farmers could use for better survival and minimal yield loss. In this study, we have screened 14 commercial oat varieties cultivated in Sweden for their seedling-stage drought stress tolerance. The drought stress of 40 % field capacity (FC) was imposed through the gravimetric method after 15 days of germination. The plants were maintained at 40% FC for three days and allowed to recover thereafter. A control batch was maintained with 90-100% FC. The plants (drought-stressed and well-watered controls) were subjected to various physiological and key biometric parameters. We monitored the relative water content (RWC), electrolyte leakage (EL), photosynthetic rate (A), transpiration rate (E), stomatal conductance (gs), maximum quantum efficiency of Photosystem II (Fv/Fm), number of tillers, and upper ground biomass. Drought stress showed a significant reduction in plant height, number of tillers, and photosynthetic parameters with no significant change in Fv/Fm for all the oat varieties. Few varieties were, nevertheless, able to recover better than the others. The identified varieties will be valuable for breeding programs and targeted modification of the oat genome, aiming to incorporate traits that enable sustainable cultivation and tolerance to anticipated climatic stresses.

Understanding the role of root, stem, and leaf characteristics on oat lodging

Céline A.M. Ferré¹, Aaron Beattie¹, J. Allan Feurtado²

¹Department of Plant Science, University of Saskatchewan, Saskatoon, SK, Canada

²Aquatic and Crop Resource Development, National Research Council of Canada, Saskatoon, SK, Canada

Lodging, the permanent displacement of stems from their upright positions, is a critical issue impacting oat harvestability, disease, and yield, which can see yield losses ranging from 25-75%. Increased lodging resistance can come from agronomic practices or new plant genetics with resistance to root- and stem-based lodging. The goal of this research was to assess the relationships between lodging and various oat root, stem, and leaf characteristics and identify the most effective traits and tool(s) for selecting lodging resistance. The study utilized both multi-environment field trials and indoor root imaging to accomplish the objectives. The field trials were completed at three locations in Saskatchewan during the summers of 2022 and 2023 with 14 varieties grown in a randomized complete block design. Data collection in the field focused on stem strength, whole plant bending resistance, root crown characteristics, and leaf angle, which were assessed between mid-milk and soft-dough stages. Field trials revealed that plant height, internode length, flag leaf angle, whole plant bending resistance, root plate angle and stem inner diameter were significantly correlated to lodging. Indoor root imaging of 22 oat varieties, grown using hydroponic 2-dimensional pouches, assessed 23 root system traits in 4-, 10-, 14-, and 17-day-old seedlings. Root imaging revealed that the number of holes in the root system and median number of roots were significantly correlated to lodging, however they had lower correlation values, and therefore may not be suitable traits for lodging resistance selection. Overall, the study demonstrated the complexity of oat lodging with an inter-connected network of traits impacting lodging including height, internode length, flag leaf angle, bending resistance, root angle and inner diameter. These traits can be used to select for and improve lodging resistance, especially in the absence of visible lodging. For root angle, a correlation between early seminal root angle in the lab and root angle in the field demonstrates the potential to use this method for early selection of lodging resistance, although further work is required to validate its use in a breeding context.

Competitive ability of oat as row spacing increases

William E. May¹, Christian Willenborg²

¹Agriculture and Agri-Food Canada, Indian Head, SK, Canada

²Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada

In a no-till environment, as the row spacing widens seeding operations become more efficient allowing more hectares to be seeded in a day; however, at the same time the crop becomes less competitive with weeds as the row spacing widens. The impact of row spacing, cultivars and weed density on the grain yield and seed quality of oat was studied using five row spacings (25, 30, 35, 40 and 50 cm), two cultivars (AC Morgan and CDC Endure) and three weed densities (0, 13 and 26 canola seeds m²). This study was conducted in Saskatchewan at Indian Head and Saskatoon in 2023 and 2024. Optimum plant densities (300 plants m²) were reached at Indian Head but not at Saskatoon. As the row spacing increased there was a linear decrease in plant density at all four site-years. There was a linear decrease in oat biomass as the row spacing widened or the weed density increased. Weed biomass increased as the row spacing widened at 2 out of 4 site years. Oat grain yield tended to decrease as the weed density increased. With the suboptimal plant densities that were reached at Saskatoon the grain yield decreased as the row spacing increased. With optimal plant densities grain yield was stable as the row spacing widened at Indian Head. If producers want to use a wider row spacing the importance of reaching an optimum plant density is critical for maintaining the grain yield of oat.

Vernalization in winter oats

Catherine J. Howarth, Alys Reid Bacon, Fiona Corke, Sandy Cowan, Irene Griffiths, Marc Loosley, Sara Tudor, Tim Langdon

IBERS, Gogerddan Aberystwyth University, Penglais, Aberystwyth, UK

It is crucial to adjust the life cycle of cereals to the agro-environments in which they are grown in order to maximize production. Flowering is a key developmental transition in the life history of plants and has a major impact on grain yield in cereals such as oats. In temperate environments with a long growing season, late flowering ensures a long vegetative phase for maximal resource acquisition resulting in high grain yield potential. In environments where the growing season is shortened due to extremes of temperature or water limitation then early flowering is preferable. The shift from the vegetative to the reproductive phase is triggered by signals from the environment and is a response to the interaction of temperature and photoperiod. Considerable genetic variation exists for the control of flowering time and plant breeders continue to select for optimal flowering time to maximize yield for specific environments. The majority of temperate cereals can be categorized based on how they react to extended cold spells (vernalization) and long days (photoperiod). Winter cultivars typically require vernalization to promote subsequent flowering and commonly exhibit a significant promotion of flowering in response to growth under long day lengths. Spring cereals differ from winter cereals in their ability to initiate flowering immediately under a favorable day-length, without cold treatment of the seed. Winter cultivars obtain sufficient vernalization when sown in the field in the autumn but this character becomes increasingly important if sowing is delayed to the late winter and early spring when temperatures are rising and day length is increasing or if winter temperatures are insufficient for vernalization to occur. For plant breeding and research, the requirement of a long period of vernalization for winter varieties results in a long period from seed to seed. Development of speed vernalization protocols combined with speed breeding have the potential to dramatically accelerate generation time. In this presentation, the role of vernalization (both duration and temperature) and of photoperiod will be explored using varieties developed over 100 years of oat breeding at Aberystwyth University.

