

PROJECT NO: BJKW32

TITLE: Developing Wheat Cultivars for Idaho

PERSONNEL: J. Chen, J. Wheeler, N. Klassen, R. Wang, W. Zhao

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JUSTIFICATION:

Idaho wheat production contributes significantly to domestic and overseas wheat markets. Nationally, Idaho ranks in the top eight states for wheat and wheat product exports. Most of wheat production in the southern part of the state is grown under irrigation, while in the northern part grown under dryland. Improved grain yield and desirable end-use quality are the two major traits required in cultivar development. Resistances to biotic and abiotic stresses have significant impacts to grain yield and end-use quality. Stripe rust has been the most important disease for both winter and spring wheat as it caused significant yield loss for growers and quality reduction for the wheat industry. The predominant spring wheat (Alturas, Louise, and Jefferson) and winter wheat (Stephen and Brundage) cultivars are being replaced by the increasing number of new wheat varieties that have better yield, improved disease resistance, and desirable end-use quality. Fusarium head blight (FHB) has emerged to the irrigated production areas in southern Idaho, especially for spring wheat, due to increasing corn production, no-till practices, and the climate change. Most of wheat cultivars are very susceptible to FHB. When an epidemic occurs the fungus in the infected grains will produce DON and causes grains unusable for human consumption and animal feeds. Snow mold and dwarf bunt are endemic diseases that limit use of winter wheat varieties in dryland production. Other diseases and pests affecting wheat production in this region include barley yellow dwarf virus (BYDV), bacterial leaf blight, physiological leaf spots, dryland crown rot, cereal cyst nematodes, and wireworm. Drought and heat are the two major abiotic stresses. Pre-harvest sprouting and late maturity alpha amylase damage are also concerns in recent years.

HYPOTHESIS & OBJECTIVES: The genetic recombination of desired genes can be selected in a favorable environment and stabilized with the proper methods. This breeding process can be accelerated using a combination of conventional breeding, wheat by maize di-haploid (DH) system, and molecular marker assisted selection (MAS). Objectives of this study are: 1) To develop desired wheat cultivars via traditional breeding; 2) To accelerate wheat cultivar development via di-haploid system and MAS; 3) To identify and validate QTL/markers associated with yield, end-use quality, resistance to biotic and abiotic stresses.

1. BREEDING PROCEDURES:

1.1. Breeder Seed Production: A two-year breeder seed production system was developed in 2012 and will be used in this grant. In FY18, we are going to plant and harvest B2 breeder seed for IDO1506 (HWW), IDO1405S (SWS, FHB), IDO1602S (HWS) and IDO1604S (HWS), B1 breeder seed for IDO1603S (HRS, H25 and FHB1 and Yr36).

- 1.2. Elite and Breeding Line Evaluation:** Yield trials are defined previously as Elite Yield Trial (EYT), Preliminary Yield Trial (PYT), and Observation Yield Trial (OYT). OYT is the first year, non-replicated trial that is planted in one or two environments depending on seed availability. PYT is the second year, replicated yield trial that is usually planted in two or three environments. EYT is the third year, replicated yield trial that is planted in four to seven locations in SE ID. Lines in the EYT will be evaluated for stripe rust by Dr. X. Chen, dwarf bunt by Dr. David Hole, FHB by us, stem rust by Drs. Yu Jin and J.M. Bonman, snow mold by Drs A. Carter and/or J. Marshall, nematodes by Dr. R. Smiley, Hessian fly by Dr. Bosque-Pérez, and Wheat Streak Mosaic Virus by Dr. M. Flower. Elite lines will also be genotyped with known functional markers and markers identified in our lab based on data generated by Dr. D. See in the ARS genotyping center at WSU and in our MAS lab. After harvesting, end-use quality of the selected lines in the EYT, PYT, and OYT from multiple locations will be assessed in the Idaho Wheat Quality Lab (Mrs O'Brein). Yield, agronomic, disease and insect resistance, and marker data will be used in selection of lines for crossing and further evaluation in the Western Regional Trials (WRT) and Tri-state Variety Trials (VYT) in the following years. In FY18 we are going to test 25 lines in WRT, 15 lines in VYT, 250 lines (50 winter and 200 spring) in EYT, 405 lines (105 winter and 300 spring) in PYT, 2580 lines (580 winter and 2000 spring) in OYT, in addition to the lines in special projects (Gp208, Gp502, Gp306).
- 1.3. Headrow Evaluation:** Headrows will be planted in Aberdeen and assessed for plant type and agronomic characteristics and disease resistance. After harvesting, test weight, seed color, protein, and flour hardness will be assessed and used in grouping of selected headrows into Observation Yield Trials in the following year. Headrow trials are also used for seed increase of F1, DH lines, and for pre-breeder seed production. In FY18 we are expecting to assess 20,000 head rows, of which 2000 rows will be sprayed with 4X Beyond herbicide to develop ClearField Plus wheat varieties.
- 1.4. Early Generation Test (F2, F3, and F4):** Around 600 populations (100 winter and 500 spring) of F2 and F3 will be advanced with modified bulk selection and 150 F4 populations (50 winter and 100 spring) will be advanced with head selection in non-replicated trials in irrigated and water stress environments in SE ID.
- 1.5. Objectives for 2017 New Crosses:** make 50 crosses between FHB resistant germplasm and adapted cultivars and breeding lines; make 50 crosses between CIMMYTT high biomass lines and adapted cultivars and breeding lines; make 50 crosses introgression of Yr5 and Yr15; make special crosses for basic research.

