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Progress Report

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Program Name: Climate Change: National Cereal

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Progress Report

Accession No. 224328

Project No. CA-D-PLS-2125-CG

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Non-Technical Summary

Climate change is causing increased abiotic and biotic stresses on barley and wheat. Examples of the impact of climate change are numerous and include: increasing CO₂ concentration reduces the ability of wheat to assimilate nitrates, higher temperatures result in changes in geographic distribution of pathogens, and altered precipitation patterns increase the likelihood of short-term crop failures and long-term production declines. These constraints, compounded by increasing demand for food, and increasing costs for fertilizer, water and other inputs, require a national breeding strategy that capitalizes on innovations in plant breeding. This project brings together the barley and wheat communities to mitigate the impact of climate change on barley and wheat production. Wheat and barley public breeding programs face similar challenges and use similar technologies. A Triticeae CAP will strengthen the integration of these research, breeding and education communities and avoid unnecessary duplications. The Triticeae CAP will evaluate a broad group of barley and wheat germplasm for disease resistance, water and nitrogen use efficiency, and yield. This germplasm will include the National Small Grains Core Collections for barley and wheat and specialized mapping, association mapping, and nested association mapping populations. The same germplasm will be characterized with thousands of molecular markers to identify the gene variants controlling the different traits. Molecular markers will then be used to accelerate the deployment of the best gene variants into commercial barley and wheat varieties. Improvements in disease resistance and water and nitrogen use efficiency will help mitigate the impact of environmental changes associated with climate change on barley and wheat productivity. An expanded centralized marker and trait database coupled with extensive analysis tools will empower breeders to efficiently identify beneficial alleles and effectively exploit large volumes of data in applied plant breeding. This integrated research project will provide a problem-based learning environment to train a new generation of plant breeders and attract new students to agricultural sciences. A nationally-coordinated plant breeding education network will be used to share expertise in different plant breeding areas in the training of 29 PhDs in plant breeding. Educational programs featuring problem-based learning, collaborations with Minority Serving Institutions and social networking technology will be developed to expand the human capital needed to train and sustain the next generation of plant breeders and to attract new students to agricultural sciences.

Accomplishments**Major goals of the project**

Climate change increases the negative impact of abiotic and biotic stresses on crop production. These constraints, compounded by increasing demand for food, and increasing costs for fertilizer, water and other inputs, require a national plan for innovative plant breeding and education. This project will change the paradigm of how we utilize germplasm resources for barley and wheat improvement from a view centered on the characterization of accessions to one centered on the discovery and deployment of valuable alleles. This project brings together the barley and wheat communities leveraging and building on the successful USDA-funded barley and wheat Coordinated Agricultural Projects (CAPs) through synergy in numerous areas. The Triticeae CAP will strengthen the integration of these research, breeding and education communities and avoid unnecessary duplications. The overall goals of the project are to phenotype and genotype diverse barley and wheat germplasm pools to discover and deploy alleles that improve yield under biotic and abiotic stresses, and to use genetic markers to rapidly deploy favorable alleles and accelerate breeding cycles. This integrated research project will provide a problem-based learning environment to train a new generation of plant breeders and attract new students to agricultural sciences. The specific objectives of this project are: 1) Discover and deploy beneficial alleles from diverse wheat and barley germplasm. 2) Accelerate breeding through marker-assisted selection and genomic selection. 3) Implement sequence-based genotyping methodologies to discover new allelic diversity. 4) Implement web-based tools to integrate marker-assisted selection and genomic selection strategies into breeding programs. 5) Develop and implement a Plant Breeding Education Network. The expected outcomes of this project include: i) A well characterized barley and wheat germplasm collection. ii)