Oat crown rust: Understanding and managing a shifty enemy in the era of genomics

Eric Nazareno¹, Erin Moreau², Eva Henningsen³, Tim Hewitt³, Melania Figueroa³, Melanie Caffè⁴, Jason Fiedler⁵, Peter Dodds³, Brian Steffenson¹, Matthew Moscou², Shahryar Kianian²

¹University of Minnesota, St. Paul, MN, USA

²USDA-ARS Cereal Disease Laboratory, St. Paul, MN, USA

³CSIRO, Canberra, ACT, Australia

⁴South Dakota State University, Brookings, SD USA

⁵USDA-ARS Cereal Crops Research Unit, Fargo, ND, USA

Oat crown rust (*Puccinia coronata* f. sp. *avenae*, Pca) is a shifty pathogen causing significant damage to oat production across the globe. To better understand how Pca has changed in the United States, 30 years of USD survey isolates (n = 5,456) tested on 30 to 40 differential lines were analyzed for overall and Pc-resistance-gene-specific virulence trends and correlations. Results showed an incredibly pathogenically diverse pathogen, with 88% of races represented by a single isolate. The pathogen undergoes drastic virulence changes that enables it to overcome host resistance genes. Virulence is also steadily increasing for most of the resistance genes in the set of 40 oat differential lines. Building upon previous partially phased genome assemblies, recent work on crown rust genomics established a chromosome-level and fully phased reference genome of a historical isolate, Pca203, using PacBio and Hi-C data. Genome wide association studies using SNPs called against these reference genomes also identified multiple virulence-associated loci containing candidate avirulence effector genes. To develop more durable resistant lines the focus was shifted to exploiting adult plant resistance (APR) gene(s). Recently, a total of nine quantitative trait loci (QTL) were identified and anchored to the oat OT3098 v1 reference genome. From these, high throughput molecular markers (KASP/PACE) were developed to enable selection of four major QTL. Further, crosses were performed to pyramid these QTL with BT1020 and BT1021 lines, which possess a unique resistance gene from *Avena strigosa*. Two advanced pyramided lines, CDL-111 and CDL-167, with three APR QTL were released to the public as breeding germplasm with the caveat of retaining the combined pyramid. Additional gene combinations with other APR QTLs are under development to further diversify the oat germplasm.

Oat bacterial blight caused by *Pseudomonas coronafaciens* in Idaho

Belayneh A. Yimer¹, Jules Butchacas², Suraj Sapkota¹, Kathy Esvelt Klos¹, Jonathan Jacobs²

¹USDA-ARS, Small Grains and Potato Germplasm Research Unit, Aberdeen, ID, USA

²Ohio State University, Department of Plant Pathology, Infectious Diseases Institute, College of Food, Agriculture, and Environmental Sciences, Columbus, OH, USA

In the summer of 2023, oat trial fields in Aberdeen, Idaho were severely infected with necrotic lesions formed on the leaves. The symptoms were necrotic streaks that resembled barley bacterial leaf streak (BLS) caused by *Xanthomonas translucens* pv. *translucens* (Xtt), which was unusually severe in barley fields in the same year and location. Hence, the initial suspicion was the disease on oats may also be BLS. To confirm that leaf samples were collected, and the pathogen was isolated on Wilbrink's media. However, the bacterial colonies grown on the media were not the typical yellowish colonies of Xtt, rather they were cream-white colonies (typical of *Pseudomonas* spp). The causative agent was identified using pathogenicity and molecular techniques. This presentation will report oat bacterial disease caused by *Pseudomonas coronafaciens* in Idaho, to the best of our knowledge, for the first time. It will also present the results of host range studies of the pathogen and the genetic resistance of selected oat germplasm to the disease.

Oat leaf blotch remover can be found in isle 1D

Peter E. Eckstein, Alexander Woitas, Tajinder Grewal, Lindsay Griffith, Aaron D. Beattie

Department of Plant Sciences/Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada

Oat leaf blotch, caused by the fungal pathogen *Pyrenophora avenae*, is usually of minor importance, but may at times significantly decrease yield while decreasing oat groat quality below minimum standards for milling. Oat disease surveys conducted from 2011-2017 in western Canada identified *P. avenae* in one third to nearly all sampled oat fields in each year of the survey. Initial screening of 15 single spore isolates collected between 2014 and 2017 against a set of nine oat cultivars indicated differential disease responses suggesting the presence of different pathotypes. To assess the genetic control of resistance to oat blotch, two recombinant inbred line populations (AC Assiniboia/S42 x CDC Dancer and OT3011 x Iowa N2052), where AC Ass/S42 and OT3011 showed resistance to the disease, were produced. Both populations were inoculated with three *P. avenae* isolates and genotyped via the Illumina iSelect platform. QTL analysis in both populations located resistance to a single, narrowly defined QTL peak at highly similar loci for all isolates. A cluster of linked markers underlying the QTL peak placed the resistance locus on chromosome 1D of the OT3098 v2 (PepsiCo 2021) genome assembly and indicated that the region was duplicated twice on chromosome 1A. The resistance locus is tightly linked to marker ES14_c2496_651 in both populations and design of a MMAS-suitable marker based on the reference sequence of ES14_c2496_651 is specific to the chromosome 1D locus only. A survey of syntenous regions in barley and wheat failed to identify similar resistance loci for the related net blotch disease of barley, nor the tan spot disease of wheat. The genomic region near ES14_c2496_651 on chromosome 1D is annotated for a cluster of three WAK1 genes that are of interest as candidate resistance genes and will be studied further as more oat genome assemblies become available.

What are the most effective markers for identifying the presence of 19 Pc genes in oat germplasm?

Rawnaq N. Chowdhury, Raja Nandety, Belayneh Admassu Yimer, Jason Fiedler, Kathy Esvelt Klos

Oak Ridge Institute for Science and Education (ORISE) Research Participant, Small Grains and Potato Germplasm Research Unit, Aberdeen, ID, USA

Crown rust caused by *Puccinia coronata* Cda. f. sp. *avenae* P. Syd. is a destructive disease, causing yield and grain quality losses in oat. Over hundred crown rust race-specific resistance genes have been identified, but the sources of race specific, seedling stage (Pc gene) resistance remain elusive in much of the oat germplasm. Identifying the genes present in specific germplasm is further complicated by the possibility that it carries multiple genes, resulting in ambiguous phenotypes. Closely linked molecular markers may be used to identify the carrier status of a particular Pc resistant allele in any given oat line. However, elevated false positive rates could lead to misidentifying carriers, potentially excluding valuable genetic material from breeding programs or inadvertently incorporating undesired traits. We report on molecular markers with genotype data in T3 linked to 19 Pc genes, along with map data in GrainGenes. A panel of Pc gene non-carrier lines was identified using phenotype data and pedigree. The false positive rate of markers was estimated as the percent of non-carriers with the allele associated with the Pc gene. Validation in this non-carrier panel of published predictive markers for four Pc genes demonstrated comparability with published data. Thirty-one SNPs associated with 15 Pc genes, which exhibited the lowest false positive rates, were assessed for their diagnostic capabilities. A total of 21 markers, for 13 Pc genes, demonstrated the ability to predict carrier status with a false positive rate of 25% in non-carrier lines. For example, the best markers for the Pc38 and Pc68 genes perfectly aligned with carrier status across all lines. PACE (PCR Allele Competitive Extension) markers were designed, and are available, for all SNPs used in this study. The markers developed in this study are intended to be used to identify which Pc genes are carried by germplasm with resistance of unknown derivation.

Oat genomics research and development activities at Agriculture and Agri-food Canada

Wubishet A. Bekele¹, Asuka Itaya¹, Nicholas A. Tinker¹, Weikai Yan¹, Kirby T. Nilsen², Yong-Bi Fu³, Mehri Hadinezhad¹, Jean-Sebastien Parent¹, Nathan Liang¹, Charlene P. Wight¹

¹Ottawa Research and Development Centre, Agriculture & Agri-Food Canada, Ottawa, ON, Canada

²Brandon Research and Development Centre, Agriculture & Agri-Food Canada, Brandon, MB, Canada

³Saskatoon Research and Development Centre, Agriculture & Agri-Food Canada, Saskatoon, SK, Canada

This presentation will provide an overview of the current research activities at Ottawa Research and Development Centre of Agriculture and Agri-Food Canada (AAFC) in collaboration with Canadian and international researchers. I will showcase examples from three key areas of research: 1. Development and application of genomics-assisted breeding tools in AAFC breeding programs. 2. Genome assemblies, genomic diversity studies, breeding-oriented genomic resources, and databases developed over the past five years. 3. Functional genomics research using the naked locus in oats as an illustrative example.