2. Doubled Haploid Production and Molecular Marker Assisted Breeding:

- 2.1.** In FY18 we are going to assess herbicide resistance in Aberdeen in around 200 DHLs derived from the cross IDO1203S/SY605CL//UI Platinum.
- 2.2.** We routinely use molecular markers for a list of traits in different stages of variety development. The traits list includes markers identified from our program and other published ones. Traits being selected via molecular markers include FHB (FHB1 and FHB 3), Hessian Fly (H25), stripe rust (Yr5, Yr15, Yr36, QTL2BS, QTL4AS), height (Rht1 and Rht2), vernalization (VRNB1), heading (PPD-D1), baking quality (GluBx7oe, GluD1, GluA3, GluB3, QTL1B-VOL). In FY18 we are going to add additional traits: dwarf bunt (QTL7DS), stem rust (Sr2, Sr39, Sr47), LMA/PHS (QTL2BS, QTL5AS, QTL3A), yield components

(SN5A, SPN6A, SPN4A).

3. Marker Development and Validation:

3.1. Identify additional molecular markers associated with dwarf bunt: The two dwarf bunt resistant lines IDO835 and UI Silver contain different QTL other than the 7DS. DHLs from the two populations (Moreland x IDO835, UI Silver x Shaan89150) were planted for the second year evaluation in a dwarf bunt nursery in Logan, UT. SNP data from the two populations will be used to conduct linkage and QTL mapping. Molecular marker associated with dwarf bunt resistance will be identified and validated in breeding lines in FY18.

3.2. Fine mapping of QTL associated with LMA and PHS (separate proposal).

3.3. QTL associated with grain cadmium content (in Dan Strawn proposal).

3.4. Molecular markers associated with yield components (USDA-ARS NIFA CAP).

3.5. Validation of FHB QTL identified from association study (USDA-ARS USWBSI project).

DURATION: Fourth of five years (2013-2018)

COOPERATION: Details were included in the progress report.

ANTICIPATED BENEFITS/EXPECTED OUTCOMES/INFORMATION TRANSFER:

New cultivars released by this project, combining improved yield with biotic and abiotic resistances, will be grown by wheat growers and be used by end-users in Idaho, the PNW, and the US to maintain or increase their productivity and competitiveness in domestic and international markets. Information on cultivars and breeding lines will be distributed to growers through the wheat breeding project website, commodity schools, IGPA meetings and magazines, and publications in Journal of Plant Registration and other journals. QTL and molecular markers identified will be used in the breeding programs in the US and the world and published in peer referred journals and presented at national and international meetings. Students involved in the projects will be trained and worked in public and private sectors after graduated.

LITERATURE REVIEW:

Development of desirable wheat varieties is dependent on the extent of genetic variation, favorable selection environments, and efficient selection methods. Genetic improvement of desirable traits for premier wheat cultivars can be achieved and accelerated by using a combination of traditional and marker-assisted breeding methodologies (Varshney et al., 2006).