Progress Report

Accession No. 224328

Project No. CA-D-PLS-2125-CG

New nested association mapping populations. iii) Eight association mapping studies. iv) Identification of novel alleles for biotic and abiotic resistance. v) New technologies to genotype large numbers of accessions at reduced costs. vi) Genotypic and phenotypic information for a large number of breeding lines. vii) Development of genotyping by sequencing technologies for barley and wheat. viii) An expanded centralized marker and trait database that serves wheat and barley breeders. ix) New tools for the breeders to analyze marker and trait datasets. x) Marker-assisted selection and genomic selection approaches to reduce the length of breeding cycles, xi) New barley and wheat germplasm and varieties better adapted to changing environments, xii) 29 well trained Ph.D. student in plant breeding. xiii) More undergraduate students interested in plant breeding and agricultural sciences. xiv) A national network to train plant breeders. xv) New collaborations with Minority Serving Institutions. These outcomes will strengthen the national network of barley and wheat public breeding programs and ameliorate the negative impacts of climate change on US food security.

What was accomplished under these goals?**Research accomplishments TCAP**

Genotyping: TCAP developed iSelect 9,000 SNP chips for barley and wheat and an iSelect 90,000 SNP chip for wheat.

These SNP platforms were used to genotype the complete core collections of barley and wheat at the USDA National Small Grain Collection. The added value of this information is attracting breeders and researchers to utilize this germplasm in their programs. The same SNP platforms were used to genotype multiple association mapping panels and biparental populations in barley and wheat (spring and winter), which were the basis of several published GWAS and QTL mapping studies.

Genotyping by sequencing (GBS) was tested and GBS bioinformatics pipelines were established. This technology generates thousands of polymorphic GBS tags and is being used to develop high-density maps of NAM populations. The low cost of GBS has also favored the implementation of genomic selection programs. TCAP enhanced the integration of USDA Genotyping laboratories and public breeding programs. The number of GBS markers increased dramatically to 636 million in wheat.

In collaboration with Nimblegen, TCAP developed exon capture platforms for barley and wheat. The first wheat platform was based on low copy number regions and was used mainly for genetic diversity studies and SNP identification. The second platform, based on 286,799 exons from 82,511 genes, was used to identify SNPs in 12 parental lines of the NAM populations, and to identify ten million mutations in 2,700 tetraploid and hexaploid lines mutagenized with EMS from previously developed TILLING populations (King et al. 2015; Uauy et al. 2009). This last resource is providing loss-of-function mutations for most wheat genes (see answer to question 5 for a detailed description).

Phenotyping: TCAP tested and implemented canopy spectral reflectance (CSR) protocols in the US barley and wheat public breeding programs. Breeders were able for the first time to see plants in the far red range! This technology was used to evaluate the National Small Grain Collection (NSGC) core collections of barley and wheat, and multiple AM and NAM populations. The water and N status of thousands of lines was evaluated using normalized indexes. These indexes were analyzed in GWAS populations and multiple QTL were identified. Several have been validated in the NAM populations. Lines with the best water and nitrogen use efficiency are being incorporated into the breeding programs' crossing blocks. Different allelic variants of the Grain Protein Content 1 (GPC-1) have been incorporated into wheat and barley commercial varieties. Some breeding programs are incorporating CSR indexes for indirect yield selection. All the phenotypic data is stored in T3.

The Triticeae toolbox database (T3): extensive phenotypic and genotypic datasets were incorporated into T3. For wheat, T3 currently includes 164 million genotype data, 636 million GBS markers, 440,000 phenotypic data for 147 traits, 334 phenotype trials, and 13,720 line records. T3 has an intuitive interface, extensive tutorials and hyperlinks to other databases. T3 now uses two-dimensional "materialized view" tables to provide quicker access. T3 has implemented useful tools to query the genotypic and phenotypic data, to perform GWAS analysis, and to provide meta analyses of QTL data for all agronomic and morphological traits.

Over the past year (Sept. 1, 2015 to Aug. 31, 2016) 5,955 unique visitors from within the United States used T3, representing a 16% increase from the previous year. T3 has also become an increasingly important source of information internationally. Over the past year, 6,251 unique non-United States visitors used T3. Major visit origination countries were Canada, United Kingdom, Germany, Australia, and China. This past year represented the first time that T3 received more international visits than domestic visits as international traffic increased by 52.0% over the previous year.