The USDA-SoyWheOatBar-3K: A rapid, inexpensive genotyping platform to enable genomics-assisted breeding of small grains

Jason D. Fiedler¹, Raj Nandety¹, Sumandeep Bazzar², Karen Beaubien³, Kevin Smith³, Melanie Caffè²

¹Cereal Crops Research Unit, Edward T. Schafer Agricultural Research Center, USDA-ARS, Fargo, ND, USA

²Department of Agronomy, Horticulture and Plant Science, South Dakota State University, Brookings, SD, USA

³Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN, USA

Molecular breeding is the use of genetic information to predict performance and can assist in quickly developing new and improved small grain germplasm. For large scale implementation of these tools, durable, robust, low-cost molecular markers - with a rapid turnaround time - are required to inform selections within breeding programs. To meet these needs, we have developed a new genotyping platform based on the Illumina Infinium II array technology that targets approximately 3,000 SNPs in wheat, oat, and barley. The markers are evenly spaced along each genome, have a high information content, and include many known-informative markers already used in selection. Validation of this platform with ~10,000 previously genotyped lines demonstrated very good technical performance, high concordance with other platforms, and ability to be upgraded to higher density sets through imputation. At least 2,000 markers were informative within a given breeding program and are sufficient for the development of highly accurate genome prediction models. The platform is highly robust with a turnaround time of only three days for usable data. The small grains content was added to a new 3,000 Soy array and has been released as the USDA-SoyWheOatBar-3K for \$14 a sample. This multi-species format also enables dual- and tri- hybridization to decrease the per-sample cost. Concordance between multi- and single-mode is ~95% for all SNPs and increases to ~99% on a high-performing subset. This new platform will enable many programs to utilize powerful molecular breeding tools to develop improved crop varieties.

A six-year head-to-head comparison of genomic versus visual selection in oat breeding for eastern Canada

Weikai Yan¹, Wubishet Bekele¹, Nick Tinker¹, Mehri Hadinezhad¹, Dan MacEachern², Genevieve Telmosse³, Holly Byker⁴, Hellen Booker⁶, Kirby Nilsen⁷, Aaron Beattie⁸, Asuka Itaya¹, Brad deHaan¹, Matt Hayes¹, Savka Orozovic¹, Li Wang¹, Charlene Wight¹, Allen Cummiskey², Isabell Morasse³, Nathan Mountain⁵, Melinda Drummond⁵, Zhanghan Zhang⁶

¹Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, Canada

²Charlottetown Research & Development Centre, Agriculture & Agri-Food Canada, PEI, Canada

³Normandin Research Station, Quebec Research & Development Centre, Agriculture & Agri-Food Canada, QC, Canada

⁴Winchester Research Station, University of Guelph, ON, Canada

⁵New Liskeard Research Station, University of Guelph, ON, Canada

⁶Elora Research Station, University of Guelph, ON, Canada

⁷Brandon & Development Centre, Agriculture & Agri-Food Canada, Brandon, MB, Canada

⁸Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada

A 6-year head-to-head comparison was conducted to compare the relative effectiveness of genomic selection (GS) vs. visual selection (VS) in oat breeding. Each year, from 2018 to 2023, the same number of lines were selected from the same breeding populations using genomic prediction and visual selection; 20 genomically predicted poor lines were also included in years 2018 to 2022. These lines were grown at three or four test locations with two replicates in eastern Canada. The results are presented here to answer the following questions: 1) Was genomic selection effective for selecting yield? 2) Was it more effective than visual selection for selecting yield? and, 3) was it more effective than visual selection for cultivar development?

Can GWAS information from oat breeding programs be used to develop higher-yield oat varieties? A case study in the SDSU oat breeding program

Guilherme Oliveira¹, Sumandeep Bazzar¹, Girma Ayana¹, Jason Fiedler², Raj Nandety², Melanie Caffè¹

¹Department of Agronomy, Horticulture, and Plant Science, South Dakota State University, Brookings, SD, USA

²Cereal Crops Research Unit, USDA-ARS, Fargo, ND, USA

Genome-wide association studies (GWAS) have been executed to identify regions controlling complex traits in oats (*Avena sativa* L.). Most studies have targeted traits related to grain yield to help oat breeders in the selection process to obtain varieties with higher productivity. However, GWAS research often employs diversity panels, and despite the benefits, applying these findings to breeding populations can be challenging due to interpopulation disparities, creating barriers to incorporating genomic knowledge into practical breeding routines. This study aimed to identify genomic regions associated with grain yield and grain yield-related traits through GWAS in breeding populations from the SDSU oat breeding program. We also explored whether this type of genetic information could be directly applied to breeding through incorporation into genomic prediction models for oat grain yield. Association mapping was conducted to investigate genetic associations for grain yield, plant height, heading date, lodging severity, snapback, and crown rust severity in six advanced oat breeding populations evaluated in multiple environments in six different years. We identified 156 significant SNPs associated with these traits, spanning 38 genomic regions across 18 oat chromosomes, highlighting a broad abundance of significant markers in the oat genome. Some genomic regions were novel, while others had been previously identified by other researchers, reinforcing the positive side to conducting GWAS studies in breeding populations, tracking which genomic information can be useful for these populations. Incorporating specific markers from significant genomic regions as fixed effects in a linear and additive genomic selection model increased prediction accuracies for grain yield. Nevertheless, these markers were not always positively associated with all grain yield-related traits. Our results demonstrated that molecular markers identified by GWAS in breeding populations can be incorporated as fixed effects into genomic selection models. However, careful consideration is essential to avoid selection for undesired phenotypes in other targeted traits.

Training set optimization and genomic prediction to improve selection efficiency for oat biomass yield in the southern US

Md Ali Babar², Samuel Adewale¹, Naeem Khan², Jordan McBreen², Sudip Kunwar¹, Janam Acharya², Victor Silva Signorini², Steve Harrison³, Noah Dewitt, Kathy Klos⁴, Jason Fiedler⁵, Raj Nandety⁵, Mary Osenga⁵, Paul Murphy⁶, Amir Ibrahim⁷, Rick Boyles⁸

¹Plant Breeding PhD Program, University of Florida, Gainesville, FL, USA

²Department of Agronomy, University of Florida, Gainesville, FL, USA

³LSU Ag Center, School of Plant, Environmental and Soil Sciences, Baton Rouge, LA, USA

⁴Small Grains and Potato Germplasm Research, USDA-ARS, Aberdeen, ID, USA

⁵Edward T. Schafer Agricultural Research Center, Fargo, ND, USA

⁶Department of Crop Science, North Carolina State University, Raleigh, NC, USA

⁷Soil and Crop Sciences Department, Texas A&M AgriLife Research, College Station, TX, USA