In addition to grain yield, improvement of bread baking quality is a vital breeding aim for hard wheat, but its measurement in early generation material is technically demanding. As a result, a number of predictive indirect assays have been developed and widely used to evaluate processing quality, including sodium dodecyl sulfate sedimentation volume, grain protein content, grain hardness, and various mixograph parameters. The end-use quality is determined by a combination of genetic factors and the growing environment of the crop (Rousset et al. 1992; Peterson et al. 1998). A major contributor to the genetic determination of bread making quality is the allelic variants at the loci encoding the high-molecular-weight glutenin subunits (HMW-GS) (Payne et

al. 1984), low-molecular weight GS (LMW-GS) and gliadins (Payne et al.1987). The gluten fraction as a whole can account for up to one-third of the variation in bread-making quality (Oury et al. 2010). This leaves more than half of the genetic determination of the end-use quality in wheat as yet undefined. Therefore, it is important to identify additional quantitative trait loci that complement the known gluten genes to achieve improved and consistent bread baking quality.

Marker-assisted breeding is vital to developing efficient breeding strategies (Brevis et al., 2010). Advances in genotyping (SNP and GBS) are decreasing molecular marker costs and increasing genome coverage to the point that new strategies are now feasible. To facilitate marker-based breeding in the small grains, the USDA-ARS has established four regional genotyping centers in Manhattan, KS; Pullman, WA; Fargo, ND; and Raleigh, NC. The integration of the genotyping laboratories in the previous CAP projects provides the foundation for the breeding programs to implement marker-assisted selection (MAS) and genomic selection (GS) strategies. MAS combining with dihaploid production will accelerate breeding cycles significantly.

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- Peterson, C.J., R.A. Graybosch, D.R. Shelton, P.S. Baezinger. 1998. Baking quality of hard winter wheat: response of cultivars to environment in the great plains. *Euphytica* 100:157–162
- Rousset, M., J.M. Carrillo, C.O. Qualset, and D.D. Kasarda DD. 1992. Use of recombinant inbred lines of wheat for study of associations of high-molecular-weight glutenin subunit alleles to quantitative traits. 2-milling and bread baking quality. *Theor Appl Genet* 83:403–412
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IDAHO WHEAT COMMISSION - BUDGET FORM

Allocated by	Idaho Wheat Commission	during FY 2016	\$	117,307
Allocated by	Idaho Wheat Commission	during FY 2017	\$	153,058

REQUESTED FY2018 SUPPORT:

	Salary	Temporary Help	Fringe	Travel	OE	Graduate Tuition/Fees	TOTALS
Idaho Wheat Commission	\$ 12,790	\$ 64,084	\$ 31,441	\$ 15,000	\$ 27,500	\$ -	150,815

TOTAL BUDGET REQUEST FOR FY 2018: \$ 150,815

BREAKDOWN FOR MULTIPLE SUB-BUDGETS:

	(PI name)	(PI name)	(PI name)	(PI name)
Salary	\$ -	\$ -	\$ -	\$ -
Temporary Help	\$ -	\$ -	\$ -	\$ -
Fringe Benefits	\$ -	\$ -	\$ -	\$ -
Travel	\$ -	\$ -	\$ -	\$ -
Operating Expenses	\$ -	\$ -	\$ -	\$ -
Graduate Student Tuition/Fees	\$ -	\$ -	\$ -	\$ -
TOTALS	\$ -	\$ -	\$ -	\$ -
Total Sub-budgets				\$ -

Explanatory Comments: (see FY2018 Guidelines for definition)

Salary: 25% of post doc.

Temporary Help: 4 full-time working for 6-8 months, 2 working in August-Sept, and 1 classified employee for June.

Fringe Benefits per UI set rates: Staff (40.9%), TH (40.9% or 7.4%)

Travel: Attend PNW QC, growers conferences, professional meeting, and travel to field nurseries.

Operating Expenses: Land charges, maintainance and rental of transportation vehicles, rental of greenhouse, and purchase field supplies.

11.21.2016 - Version

ANNUAL REPORT

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ADDRESS: Jianli Chen, University of Idaho Aberdeen Research & Extension Center, Aberdeen, ID 83210; 208-397-4162, ext. 229; jchen@uidaho.edu

COOPERATION:

University of Idaho: J. Marshall, K. O'Brien, D. Fu, Y. Wang, K. Schroeder, N. Bosque-Perez, D. Strawn, J. Kuhl, O. Welsh, X. Liang, A. Lin, A. Rasheed, Ch. Roger;

USDA-ARS: J. Bonman, G. Hu, X. Chen, D. Angle, K. Campbell, D. See, S. Xu, J. Yue, M. Guttieri, X. Shao, G. Brown-Guedira, Sh. Zhnog;

OSU: R. Zemetra, M. Flower, R. Smiley, A. Russ; KSU: A. Akhunov, G. Zhang;

WSU: R. Higginbotham, A. Carter, M. Pumphrey, T. Murray; MSU: E. Olson;

U.C. Davis: Jorge Dubcovsky, J. Zhang; MSU: L. Talbert, J. Herman.