Population development: An important legacy of TCAP is the development of publicly-available and fully genotyped AM panels, NAM populations, a wild barley introgression population, and several biparental populations. These genetic resources have been genotyped using the iSelect SNP chips, GBS and exon-capture, providing valuable tools for the rapid identification of associations between molecular markers and traits.

Publications: Scientific knowledge was disseminated through 283 peer reviewed articles that were referred 5,674 times during the five years of the project. These included publications in Science, Nature, Nature Genetics, PNAS, Plant Cell, Genome Biology, etc.

Varieties and Germplasm: TCAP coPIs released 82 commercial varieties and 98 improved germplasm. An economic study based on 2012 data estimated that \$17.2 million per year were added to current barley and wheat varieties by CAP projects. A survey of the acreage of wheat and barley varieties planted in 2014 in the US showed that varieties released by the barley

Progress Report

Accession No. 224328

Project No. CA-D-PLS-2125-CG

and wheat CAPs covered 8.5 million acres documenting the economic impact of this grant to the wheat industry and the US agriculture.

WheatCAP and TCAP Awards: The WheatCAP program received the 2007 USDA-NRI "Discovery Award" for best research program and the 2011 U.S. Department of Agriculture (USDA) Secretary's Honor Award. The TCAP received the USDA-NIFA Partnership Award. Members of the TCAP group received the Wolf Prize in Agriculture (J. Dubcovsky), the Lifetime Achievement Award from the National Association of Plant Breeders (S. Baenziger), and the Plant Breeding Impact Award (B. Carver) for projects associated with the two CAP grants.

What opportunities for training and professional development has the project provided?

Education accomplishments TCAP

The extensive resources invested by TCAP in student training, and the coordinated activities developed by the PBTN at a national level have resulted in a well-trained and well-integrated workforce. The online communication tools developed by PBTN have reduced the isolation of students placed in smaller institutions and have increased collaboration among students. The PBTN tools are used by breeding programs and students around the globe and the platform has been adopted by other crop species in the USA. A total of **56 graduate students completed their programs** (10 MS and 46 PhD. Proposal target was 30). All graduated students (except one that took a year off to write) are working in industry or academia, documenting the demand for TCAP students (see also industry letters in Appendix 1). Ten additional graduate students that started later are expected to graduate by 2017 (96% expected graduation rate).

Evaluation of the TCAP educational program by education experts has shown that TCAP students have a broader perspective of plant breeding than students outside the program. This group of students will provide the continuity and leadership required for sustainable plant breeding activities in the US. An economic impact analysis of the TCAP education program concluded that the future return to the plant breeding sector will be \$1.11 to \$2.50 for every \$1 invested (using conservative assumptions).

How have the results been disseminated to communities of interest?

Results for this project have been disseminated through 287 scientific articles that have been crossreferenced 6314 times documenting their high impact. The applied results of this project have been presented to wheat and barley researchers in scientific meetings and to wheat and barley growers and members of the wheat industry at field days, farm advisors meetings, and industry collaborators meetings. Results have been also made available through dedicated web pages. Our efforts directly reach the barley and wheat growers and industry by releasing improved varieties that cover roughly 8.5 million acres. The international wheat and barley research communities had access to the new association mapping and sequencing information through publications in peer-reviewed journals, presentations in national and international conferences, and sequences deposited in GenBank and T3. To facilitate access to the new molecular markers for different traits, we incorporate detailed protocols to the publicly available MASWheat website .

What do you plan to do during the next reporting period to accomplish the goals?

A No Cost Extension for one year was completed in 2016. A new WheatCAP grant was prepared and submitted to USDA and was approved for funding. The TCAP will transition to the new grant WheatCAP with a similar team and the incorporation of several new young researchers.