⁸Pee Dee Research & Education Center, Clemson University, Florence, SC, USA

In the southern US, oat has been extensively used as a winter forage crop for silage, grazing, and hay for different classes of livestock including beef and dairy due to its high-quality early fall-winter forage production, high tillering, and regrowth potential. Phenotyping of oat forage yield is time consuming, labor intensive, destructive, and difficult to harness over large areas. Genomic prediction has been demonstrated to increase genetic gain and breeding efficiency of complex traits in plant breeding programs. The objectives of this study were to optimize training population size and determine the accuracy of different genomic selection models for biomass yield prediction in oats. The southern oat panel used for the study consists of 420 oat lines, mostly elite lines with favorable agronomic performance developed by public oat breeding programs in Southern US. The panel was phenotyped in Citra, Florida for height, growth stage and habit, and dry matter yield from 2022 to 2024 and genotyped using GBS which resulted in 10,386 SNP markers. Harvesting of oat biomass was done at three different times during the growing season to obtain respective biomass-related traits. During harvest, representative fresh samples were collected and oven dried. The results showed significant genotypic differences for dry matter yield from the three harvests with moderate heritabilities. Overall, genomic best linear unbiased prediction, Bayes B and random forest models gave similar prediction accuracies ranging from 0.26-0.43 for biomass yield from the three harvests. In the multivariate models that involved biomass yield with correlated traits (height and growth habit), prediction accuracies of biomass yield were higher (0.35-0.68) than in the univariate model. Higher predictive abilities of 0.55 and 0.68 were observed for dry matter yield for biomass harvests 1 and 2 respectively, when canopy height was included in the genomic prediction model. Prediction abilities increased as population size increased. The coefficient of determination training optimization approach gave the highest prediction accuracy of 0.68 for population size 350. The results of this study will help to accelerate early yield testing stage by identifying superior genotypes with the best combination of genes to improve genetic gain in oat breeding program.

Beyond milling – the other uses of oat

Stephen Harrison¹, Aaron D. Beattie²

¹LSU Ag Center, School of Plant, Environmental and Soil Sciences, Baton Rouge, LA, USA

²Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada

Breeding oat to have suitable milling and nutritional characteristics is a significant effort associated with many breeding programs in North America to meet the needs of the large milling industry. However, in the United States only about 33% of the 2.5 million acres seeded in 2023 were harvested for grain, indicating that a large percentage of the acres are devoted to other uses. Even in Canada where a large portion of the 3.6 million oat acres are targeted for the milling industry, about 20% of the acres are used for forage to service the dairy and beef cattle industries. Use of oat as a winter pasture forage, cover crop, wildlife food, silage or for winter feeding as hay or swath grazed provide animals a high-quality feedstock. The benefits and breeding of oat for this non-milling uses will be discussed, along with recent examples of improved varieties.

Content and profile of immunogenic gluten-like proteins in Canadian oat

Yuxiu (Iris) Chen, Xiao Qiu

Department of Food and Bioproduct Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada

Oat is a functional food due to the presence of some unique healthy compounds. However, oat also contains a small amount of avenins, a group of prolamins similar to wheat gluteins that can cause adverse immune responses in the small intestine leading to an enteropathy disorder called Celiac disease. Therefore, recommendation of oats as gluten-free diets for celiac patients remains highly controversial. A total of 24 representative oat cultivars selected from East and West Canada were analyzed for the contents and profiles of immunogenic gluten-like proteins. Four different protein fractions in the oat cultivars including albumins, globulins and avenins (gliadin-like protein) and avenins (glutenin-like protein) were sequentially isolated and quantified. Gliadin-like avenins were in range of 6 to 17% while glutenin-like avenins were in a range from 5 to 11% of the total proteins in oats. Almost all cultivars possessed immunogenic gluten-like proteins measured by monoclonal antibodies against immunogenic epitopes at levels of less than or close to 20 ppm, except for one cultivar (Reid) that contained the immunogenic proteins substantially higher than the gluten-free standard. A few highly immunogenic avenin proteins with a size of 30 kDa to 50 kDa were exclusively found in the cultivar. These results suggest that considerable variations in the content and profile of immunogenic gluten-like proteins in oats, but most of them are safe and suitable for consumption for all consumers including Celiac disease individuals. This work not only provides the reference information on oats for consumption by celiac patients, but also lays a foundation for identification of the immunogenic proteins and genes for breeding oats without immunogenic proteins.

Distribution of trigonelline in oat groats and its preventing high-fat-diet induced muscular dysfunction mechanism in mice

Xinzhong Hu, Rui Dong, Tian Ren, Xiaolong Wang

College of Food Engineering and Nutritional Science, Shaanxi Normal University, Xi'an, Shaanxi, China

Oat accumulated contains about 111.70 - 230.00 $\mu\text{g/g}$ of trigonelline, which is 22 times higher than that in wheat and rice. Trigonelline does not uniformly distribute in oat groats, it is the most abundant in bran (around 163.54 - 265.23 $\mu\text{g/g}$), and is evenly distributed in the endosperm parts (around 62.10 - 95.15 $\mu\text{g/g}$). Oat bran rich in trigonelline significantly ameliorated high fat diet (HFD)-induced skeletal muscle function abnormalities, as evidenced by improvement in mice grip strength and endurance treadmill running distance, accompanied with the regulation of muscle functions related gene expressions, namely *Fis1*, *Cytc*, *Myh2* and *Myh4*. Oat bran suppressed the production of systematic inflammatory cytokines while promoted superoxide dismutase and glutathione. Furthermore, oat bran significantly impacted gut microbiota composition by promoting short chain fatty acids (SCFAs) producers and certain probiotic genera, along with the enhancement of SCFAs. In vitro experiment furtherly verified that trigonelline could prevent the accumulation of lipid droplets, regulate inflammatory cytokines in skeletal muscle cells, and performed as methyl donor in complete metabolism homeostasis, and with that can account for the settled lactate intensity during exercise training in mice. This research provides valuable insights into the potential benefits of incorporating oat bran into a high-fat diet for preventing skeletal muscle dysfunction in mice.

Assessing the impact of genotype x environment on oat protein isolate structure-function characteristics

Maneka Malalgoda

Department of Food and Human Nutritional Sciences, University of Manitoba, Winnipeg, MB, Canada

The objective of the study was to examine the impact of genotype x environment (GxE) on oat protein isolate (OPI) structure, and functionality and composition. Three oat genotypes (Summit, AC Morgan, and CS Camden) grown in three different environments in the Canadian Prairies (Manitoba, Alberta, and Saskatchewan) were used in this study. An optimized alkaline extraction - isoelectric precipitation method was used to prepare OPI from defatted oat flour, and the resulting OPI was evaluated for structural characteristics, such as protein molecular weight distribution, surface hydrophobicity, and denaturation characteristics, as well as functional properties, such as solubility, emulsification, foaming and gelation. OPI composition was analyzed using SE-HPLC and LC-MS was used to oat globulin proteins further. The results indicated that oat protein content, protein profile, and functional properties are impacted by genotype and the environment. For example, surface hydrophobicity was impacted by growing environment with samples from Alberta showing the highest surface hydrophobicity. The water solubility of OPI was significantly impacted by GxE, where the solubility ranged from 13-30%. Samples Alberta - Summit exhibited the highest foaming capacity, while all samples tested had good foaming stability >70%. The SE-HPLC analysis differentiated OPI into four major fractions: polymeric globulin, avenins, glutelins and albumins as well as smaller peptides. The SE-HPLC analysis demonstrated that overall OPI composition is impacted by growing environment. LC-MS analysis was able to identify eight major types of proteins in OPI, globulins being the most prominent. Additionally, the results indicated that certain environment and genotype combinations could result in enhanced globulin protein quality, given the positive and negative associations between specific globulin proteins and certain genotypes and environment combinations. Overall, the results show that GxE significantly impacts OPI structure, function, and composition, emphasizing the need for additional research in this area so that that oat can be successfully utilized as a protein source of consistent quality.