USU: D. Hole; CSU: S. Haley, P. Byrne; UMN: J. Anderson, Y. Dong; LSU: Steve Harrison.

Industry: B. Wilkin; R. McLean; F. Curtis, J. Peterson, J. Kalous; G. Weaver, Sh. White, G. Gang, H. Jie.

ACCOMPLISHMENT:

Using an integrated approach combining of traditional breeding, wheat by maize dihaploid (DH) system, and molecular marker assisted selection, we evaluated around **10,000 yield plots** planted in Aberdeen, Kimberly, Tetonia, Soda Springs, Rockland, and Arbon Valley and around 20,000 headrows in Aberdeen.

The breeding program assisted in market launch of the two released spring wheat cultivars, UI Stone and UI Platinum. Production of UI Stone and UI Platinum brought back royalty to university. **UI Sparrow (IDO1108) was officially released** in August this year. UI Sparrow was developed using wheat x maize dehaploid technology. This cultivar has high yield, immune resistance to dwarf bunt, high level of resistance to stripe rust and snow mold. It is adapted in reduced irrigation and high rainfall dryland production in ID and WA. One private company is interested in licensing in 2017. We planted large strip trials in Aberdeen, Kimberly, Rockland, and Arbon Valley and will do field demonstration to growers and industry and other state holders in summer 2017. We also harvested **breeder seed for IDO1506 (HWW), IDO1602S (HWS), IDO1604S (HWS), IDO1405S (SWS)**, and submitted five lines for quality evaluation to PNW Quality Council. In addition, we did seed increase for UI Stone and 10 germplasm lines.

In acknowledgements of IWC support, we **published one referred paper in TAG**, submitted two manuscripts, and prepared three manuscripts for 2017. One 2015 published paper was **awarded**

the first place of outstanding papers in plant genetic resource. We also did three oral and two poster presentations at an international meeting and one oral at national meeting, six outreach and 10 field day presentations. IWC support directly or indirectly helped us in getting **new competitive grant** (10M, \$432K to UI for five years) and additional industry grants for a total of \$330,487 (IWC support \$184,562) in FY17.

The specific progresses were summarized below:

Molecular marker-assisted breeding. We routinely use molecular markers for a list of traits in different stages of variety development. The traits list includes markers identified from our program and other published ones. Traits being selected via molecular markers include FHB (FHB1 and FHB 3), Hessian Fly (H25), stripe rust (Yr5, Yr15, Yr36, QTL2BS, QTL4AS), height (Rht1 and Rht2), vernalization (VRNB1), heading (PPD-D1), baking quality (GluBx7oe, GluD1, GluA3, GluB3, QTL1B-VOL). This year we extracted DNA for 570 lines in our lab and genotyped them with 20 markers in Western Regional Genotyping Lab in Pullman, WA. As a result of marker-assisted selection from this and previous years **we selected two hard red spring wheat lines IDO1603S and IDO1605S that have high yield, resistance to hessian fly, stripe rust, and good bread-baking quality. We are expecting to release one of them in 2017 or 2018.**

Use wheat x maize dihaploid technology to facilitate breeding and QTL mapping.

Around 189 DHLs from UI Platinum x LCS Star produced in 2015 were planted in Aberdeen and Soda and tested for grain cadmium content this year. We are going to genotype this population with 90K SNP platform and plant it in Aberdeen, Soda, and Ashton in 2017 and identify QTL associated with grain cadmium content in 2018.

One DH population (120 DHLs) derived from UI Platinum x SY Capstone in 2014 was genotyped by 90K SNP platform and assessed in multiple locations for yield and yield components, stripe rust, stem rust, bread baking quality, and falling numbers in 2015 and 2016. One dissertation and two manuscripts will be developed by a visiting Ph.D student in 2017. Findings related to QTL of yield components were orally presented at 2016 ASA and CSSA meeting. **New KASP markers were developed for yield components and LMA and will be used in MAS.** The new KASP markers will also be used in fine mapping and cloning project being supported by a newly funded USDA-NIFA grant (10M, SA\$432,685) in coming five years.