Participants

Actual FTE's for this Reporting Period

Role	Non-Students or faculty	Students with Staffing Roles			Computed Total by Role
		Undergraduate	Graduate	Post-Doctorate	
Scientist	0	0	0	0	0
Professional	0	0	0	0	0
Technical	0	0	0	0	0
Administrative	0	0	0	0	0
Other	0	0	0	0	0
Computed Total	0	0	0	0	0

Accession No. 224328

Project No. CA-D-PLS-2125-CG

Student Count by Classification of Instructional Programs (CIP) Code

{NO DATA ENTERED}

Target Audience

The audiences targeted by this project include barley and wheat researchers, breeders (public and private), growers and members of the barley and wheat industry. The applied results of this project have been presented to wheat and barley researchers in scientific meetings and to wheat and barley growers and members of the wheat industry at field days, farm advisors meetings, and industry collaborators meetings. Results have been also made available through dedicated web pages.

Our efforts directly reach the barley and wheat growers and industry by releasing improved varieties that cover roughly 8.5 million acres. This last number documents well the large audience reached by the TCAP project and the economic impact of this grant to the wheat industry and the US agriculture. The targeted audience is further expanded when public wheat and barley varieties are used by the milling, baking, malting, and brewing industries that contribute additional jobs and value to the economy. Private breeding companies are also part of the audience of this project since they routinely use public varieties in their crossing blocks, transferring part of this value to the private sector and further multiplying the economic benefits of the public breeding activities.

The international wheat and barley research communities had access to the new association mapping and sequencing information through publications in peer-reviewed journals, presentations in national and international conferences, and sequences deposited in GenBank and T3. Since the last report, TCAP participants published 38 new peer reviewed scientific articles. Publications from the six years of the project have been cross-referenced 6,314 times (average 22 times per publication) documenting the impact of TCAP research. In addition, 17 new cultivars and 5 new germplasm were released during the sixth year of the project.

All the genotypic and phenotypic data generated by the TCAP project are well organized and safely stored in the T3 database. This database works in close collaboration with GrainGenes. The T3 database is also providing the tools to retrieve and analyze this valuable information and has accelerated the time from data collection to data availability in a public form.

The information of molecular markers for new disease resistance genes, nitrogen use efficiency genes and drought tolerance genes identified and mapped in this project reach a wide national and international audience of barley and wheat breeders. They incorporate these beneficial alleles into their own varieties, which limits applications of costly fungicides and reduces the need for N fertilization, increasing growers' profitability and benefiting the environment. To facilitate access to the new molecular markers for different traits, we incorporate detailed protocols to the publicly available MASWheat website (<http://maswheat.ucdavis.edu/protocols/>).

In the education area the targeted audience included graduate and undergraduate students as well as students from Minority Serving Institutions (MSIs). The online communication tools developed by PBTN have reduced the isolation of students placed in smaller institutions and have increased collaboration among students. The PBTN tools are used by breeding programs and students around the globe and the platform has been adopted by other crop species in the USA. All graduated students (except one that took a year off to write) are working in industry or academia, documenting the demand for TCAP students.

The online PBTN environment was used to deliver webinars and courses further expanding the audience of this project. Graduate students participated in a face-to-face workshop in collaboration with industry, and in a poster session at PAG. Undergraduate students were supported through online meetings. TCAP supported attendance of students at the National Association of Plant Breeders Meeting and to PAG. PBTN has provided an excellent communication tool for the project. Information about research and education was shared both internally and externally through TCAP seminar series, quarterly newsletters and meetings at PAG. Evaluation tools were refined; surveys and interviews were performed; and evaluation reports were created. Evaluation information was used to produce talks, posters and papers.

This project brings together the barley and wheat communities into a Coordinated Agricultural Project to mitigate the impact of climate change on barley and wheat production by strengthening the integration of these communities and avoiding unnecessary duplications.