Composition and techno-functional properties of oat bran from Canadian oat varieties

Marta S. Izydorczyk

Grain Research Laboratory, Canadian Grain Commission, Winnipeg, MB, Canada

Oats and oat products have attracted consumer, research, and commercial interests due to the health benefits associated with their consumption. Oat bran, if sufficiently enriched in β -glucans (BG), can carry a health claim associated with the ability of its BG to reduce the risk of heart disease. Oat bran as defined by AACC International should contain a minimum of 5.5% BG and comprise no more than 50% of the originating clean oat groats or rolled oats. Oat bran produced from recently developed Canadian oat varieties can easily surpass the minimum requirement stipulated in the current definition and become a product enriched not only in BG, but also in other dietary fibre components, vitamins, and valuable oat proteins. The objectives of this project were to evaluate the effects of milling conditions used to prepare bran fractions on their composition and techno-functional properties. Nine Canadian oat genotypes, including older varieties AC Morgan, Summit, CS Camden, and CDC Dancer, as well as recently registered varieties CDC Haymaker, AAC Douglas, CDC Endure, CDC Arborg, and Ore3542M, were used in the study. Preliminary milling trials established that the optimal roller milling conditions to produce oat bran involved grinding with dull to dull roll disposition and a roll differential speed of 2:1. The milling flow consisted of two corrugated roll passages (B1 and B2), processing of the ground material held on a 450 μm sieve using a bran finisher, and was followed by sifting. Coarse bran products were obtained when the roll gaps of B1 and B2 were set at 200 and 150 μm , respectively, whereas fine bran products were produced when the roll gaps were reduced to 100 and 50 μm , respectively. The coarse and fine bran products differed significantly in particle size. The mass median diameter (d_{50}) for coarse bran ranged from 570 to 620 μm , whereas for fine bran from 280 to 350 μm . The yield of coarse bran ranged from 38 to 42% and for fine bran from 40 to 46%, depending on the oat genotype. The content of BG in fine bran was 1 to 2 % higher than in coarse bran. The content of BG in fine bran was twice as high as in the groats and ranged from 8 to 10.6% depending on genotype. The protein content in fine and coarse bran fractions was similar and about 1.3 times higher than in groats in both products. There were significant differences in swelling and water-holding capacity among the bran preparations. The fine bran exhibited higher water hydration capacity and swelling than coarse bran. Bran products from different oat genotypes exhibited a wide range in cold paste (64°C) viscosity attributable to variations in total and soluble BG. In conclusion, our study clearly demonstrated that bran produced from the current Canadian oat varieties using optimal processing methods offers many health and functional benefits.

POSTER ABSTRACTS

Adapting Oats to the Final Frontier

Hanna M. Haikka¹, Juho Hautsalo², OatFrontiers Consortium

¹Boreal Plant Breeding Ltd., Finland

²Natural Resources Institute (LUKE), Finland

Interreg Northern Periphery and Arctic (NPA) is a European Union funding program promoting transnational cooperation in Northern Europe. It supports innovative, sustainable solutions to improve life in remote, sparsely populated areas. The NPA fosters community resilience through effective collaboration across seven countries. OatFrontiers targets Northern Periphery Areas (NPA), regions which hold potential for cereal cultivation expansion but face numerous challenges due to isolation, low population density, and limited economic diversity. These areas, heavily reliant on dairy and meat production, are both impacted and benefited by climate change. While climate change may create new opportunities for cereal farming as temperatures rise, it also introduces stress factors such as droughts, diseases, and unpredictable weather patterns. The project's objective is to enhance oat production in Northern Scandinavia, Iceland, and Western Ireland, promoting economic diversification and infrastructure development in these peripheral communities. Oats are chosen for their health benefits, increasing food demand, resilience, and lower fungicide requirements compared to wheat and barley. A consortium of local plant breeders and R&D partners aims to develop and pilot uniquely diverse pre-breeding oat material. This involves addressing two major challenges in modern oat breeding: limited genetic diversity and insufficient understanding of photoperiod response. By gathering and testing a set of 400 diverse oats, including modern cultivars, material from the Nordic genebank, NordGen, as well as Irish heritage lines, and *Avena sterilis*-based crosses, the project will generate new genetic information and field performance data from NPA locations. The outcomes include identifying suitable cultivars from the current oat gene pool, developing new pre-breeding material with needed diversity, conducting genetic and pilot studies to understand adaptation to photoperiod and stress factors, and fostering collaboration among the oat R&D sector and producers. This transnational cooperation aims to overcome financial and resource limitations, sharing risks and costs to achieve common goals. Increased oat cultivation in the NPA will provide economic benefits to farmers, support local industries, promote healthier diets, and optimize land use. By piloting diverse oat material, the project will introduce resilient, high-quality cultivars, contributing to sustainable farming and economic growth in these regions.

Advancing oat breeding and research at UC Davis

Isabel A. del Blanco, Xiaofei Zhang

Plant Sciences Department, University of California, Davis, CA, USA

California is one of the major oat-producing states in the USA, planting approximately 100,000 acres annually. These oats primarily serve as animal feed for dairy cattle, the largest industry in California, with 10% harvested for grain. As public awareness of the health benefits of oat grows, so does the market demand for oat-based food products. The significant acreage and increased demands underscore the necessity for developing new oat cultivars specifically adapted to California's unique climate and agricultural needs. The oat breeding and research at UC Davis focus on several key objectives: 1) Yield and Quality Enhancement - developing oat varieties with higher yields, improved lodging resistance, increased test weight, and superior end-use quality; 2) Disease Resistance - improving resistance to Yellow Dwarf Virus (BYDV/CYDV), which causes significant damage to oats, including leaf discoloration, stunting, and plant death. The program also targets resistance to crown rust, stem rust, powdery mildew, and leaf blotch; 3) Adaptation to Rotations - selecting early flowering genotypes that fit well into rotations with other crops, such as rice and corn. To achieve these objectives, the program uses conventional pedigree breeding to create new genetic combinations and select advanced lines for variety release. We also actively participate in the International Oat Nursery (ION) and Uniform Early Performance Oat Nursery (UEPON) for varietal evaluation and disease screening. In recent years, we have made significant achievements in variety development. Two candidate varieties for dual purpose: forage and grain production will be released within the next 1-2 years. The UC Davis oat program remains at the forefront of oat research by exploring new technologies to increase breeding efficiency, such as speed breeding, Doubled Haploid technology, and genome editing. By combining conventional and cutting-edge technologies, we aim to develop superior oat cultivars that support sustainable agriculture and meet the diverse needs of both producers and consumers.