Identify QTL for resistance to fusarium head blight. This is my hatch project with additional finding from USDA-ARS USWBSI. I hired one postdoc (50%) conducted association mapping of FHB resistance in 190 spring wheat lines from PNW. The 170 lines were assessed in the second year in Aberdeen, ID and St. Paul, MN under collaboration. **Research findings were presented at 2016 ASA and CSSA meeting and at 2016 National FHB Forum.** One manuscript is expected to submit in January, 2017. FHB resistant germplasm identified will be used as parental lines in crossing in 2017. Molecular markers identified will add to the trait lists in MMAB.

Identify molecular markers associated with dwarf bunt: We published a paper in TAG for a novel QTL associated with dwarf bunt resistance and PCR-based markers on 7DS. We also

assessed dwarf bunt resistance in two additional DH populations (Moreland x IDO835, UI Silver x Shaan89150) in a dwarf bunt nursery in Logan, UT. SNP data from the two populations were analyzed and linkage maps were constructed. QTL will be identified when additional dwarf bunt data become available in 2017 and 2018. **We submitted a pre-proposal to NSF to do fine mapping of the 7DS QTL and identify additional QTL for five important dwarf bunt genes Bt8, Bt9, Bt10, Bt11, and Bt12 under collaboration with scientists in Austria and**

Develop herbicide resistant spring wheat cultivars.

We completed a field screening for a total of 2000 headrows. The harvested headrows have been screened again in greenhouse before planting them in the field in spring 2017. Around 200 DHLs from the cross IDO1203S/SY605CL/UI Platinum are being produced to speed up the variety development of two-gene Clearfield. These DHLs will be sprayed by Beyond after seed increased in greenhouse in 2017.

Breeding using EMS mutagenesis. Out of 390 EMS-induced lines in Moreland background, sixty lines were advanced and planted in fall of 2016. Some of these lines showed significantly increased yield than Moreland and have good resistance to stripe rust. A couple lines can be released as Moreland replacement and some other lines can be used in functional analysis in the future.

Publications and presentations

- J. Chen, M. J. Guttieri, J. Zhang, D. Hole, E. Souza, B. Goates. 2016. A novel QTL associated with dwarf bunt resistance in Idaho 444 winter wheat. *Theor Appl Genet.* 129(12): 2313-2322. DOI 10.1007/s00122-016-2783-2.
- Liu, Y., P. Li, J. Zhang, Y. Hu, and J. Chen. 2016. Dwarfing genes *Rht4* and *Rht-B1b* affect plant height, agronomic traits, and kernel quality traits in common wheat under two water regimes. Accepted by *Field Crops Research*.
- Liang, X., D. Strawn, J. Chen, and J. Marshall. 2016. Cadmium accumulation in spring wheat grains is influenced by cadmium bioavailability and root length. Submitted.
- Chen, J., R. Wang, J. Zhang, D. Hole, M. J. Guttieri, E. Souza, B. Goates. 2016. Validation and marker assisted selection for a novel QTL *Q.DB.ui-7DS* associated with dwarf bunt resistance of winter wheat. Oral presentation and abstract in the proceedings of ASA, CSSA and SSSA Int'l Annual meeting, Phoenix, AZ, Nov. 15-18.
- Tyler, G., J. Chen, R. Wang, J.M. Bonman. 2016. Association mapping of yield components in 2-Row spring barley from the USDA National Small Grains Collection. Oral presentation and abstract in the proceedings of ASA, CSSA and SSSA Int'l Annual meeting, Phoenix, AZ, Nov. 15-18.
- Liu, Y., R. Wang, J. Chen, D.R. See. 2016. Genome-wide linkage mapping of QTL for yield component in UI Platinum/SY Capstone double haploid population. Oral presentation and abstract in the proceedings of ASA, CSSA and SSSA Int'l Annual meeting, Phoenix, AZ, Nov. 15-18.
- Wang, R., J. Chen, J. Zhang, W. Zhao, J. Wheeler, N. Klassen, J.A. Anderson, D.R. See and Y. Dong. 2016. Genome-Wide Association Mapping of Resistance QTL to Fusarium Head Blight in Spring Wheat Lines Grown in Pacific Northwest and CIMMYT. Poster presentation and

abstract in the proceedings of ASA, CSSA and SSSA Int'l Annual meeting, Phoenix, AZ, Nov. 15-18 and in the proceedings of 2016 FHB forum, St. Louis, MO, Dec. 4-6.