Products

Progress Report

Accession No. 224328	Project No. CA-D-PLS-2125-CG
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Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Baenziger, P. S., R. A. Graybosch, T. Regassa, R. N. Klein, G. R. Kruger, D. K. Santra, L. Xu, D. J. Rose, S. N. Wegulo, Y. Jin, J. Kolmer, G. L. Hein, M.-S. Chen, G. Bai, R. L. Bowden and J. Poland. 2016. Registration of 'NE05548' (Husker Genetics Brand Panhandle) Hard Red Winter Wheat. *J. Plant Registrations*. 10:276-282

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Bajgain, P., M.N. Rouse, and J.A. Anderson. 2016. Comparison between genotyping by sequencing and SNP-chip genotyping for QTL mapping in wheat. *Crop Sci*. 56: 1–17.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Bajgain, P., M.N. Rouse, T.J. Tsilo, G.K. Macharia, S. Bhavani, Y. Jin Y, and J.A. Anderson. 2016. Nested association mapping of stem rust Rrsistance in wheat using genotyping by sequencing. *PLoS ONE* 11(5): e0155760.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Bulli, P., J. Zhang, S. Chao, X. Chen, and M. Pumphrey. 2016. Genetic architecture of resistance to stripe rust in a global winter wheat germplasm collection. *G3*: doi: 10.1534/g3.116.028407

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Checovich, M. L., A. Galatro, J. Moriconi, M. Simontacchi, J. Dubcovsky, G. E. Santa-María. 2016. The stay-green phenotype of TaNAM-RNAi wheat plants is associated with maintenance of chloroplast structure and high enzymatic antioxidant activity. *Plant Physiology and Biochemistry*. 104: 257-265

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Chen, J., M. J. Guttieri, J. Zhang, D. Hole, E. Souza, and B. Goates. A novel QTL associated with dwarf bunt resistance in Idaho 444 winter wheat. *Theor Appl Genet*. 129:2313-2322.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Cruz, C.D., G.L. Peterson, W.W. Bockus, P. Kankanala, J. Dubcovsky, K.W. Jordan, E. Akhunov, F. Chumley, D.F. Baldelomar, and B. Valent. 2016. The 2NS translocation from *Aegilops ventricosa* confers resistance to the *Triticum* pathotype of *Magnaporthe oryzae*. *Crop Science* 56:990–1000.

Progress Report

Accession No. 224328	Project No. CA-D-PLS-2125-CG
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Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Froese, P.S., A.H. Carter (2016) Single nucleotide polymorphisms in the wheat genome associated with tolerance of acidic soils and aluminum toxicity. *Crop Science* 56:1662-1677

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Froese, P.S., T.D Murray, A.H Carter (2016) Quantitative Cephalosporium stripe disease resistance mapped in the wheat genome. *Crop Science*: 56:1586-1601

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Gao, L., J. Kielsmeirer-Cook, P. Bajgain, X. Zhang, S. Chao M.N. Rouse, and J.A. Anderson. 2015. Development of genotyping by sequencing (GBS) and array derived SNP markers for stem rust resistance gene Sr42. *Mol. Breeding* 35:207

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Gao, L., M.K. Turner, S. Chao, J. Kolmer, and J.A. Anderson. 2016. Genome wide association study of seedling and adult plant leaf rust resistance in elite spring wheat breeding lines. *PLoS ONE* 11: e0148671.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Gizaw S.A., K. Garland-Campbell K, A.H. Carter (2016) Use of spectral reflectance for indirect selection of yield potential and stability in Pacific Northwest winter wheat. *Field Crops Research* 196:199-206.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Gizaw S.A., K. Garland-Campbell K, A.H. Carter (2016) Evaluation of agronomic traits and spectral reflectance in Pacific Northwest winter wheat under rain-fed and irrigated conditions. *Field Crops Research* 196:168-179.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Accepted	2016	YES

Citation

Grogan, S.M. J. Anderson, P.S. Baenziger, K. Frels, M.J. Guttieri, S.D. Haley, K.-S. Kim, S. Liu, G.S. McMaster, M. Newell, P.V. Vara Prasad, S.D. Reid, K.J. Shroyer, G. Zhang, E. Akhunov, and P.F. Byrne. 2016. Phenotypic plasticity of winter wheat heading date and grain yield across the U.S. Great Plains. *Crop Science* 56:1-44.