One hundred years of comparative genetic and physical mapping in cultivated oat: an inventory of hexaploid oat genes and QTL

Charlene P. Wight¹, Victoria C. Blake^{2,3}, Eric N. Jellen⁴, Eric Yao^{2,5}, Taner Z. Sen^{2,5}, Nicholas A. Tinker¹

¹Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, Canada

²Western Regional Research Center, Crop Improvement and Genetics Research Unit, United States Department of Agriculture-Agricultural Research Service, Albany, CA, USA

³Department of Plant Sciences and Plant Pathology, Montana State University, Bozeman, MT, USA

⁴Department of Plant & Wildlife Sciences, Brigham Young University, Provo, UT, USA

⁵Department of Bioengineering, University of California, Berkeley, CA, USA

A comprehensive inventory of genes and quantitative trait loci (QTL) mapped in cultivated oat (*Avena sativa* L.) and their most likely locations on the OT3098 v2 reference sequence (found on the GrainGenes website - <https://wheat.pw.usda.gov/jb?data=ggds/oat-ot3098v2-pepsico>; Yao, et al., 2022) has been completed (Wight, et al., 2024). First, comparative mapping was used to identify the locations of genes and QTL on the 2018 oat consensus map (Bekele, et al., 2018). The consensus map linkage groups were then divided into cM regions defined by SNP markers. These were matched to locations on the physical chromosomes of OT3098 v2. Most of the genes and QTL could be assigned to positions on both maps. However, large areas of reduced recombination (centromeres, breakpoints) resulted in many of the assigned regions on the physical map being quite long. A number of resources (https://oatnews.org/oatnews_pdfs/2020/oatnews_2024_Wight.pdf) were created during this work, including genome browser tracks. Examples of some of the tools will be presented on the poster. References: Bekele, WA, et al. (2018) Haplotype-based genotype-by-sequencing in oat genome research. *Plant Biotechnology J.* <https://doi.org/10.1111/pbi.12888> Wight, CP, et al. (2024) One hundred years of comparative genetic and physical mapping in cultivated oat (*Avena sativa* L.). *Crop and Pasture Science* 75, CP23246. <https://doi.org/10.1071/CP23246> Yao, E, et al. (2022) GrainGenes: A data-rich repository for small grains genetics and genomics. *Database* <https://doi.org/10.1093/database/baac034>

Genetic mapping and validation of *Avena sterilis*-derived crown rust resistance genes *Pc40* and *Pc46* in cultivated oat

Xiangmin Zhang, Aaron D. Beattie

Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada

Oat crown rust, caused by *Puccinia coronata* f. sp. *avenae* P. Syd. & Syd. (*Pca*), is the largest on-going threat to oat production in Canada and worldwide. With the decreasing cost associated genotyping and ever-improving oat genome assemblies, it is now possible to not only develop markers linked to crown rust resistance genes, but also understand their chromosome locations and allelic relationships among the large number of reported resistance genes. Such information will allow oat breeders to understand which combinations of resistance genes can be pyramided together and test the effectiveness of such pyramids. Although the presence of some genes have been known for decades, their current distribution within oat germplasm and effectiveness is unclear. For example, although the *Pc45* gene was reported in 1971 it remains a useful gene within regions of western Canada and Ontario. It is likely that other such useful genes exist within the current pool of reported genes. Crown rust resistant genes *Pc40* and *Pc46* were originally identified in the wild hexaploid species, *Avena sterilis*, and transferred into cultivated oat (*Avena sativa*). *Pc40* was mapped to Mrg17 on the oat consensus map within the 7.84-10.08 Mbp interval on chromosome 6C of the OT3098 v2 assembly. Markers GMI_ES05_c20576_219 and avgbs_122060, when combined individually with avgbs_213353, resulted in a prediction accuracy of 94% and 100%, respectively, in a 114 member oat diversity panel. The *Pc46* gene was identified on Mrg19 of the oat consensus map, located within the 469.26-472.79 Mbp interval of chromosome 3D. Markers avgbs_122535 and avgbs_67655 together predict the absence of *Pc46* gene within the oat diversity panel with an accuracy of 97%. The KASP assays developed for *Pc40* and *Pc46* in this study will be useful to incorporate these genes into oat breeding lines to assess their utility with crown rust gene pyramids.

Identification and fine mapping of the powdery mildew resistant gene PmBY642 in a hexaploid oat (*Avena sativa* L.)

Tao Liu^{1,2}, Hong Chen^{1,2,3}, Wenhui Tian^{1,2,3}, Aijie Ma^{1,2,3}, Guoqing Wang^{1,2,3}, Jingqing Xu^{1,2}, Bo Zhang^{1,2}

¹Qinghai Province Key Laboratory of Crop Molecular Breeding, Northwest Institute of Plateau Biology, Chinese Academy of Sciences, Xining, Qinghai, China

²Key Laboratory of Adaptation and Evolution of Plateau Biota, Northwest Institute of Plateau Biology, Chinese Academy of Sciences, Xining, Qinghai, China.

³University of Chinese Academy of Sciences, Beijing, China

Powdery mildew, caused by *Blumeria graminis* DC. f. sp. *avenae*, is one of the most destructive diseases that threatens oats yield and quality. In the study, oat line BY642, with all-stage resistance (ASR) to powdery mildew, was crossed with susceptible lines BY133 and BY119 to create two bi-parental populations, respectively. Resistance to powdery mildew was evaluated in the field and laboratory through inoculating with Bgt isolated. Bulk segregant RNA-Seq (BSR-seq) and DNA-base bulk segregant analysis (BSA-seq) were conducted to screen candidate variation loci as well as a partial high-density genetic map constructed subsequently. The resistance gene has been fine mapped in a range of 0.85 cM interval with 624.92 kb physical distance on chromosome 1A, which could explain 35.49% of the phenotypic variation, temporary annotated as PmBY642. A large segment missing was detected in the corresponding candidate regions of PmBY642 in the reference genome. Two markers (1A109 and 1A140) tightly linked to PmBY642 have been successfully applied for marker-assisted selection (MAS) breeding, and a series of oat lines containing PmBY642 with high resistance to powdery mildew were created. The results enriched the oat powdery mildew resistance gene pool and valuable for breeding powdery mildew resistance oat cultivars. Keywords Oats; powdery mildew; fine mapping, marker-assisted selection.

Oat through the lens: image analyses assessing variation in root and panicle architecture

Daiqing Huang¹, Xuan Yang¹, Céline A.M. Ferré², Shengjian Ye¹, Michael W. Taylor², Aaron D. Beattie², J. Allan Feurtado¹

¹Aquatic and Crop Resource Development, National Research Council of Canada, Saskatoon, SK, Canada

²Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada

The digitization of crop phenotypes through image-based approaches creates opportunities to increase the speed and precision of crop trait selections and narrow the genotype-to-phenotype knowledge gap. We have been developing and utilizing both 2- and 3-dimensional imaging approaches to characterize variation in oat root systems and panicle architecture. The major goal of the research is to identify traits which promote climate resilience and sustainable agriculture with an initial focus on improvement of oat lodging resistance. To distinguish key traits for root anchorage, a high-throughput 2D phenotyping platform was utilized to image and analyze root system size, topology, and morphology traits in 22 cultivars relevant to western Canada ranging in lodging resistance. Initial results suggest that variation in oat root anchorage can be impacted by both: (1) traits influencing soil exploration capacity such as root angle and (2) traits related to soil gripping capacity such as lateral root density. Analysis of root system variation across a diverse collection of 113 oat genotypes revealed significant variation in root angle, number, and overall complexity and biomass, suggesting the potential to select for various root traits including those impacting lodging resistance. For panicle analysis, in addition to 2D image analysis, a workflow was established to reconstruct realistic 3D models for trait analysis. Digital analyses of 14 oat cultivars from two field environments, revealed significant variation in panicle architecture traits such as height, width, branching angle, and compactness. We are working toward associating panicle traits to oat productivity and parameters, such as drag area, which has been suggested to influence lodging. Overall, our results are making available the methodologies and data to enable more accurate trait selections and robust breeding decisions for increasing oat genetic gain.