Progress Report

Accession No. 224328

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Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Grogan, S.M., G. Brown-Guedira, S.D. Haley, G.S. McMaster, S.D. Reid, J. Smith, P.F. Byrne. 2016. Allelic variation in developmental genes and effects on winter wheat heading date in the U.S. Great Plains. PLOS ONE 11: e0152852

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Haas, M., Menke, J., Chao, S., Steffenson, B. J. 2016. Mapping quantitative trait loci conferring resistance to a widely virulent isolate of *Cochliobolus sativus* in wild barley accession PI 466423. Theor. Appl. Genet. 129:1831-1842.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Hoffstetter, A., A. Cabrera, and C. Sneller. 2016 Identifying quantitative trait loci for economic traits in an elite soft red winter wheat cultivar development population. Crop Sci. 56:547-558.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Hoffstetter, A.L., A. Cabrera, M. Huang, and C. Sneller. 2016. Optimizing training population data and validation of genomic selection for economic traits in soft winter wheat. G3 doi: 10.1534/g3.116.032532

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Huang, M., A. Cabrera, and C. Sneller. 2016. Genomic selection for wheat traits and trait stability. Theor. Appl. Genet. 129:1697-1710.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Leng, Y., R. Wang, S. Ali, M. Zhao, S. Zhong. 2016. Sources and genetics of spot blotch resistance to a new pathotype of *Cochliobolus sativus* in a USDA barley core collection. Plant Disease. 100: 1988-1993

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Li, K., J. Hegarty, C. Zhang, A. Wan, J. Wu, G. Brown-Guedira, X. Chen, M. Muñoz-Amatriaín, D. Fu, and J. Dubcovsky. 2016. Fine mapping of barley locus Rps6 conferring resistance to wheat stripe rust. Theor Appl Genet. 129:845-859.

Progress Report

Accession No. 224328

Project No. CA-D-PLS-2125-CG

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Mascher, M., V.J. Schunemann, U. Davidovich, A. Himmelbach, S. Hubner, T. Fahima, A. Korol, M. David, N. Marom, S. Riehl, M. Schreiber, S.H. Vohr, R.E. Green, I.K. Dawson, J. Russell, B. Kilian, G.J. Muehlbauer, R. Waugh, J. Krause, E. Weiss and N. Stein. 2016. Genomic evidence from 6000-year old grains sheds new light on barley domestication history. *Nature Genetics* 48:1089-1093

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Narayanan, S., P.V.V. Prasad, R. Welti. 2016. Wheat leaf lipids during heat stress: II. Lipid experiencing coordinated metabolism are detected by analysis of lipid co-occurrence. *Plant Cell and Environment*. 39:608-617.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Narayanan, S., P. Tamura, M. Roth, P.V.V. Prasad, R. Welti. 2016. Wheat leaf lipids during heat stress: I. High day and night temperatures results in major lipid alternations. *Plant Cell and Environment*. 39:787-803.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Naruoka, Y., K. Ando, P. Bulli, K. T. Muleta, S. Ryneerson, and M.O. Pumphrey. 2016. Identification and validation of SNP markers linked to the stripe rust resistance gene Yr5 in wheat. *Crop Science*. 56: 3055-3065.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Nasseer, A. M., J. M. Martin, H.-Y. Heo, N. K. Blake, J. D. Sherman, M. Pumphrey, K. D. Kephart, S. P. Lanning, L. E. Talbert. 2016. Impact of a quantitative trait locus for tiller number on plasticity of agronomic traits in spring wheat. *Crop Sci*. 56:595-602.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Nice, L.M., B.J. Steffenson, G.L. Brown Guedira, E.D. Akhunov, T.J.Y. Kono, P.L. Morrell, R. Horsley, K.P. Smith and G.J. Muehlbauer. 2016. Development and genetic characterization of an advanced backcross – nested association mapping (AB-NAM) population of wild x cultivated barley. *Genetics* 203:1453-1467.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Nirmala, J., S. Chao, P. Olivera, B. Abeyo, M. Imtiaz, E. Akhunov, M.O. Pumphrey, Y. Jin and M.N. Rouse. 2016. Markers linked to wheat stem rust resistance gene Sr11 effective to *Puccinia graminis* f. sp. *tritici* race TKTTF. *Phytopathology*. 106:1352-1358.

Progress Report

Accession No. 224328

Project No. CA-D-PLS-2125-CG

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Richards, J., Chao, S., Friesen, T.L., Brueggeman R. 2016. Fine mapping of the barley chromosome 6H net form net blotch susceptibility locus. *G3*. 6:1809-1818.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Russell, J., M. Mascher, I.K. Dawson, S. Kyriakidis, C. Calixto, F. Freund, M. Bayer, I. Milne, T. Marshall-Griffiths, S. Heinen, A. Hofstad, R. Sharma, A. Himmelbach, M. Knauft, M. van Zonneveld, J.W.S. Brown, K. Schmid, B. Kilian, G.J. Muehlbauer*, N. Stein and Robbie Waugh. 2016. Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. *Nature Genetics* 48:1024-1030

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Schönhofen, A., B. Hazard, X. Zhang, and J. Dubcovsky. 2016. Registration of common wheat germplasm with mutations in SBEII genes conferring increased grain amylose and resistant starch content. *J. Crop Reg.* 10:200-205.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Simmonds, J., P. Scott, J. Brinton, T.C. Mestre, M. Bush, A. Del Blanco, J. Dubcovsky, C. Uauy. 2016 A splice acceptor site mutation in TaGW2-A1 increases thousand grain weight in tetraploid and hexaploid wheat through wider and longer grains *Theor Appl Genet.* 129:1099–1112.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Turner, M.K, Y. Jin, M.N. Rouse, and J.A. Anderson. 2016. Stem rust resistance in 'Jagger' winter wheat. *Crop Sci.* 56:1–7.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Varella, A. C., L. E. Talbert, M. L. Hofland, M. Buteler, , J. D. Sherman, N. K. Blake, H.Y. Heo, J. M. Martin, D. K. Weaver. 2016. Temporal patterns of pith expression and retraction in wheat stems and its effect on resistance to the wheat stem sawfly. *Plant Breeding*, 135:546-551.

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

Wang, R., Y. Leng, S. Shrestha, and S. Zhong. 2016. Coordinated and independent functions of velvet-complex genes in fungal development and virulence of the fungal cereal pathogen *Cochliobolus sativus*. *Fungal Biology* 120:948-960.

Progress Report

Accession No. 224328

Project No. CA-D-PLS-2125-CG

Type	Status	Year Published	NIFA Support Acknowledged
Journal Articles	Published	2016	YES

Citation

38. Wang, X., B. Yang, K. Li, Z. Kang, D. Cantu, J. Dubcovsky. Conserved *Puccinia striiformis* effector interacts with wheat NPR1 and reduces induction of Pathogenesis-Related genes in response to pathogens. *Mol. Plant Microbe Int.* <http://dx.doi.org/10.1094/MPMI-10-16-0207-R>.

Patent(s) and Plant Variety Protection(s)

Application Number	Application Filing Date	Title
201600390	08/09/2016	Hard White Spring Wheat 'Patwin-515HP'
201700009	09/11/2016	Malting barley 'Tahoe'
201600078	02/02/2016	Soft White Spring Wheat 'Seahawk'
201600077	02/02/2016	Hard Red Spring Wheat 'Alum'
201600076	02/02/2016	Hard Red Spring Wheat 'Chet'
2016000298	06/30/2016	Hard Red Spring Wheat 'Lanning'

Other Products**Product Type**

New Germplasm

Description

'Shelly' (PVP application in progress) is a hard red spring variety released by the MN wheat breeding program. Shelly has grain yields comparable to the highest yielding varieties in the region, but has higher grain protein. Shelly also has moderate resistance to *Fusarium* head blight, containing Fhb1.