Robustness of oats for the nordic region (RobOat)

Hanna M. Haikka¹, Marja Jalli², PPP RobOat Consortium

¹Boreal Plant Breeding Ltd., Finland

²Natural Resources Institute Finland (Luke), Finland

RobOat focuses on pre-breeding and especially on adaptation of oats to environmental and climatic changes in the Nordic region. The project is funded by Nordic countries through the Nordic Council of Ministers and plant breeding entities, and it is coordinated by the Nordic Genetic Resource Center (NordGen). The collaboration between plant breeding companies and public institutions aims to enhance the resilience of oat cultivars in response to the unique Nordic climate conditions. The project targets the development of future oat cultivars by utilizing a diverse range of genetic resources to meet the increasing demand for healthy and high-quality oat materials. The key objectives include broadening the genetic base of Nordic oats by utilizing less explored oat germplasm from NordGen, and phenotyping for resilience against abiotic and biotic stresses. Improving phenotyping methodologies is another critical objective. The focus is on the development and standardization of reliable methods for drought and water logging evaluation and disease resistance. Additionally, enhancing genomic tools by applying the latest genomic analyses to complement existing genetic tools (genomic selection) and to develop new ones (new genetic markers and candidate genes) is in the focus. In later steps, we develop segregating populations for genome mapping analyses. Whole genome sequencing and large chromosome rearrangements are studied for understanding breeding barriers. Research activities involve phenotyping trials to test drought and water logging tolerance as well as crown rust and semi loose smut resistance both under controlled conditions and normal field trials. Genotyping and genomic studies will use genotyping-by-sequencing (GBS) for selected oat lines, and conduct amplicon sequencing and RNA-seq to study genetic responses to stresses. Marker development will utilize data for Genome-Wide Association Studies (GWAS) to develop markers, and select parent lines for creating populations for fine genetic mapping and gene discovery. RobOat aims to provide resilient oats to meet the Nordic Nutrition Recommendations 2023 and the European Green Deal Strategy. By addressing the challenges posed by climate change and disease prevalence, RobOat seeks to ensure a stable supply of oats for the Nordic countries, contributing to sustainable agriculture and food security.

Screening oats breeding lines for nutritional traits using a robust and effective NIRS technique

Mehri Hadinezhad, Judith Fregeau-Reid, Savka Orozovic, Weikai Yan

Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, Canada

Plant breeding is a dynamic, multi-disciplinary endeavour that aligns grower aspirations with the demands of national and international markets. While high yield and disease resistance remain critical objectives, achieving a superior quality profile is paramount for oat breeders. Key quality considerations are protein, oil, and β -glucan. Oat varieties should have an adequate level of protein. However, the presence of lipids in oats can disrupt the milling processes. As such, minimizing lipid content is a preferred target. Oat's most crucial nutritional trait is β -glucan (oats soluble fibre) because of its proven health benefits. Developing new oat varieties high in β -glucan would facilitate the expansion of oats markets and provide healthier oat-based products to Canadians. At Grain Quality Laboratory (GQL), Ottawa Research and Development Centre, an in-house built robust and effective NIRS technology has been developed to simultaneously analyze oats breeding lines for their protein, lipid, and β -glucan content. Oat samples are dehulled, heat-treated, hand-sorted (to discard debris and unde-hulled grains), milled and scanned. Wet chemistry techniques are applied yearly on a subsample set to validate the calibration performance. In addition, an attempt was made to develop a calibration based on whole oat grains after dehulling (groat) and compare its performance with the ground oat calibration. The oat whole grain calibration would eliminate the milling step, which is time-consuming and labour-intensive, especially when screening thousands of oats lines per year. Oat samples from multiple growing regions and four crop years were evaluated using both calibrations. The developed oat whole grain model ranked the oat genotypes similar to the ground oat model for all traits. This effort has contributed to the release of the following oat cultivars with high β -glucan: AAC Excellence, AAC Reid, AAC Captain, AAC Wight, and AAC Fedak and oat cultivars with low oil content, including AAC Nicolas, AAC Richmond, and AAC Anthony.

The new IONC oat nomenclature rules

Eric N. Jellen¹, Charlene P. Wight², Manuel Spannagl³, Victoria C. Blake⁴, James Chong⁵, Matthias H. Herrmann⁶, Catherine J. Howarth⁷, Yung-Fen Huang⁸, Jia Juqing⁹, Andreas Katsiotis¹⁰, Tim Langdon⁷, Chengdao Li¹¹, Robert Park¹², Nicholas A. Tinker², Taner Z. Sen⁴

¹Brigham Young University, Provo, UT, USA

²Agriculture and Agri-Food Canada, Ottawa, ON, Canada

³Helmholtz Center Munich, Neuherberg, Germany

⁴USDA-Agricultural Research Service, Albany, CA, USA

⁵Agriculture and Agri-Food Canada, Morden, MB, Canada

⁶Julius Kuehn Institute, OT Gross Lüsewitz, Sanitz, Germany

⁷Institute of Biological, Environmental, and Rural Sciences, Aberystwyth, UK

⁸National Taiwan University, Taipei, Taiwan

⁹Shanxi Agricultural University, Taigu, China

¹⁰Cyprus University of Technology, Limassol, Cyprus

¹¹Murdoch University, Murdoch, WA, Australia

¹²University of Sydney, Narellan, NSW, Australia

The increasing number of high-quality oat reference genomes has necessitated the development of a universal system for naming oat genomes and subgenomes, chromosomes, genes, gene models, and quantitative trait loci. Consequently, the International Oat Nomenclature Committee (IONC) recently published a series of resources, policies, procedures, and conventions into a single international nomenclature standard. We present those standards here.

The Oat Newsletter

Charlene P. Wight¹, Catherine J. Howarth², Jean-Luc Jannink³, Gerard R. Lazo⁴, Steve Michel⁴, S. Shea Miller¹, Marcelo T. Pacheco⁵, Nicholas A. Tinker¹, Zongwen Zhang⁶, Pamela K. Zwer⁷, Taner Z. Sen⁴

¹ORDC, Agriculture and Agri-Food Canada, Ottawa, ON, Canada

²IBERS, Aberystwyth University, Aberystwyth, Ceredigion, UK

³USDA-ARS and Cornell University, Ithaca, NY, USA

⁴USDA-ARS Western Regional Research Center, Albany, CA, USA

⁵UFRGS, Porto Alegre, Rio Grande do Sul, Brazil

⁶Institute of Crop Sciences, CAAS, Beijing, China

⁷SARDI, Waite Campus, Adelaide, SA, Australia

The first Oat Newsletter was published by the National Oat Conference (USA) in 1950. It was published once a year and sent out by regular mail. The newsletter was designed to supplement the Uniform Nursery reports by providing research updates, meeting information, community information, and reports from oat research stations concerning yields, disease outbreaks, etc. Past issues contain a fascinating history and are well worth reading. The Oat Newsletter today is a dynamic, on-line publication (<https://oatnews.org>) sponsored by the American Oat Workers™ group and hosted by the GrainGenes team at USDA-ARS. Members of the oat community are encouraged to submit research reports, community news, and other information to the editor at any time (oatnewsletter@gmail.com). Research reports are reviewed by two members of the newsletter committee. Newer volumes of these reports have their own sections under the “Research” tab in the newsletter. The “Archives” section contains copies of the newsletter published from 1950-2006. The website is updated regularly, with notifications sent out by email to a list of subscribers. In addition, “OatMail” is available as an email forum for discussion. Details can be found under the “About” tab, where instructions to authors can also be found. Other tabs include those for “Community News”, “Meetings”, “Nomenclature”, “Germplasm”, “Pathology”, and “Links”. When it comes to maintaining and developing the newsletter, the help of the oat community at large is needed and welcome. To quote K.S. Quisenberry in the inaugural edition of the Oat Newsletter, “Its success will depend on the cooperation of all workers.” Your input is always appreciated!

The Triticeae Toolbox

Jean-Luc Jannink, Clay Birkett David Waring

US Department of Agriculture, Agricultural Research Service, Cornell University, Cornell, NY, USA

In the current era of genomics-assisted breeding there is great value in sharing across breeding programs: even if the programs evaluate different accessions, many of the same haplotypes segregate across programs. Combining data enables larger analyses that improve effect estimation and selection of those haplotypes. USDA has long organized central services for public-sector breeding programs (e.g., the USDA Genotyping Labs). The Triticeae Toolbox (T3) aims to become a centralized USDA service for the benefit of data sharing for wheat, barley, and oat breeding programs. To make the effort to uploading data to T3 worth it, we are: 1. Simplifying data upload with easy templates 2. Providing breeding operation functions to make uploading data simultaneous with collecting it 3. Making it easy to consolidate data across many trials for joint analyses 4. Providing functions to help data analysis across multiple datasets, such as marker imputation. Developments in digital data collection and management, as well as in statistical analyses, are such that these objectives are achievable. The success of these efforts will increase the genetic gain generated by public investments in small grains breeding. The accumulated data within T3 will also provide a powerful resource for the basic exploration of the genotype to phenotype map in small grains.

Understanding the genetic basis of stem rust resistance in southeastern US oat through genome wide association study

Janam Prabhat Acharya¹, Md Ali Babar¹, Naeem Khan¹, Jordan McBreen¹, Victor Silva Signorini¹, Sudip Kunwar², Samuel Adewale², Kathy Klos³, Stephen Harrison⁴, Noah DeWitt⁴, Flavia Furlan⁴, Amir Ibrahim⁵, Daniel Hathcoat⁵, Jason Fiedler⁶, Raja Sekhar Nandety⁶, Mary Osenga⁶, Paul Murphy⁷, and Rick Boyles⁸

¹Department of Agronomy, University of Florida, Gainesville, FL, USA

²Plant Breeding PhD Program, University of Florida, Gainesville, FL, USA

³Small Grains and Potato Germplasm Research, USDA-ARS, Aberdeen, ID, USA

⁴LSU Ag Center, School of Plant, Environmental and Soil Sciences, Baton Rouge, LA, USA

⁵Soil and Crop Sciences Department, Texas A&M AgriLife Research, College Station, TX, USA

⁶Edward T. Schafer Agricultural Research Center, Fargo, ND, USA

⁷Department of Crop Science, North Carolina State University, Raleigh, NC, USA

⁸Pee Dee Research & Education Center, Clemson University, Florence, SC, USA

Stem rust (SR), caused by *Puccinia graminis* f. sp. *avenae* Eriks (Pga), presents a considerable threat to oat production, leading to yield and quality reductions. Ongoing efforts in southeastern US universities aim to develop oat varieties with varying resistance levels to this pathogen. However, the specific genetic factors governing the response of southern oat varieties to SR remain elusive. This study seeks to elucidate these genetic mechanisms. Utilizing the Southern Oat Association Panel (SOAP) comprising 440 elite oat lines from public breeding programs in the Southern US, we conducted experiments at selected sites in Citra, FL, Castroville, TX, Baton Rouge, and Winnsboro, LA, known for oat rust disease prevalence. Employing a RCB design with three replicates, susceptible checks were strategically placed to ensure uniform infection distribution. Days to heading and relative maturity were considered as covariates for subsequent analyses. SR phenotypes were visually evaluated during mid and late dough stages in the field, assessing infection response (rated R to S) and severity (rated 0 to 100) according to modified Cobb scale. Additionally, the Average Coefficient of Infection (AIC) was calculated. Genotyping was performed using the genotype by sequencing (GBS) method, with data filtered for multiallelic and monomorphic SNPs. SNPs with a relative minor allele frequency below 0.05 and those missing more than 20% of data were excluded. Preliminary genome-wide association studies (GWAS) revealed significant associations of SNPs with SR using Bonferroni correction as a threshold. Multiple marker-trait associations (MTAs) were identified and an MTA for SR resistance on chromosome 1A was identified across all locations and over time. These findings highlight a notable level of resistance against virulent SR races within the SOAP genotypes that could help to explore potential utilization of these associations.

Vegetative indices data boost genomic selection models in predicting oat grain yield

Guilherme Oliveira¹, Sumandeep Bazzar¹, Maitiniyazi Maimaitijiang², Jiyul Chang¹, Jason Fiedler³, Melanie Caffè¹

¹Department of Agronomy, Horticulture, and Plant Science, South Dakota State University, Brookings, SD, USA

²Department of Geography and Geospatial Sciences, SDSU, Brookings, SD, USA

³Cereal Crops Research Unit, USDA-ARS, Fargo, ND, USA

Traditional genomic selection (GS) methods have been improved by integrating information about major genes into these models. However, for complex traits like grain yield (GYL), this approach may be limited due to the absence of large-effect loci directly affecting this trait. Drawing on insights from phenomics research, the implementation of vegetative indices data has improved crop yield modeling. This suggests that incorporating major genes information affecting these variables might be a viable strategy for enhancing GS models to improve GYL prediction. Therefore, the study aimed to collect vegetative indices using a sensor mounted on an unmanned aerial vehicle (UAV) in oat breeding populations and identify genomic regions associated with these vegetative indices, incorporating them as fixed effects in linear and additive genomic models and evaluating their capability to increase oat GYL predictions accuracies. The UAV flights were conducted in four distinct environments. In each environment, five vegetative indices associated with biomass and chlorophyll levels, which are linked to grain yield (GYL), were collected. Data was gathered from four separate drone flights in each environment, resulting in 20 vegetative indices variables (4 flights x 5 indices). Additionally, the average values of these vegetative indices from the four flights were calculated, providing 5 more variables. In total, including the GYL, 26 variables were collected in each environment (20 individual vegetative index variables, 5 average vegetative index variables, and GYL). Conducting a genome-wide association study (GWAS), fifty-seven molecular markers across twenty of the twenty-one oat chromosomes were identified in association with some of the analyzed vegetative indices. In addition, the broad heritability of the vegetative indices ranged from values close to 0 (no significant associations) to 0.89. These results indicate the presence of genomic variability for the traits related to these vegetative indices in the oat breeding populations under investigation with a complex genetic architecture. Using only the most significant markers (lowest p-values), prediction accuracies for grain yield increased by 7.5-10% in multi-environmental scenarios. These results support the use of vegetative indices for improving GS accuracy for oat grain yield and highlight the benefit of a joint application of phenomics and genomics.