Product Type

New Germplasm

Description

'UI Sparrow' soft white winter wheat adapted to irrigated and drylands in ID and WA with very good winter hardiness. UI Sparrow has immune resistance to dwarf bunt (for organic wheat production) and to all predominant races of stripe rust except for PSTv-40 (but has HTAP resistance).

Product Type

New Germplasm

Description

VA10W-96 is an early maturing SRW wheat variety having high test weight and resistance to powdery mildew, leaf rust, and stripe rust.

Product Type

New Germplasm

Description

VA10W-119 is an early maturing SRW wheat variety having high test weight and gene H13 conferring resistance to Hessian fly.

United States Department of Agriculture
Progress Report

Accession No. 224328

Project No. CA-D-PLS-2125-CG

Product Type

New Germplasm

Description

VA11W-106 is a broadly adapted, high yielding, full season SRW wheat variety having resistance to powdery mildew, leaf rust and stripe rust.

Product Type

New Germplasm

Description

Vision 50 (VA09HRW-64) is a broadly adapted HRW wheat variety that is resistant to leaf and stripe rusts.

Product Type

New Germplasm

Description

Langin' (CO11D446) is a hard red winter wheat developed by the Colorado Agricultural experiment station and released in fall 2016. DNA marker assays for high molecular weight glutenin subunits have shown that Langin carries the Glu-A1b, Glu-B1b, and Glu-D1d high molecular weight glutenin alleles, that it does not carry the 1RS wheat-rye translocation, and it carries the Sbm1 allele conferring resistance to wheat soilborne mosaic virus".

Product Type

New Germplasm

Description

'MT1173' is a Clearfield variety with two genes for resistance to imidazolinone herbicides. Initial selection of herbicide resistance was accomplished using molecular markers. The variety has been licensed to a private company for commercialization.

Product Type

New Germplasm

Description

OH08-206-69, soft red winter wheat line released in the fall of 2016 as a public variety.

Product Type

New Germplasm

Description

OH09-207-68, soft red winter wheat line released in the fall of 2016 for licensing.

Product Type

New Germplasm

Description

OH07-263-3, soft red winter wheat line released in the fall of 2016 for licensing.

Product Type

New Germplasm

Description

PI 676269: synthetic hexaploid wheat developed at UC Davis carrying loss of function mutations at all three VRN2 loci (first vrn2-null spring hexaploid wheat).

Progress Report

Accession No. 224328

Project No. CA-D-PLS-2125-CG

Product Type

New Germplasm

Description

PI 675644-675647: four mutant combinations of Sbella and Sbellb mutants in hexaploid wheat. The quintuple mutant (PI 675647). Presented 63% increase in amylose and 1,057% increase in resistant starch relative to the control, and differed in starch viscosity parameters

Product Type

Databases

Description

Phenotype and genotype data in the Triticeae Tool Box (T3) has been expanded. In September 2016, T3 included 164 million genotype data, 636 million GBS markers, 440,000 phenotypic data for 147 traits, 334 phenotype trials, and 13,720 line records.

Product Type

Databases

Description

WheatExp is an expression database and visualization tool to analyze and compare homoeologue-specific transcript profiles across a broad range of tissues from different developmental stages in polyploid wheat. Beginning with publicly-available RNA-seq datasets, a pipeline was developed to distinguish between homoeologous transcripts from each annotated gene in the hexaploid bread wheat genome. The database can be queried either by BLAST or by searching for a known gene of interest by name or functional domain. WheatExp is hosted on the GrainGenes website and can be accessed at the following URL <http://wheat.pw.usda.gov/WheatExp/>.

Changes/Problems

{Nothing to report}