

**PROJECT NO:** BJKV32

**TITLE:** Developing Wheat Cultivars for Idaho

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

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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 some 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.

**PROCEDURES:**

**Breeder Seed Production:** A two-year breeder seed production system was developed in 2012 and used in this grant. The first year breeder seed production (B1) is to grow 400 headrows from 400 heads selected from a plot in the elite line strip trials (Gp10 and Gp100). The B1 headrows

are selected based on uniformity and disease resistance if occurs. The selected B1 headrows are individually harvested and tested for protein and test weight and some of headrows with low test weight will be discarded. The final selected headrows are planted in yield plots in the second year breeder seed production (B2), simultaneously, a tea-spoon grain of each B2 plots are tested in disease nurseries (stripe rust, dwarf bunt, FHB). The B2 plots are selected based on uniformity and disease resistance and composited to form final breeder seed for foundation seed production in the following year.

In FY17, we are expecting to harvest B1 breeder seed for one hard white winter line IDO1506, and two hard white spring wheat lines IDO1602S and IDO1604S. We are going to plant breeder seed for two hard red winter lines IDO1607DH and IDO1609DH; two hard white winter lines IDO1606DH and IDO1608DH; three hard red spring wheat lines with Hessian Fly resistance and/or FHB resistance IDO1601S, IDO1603S and IDO1605S.

**Elite and Breeding Line Evaluation:** Yield trials are defined 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. Yield, agronomic, disease and insect resistance, and marker data will be used in selection of lines for crossing and evaluation in the Western Regional Trials (WRT) and Tri-state Variety Trials (TVT) in the following years. In FY17 we are going to test 25 lines in WRT, 15 lines in TVT, 350 lines (150 winter and 200 spring) in EYT, 380 lines (80 winter and 300 spring) in PYT, 2250 lines (750 winter and 1500 spring) in OYT, in addition to the lines in special projects.

**Headrow Evaluation:** Headrows will be planted in Aberdeen and be 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 fall of 2015, we planted around 3840 winter wheat headrows (2560 F5, 400 F1, 400 breeder, and 480 others). In the spring of 2016, we are going to plant approximately 20,000 spring wheat headrows (18,000 F5, 600 F1, 800 breeder, and 600 others).

**Early Generation Test (F2, F3, and F4):** A total of 660 populations (160 winter and 500 spring) of F2 and F3 will be advanced with modified bulk selection and 180 F4 populations (30

winter and 150 spring) will be advanced with head selection in non-replicated trials in irrigated and water stress environments in SE ID. Out of 150 F4 spring wheat populations, fifty will be inoculated in a FHB nursery with corn spawn. Head selection will be conducted based on FHB resistance when infection is established. In addition, fifty BC2F2 spring wheat populations will be sprayed with 4X Beyond herbicide to develop ClearField Plus wheat varieties.

**Molecular Marker Assisted Breeding:** After completed marker-assisted pyramiding of FHB1, H25, and Yr36 we are going to move our effort on pyramiding of novel stem rust resistance genes Sr39 and Sr47 to Ug99 with FHB1, H25, and Yr36 using markers developed by Klindworth et al. (2012). A new Post Doctorate and Weidong Zhao will conduct this project.

**Marker Development and Validation:**

**Molecular markers associated with FHB:** We will plant the 190 PNW spring wheat lines in a field scab nursery and greenhouse for the second year evaluation of FHB resistance. QTL will be identified using two years disease data and good SNPs derived from 90K. A new Post Doctorate and Weidong Zhao will conduct this project.

**Molecular markers associated with dwarf bunt:** DH lines from the two DH 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 FY17. A new Post Doctorate and Weidong Zhao will conduct this project.

**Molecular markers associated with end-use quality in hard white background:** Two hard white DH populations were developed from UI Silver x Shaan89150 and Capstone x UI Platinum to identify markers associated with bread baking quality. The two populations have been genotyped by GBS, SNP, and SSR this year. The bread baking quality of the two populations will be assessed in 2016. A visiting Ph.D student from P. R. China will coordinate this study.

**Molecular markers associated with grain cadmium content:** Two hard white spring wheat DH populations (UI Platinum x LCS Star and UI Platinum x LCS Atoma) will be planted in two high Cd environments Ashton and Soda in the spring of 2017 and 2018. Grain samples harvested from the two locations will be tested for Cd content in Moscow each year. The two populations will be genotyped by 90K SNP in 2017. Molecular markers associated with Cd content will be identified in 2018.

**DURATION:** Third of five years (2013-2018)

**COOPERATION:**

University of Idaho: J. Marshall, K. O'Brien, D. Fu, Y. Wang, C. Schroeder, N. Bosque-Perez, D. Strawn, J. Kuhl.

USDA-ARS: J. Bonman, G. Hu, X. Chen, D. Angle, K. Campbell, D. See, S. Xu, J. Yue.  
OSU: R. Zemetra, M. Flower, R. Smiley; WSU: R. Higginbotham, A. Carter, M. Pumphrey et al.  
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.  
Thresher: B. Wilkin; GrainKraft: R. McLean; LimaGrain: Jean-Bruno, F. Curtis; Ardent: G. Weaver; Syngenta: J. Moffatt

#### **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.

#### REFERENCES:

- Brevis, J.C., C.F. Morris, F. Manthey, and J. Dubcovsky. 2010. Effect of the grain protein content locus *Gpc-B1* on bread and pasta quality. *J Cereal Sci* 51:357-365.
- Klindworth, D.L., Z. Niu, S. Chao, T.L., Friesen, J.D. Faris, X. Cai, S.S. Xu. 2012. Introgression and Characterization of a Goatgrass Gene for a High Level of Resistance to Ug99 Stem Rust in Tetraploid Wheat. In: *Genes, Genomes, Genetics* 2:665-673.
- Oury, FX., H. Chiron, A. Faye, O. Gardet, A. Giraud, E. Heumez, B. Rolland, M. Rousset, M. Trottet, G. Charmet, G. Branlard. 2010. The prediction of bread wheat quality: joint use of phenotypic information brought by technological tests and the genetic information brought by HMW and LMW glutenin subunits. *Euphytica* 171(1):87-109
- Payne, P.I., E.A. Jackson, L.M. Holt, C.N. Law. 1984. Wheat storage proteins: their genetics and their potential for manipulation by plant breeding. *Phil Trans R Soc Lond Ser B* 304:359-371
- Payne, P.I., M.A. Nightingale, A.F. Kattiger. 1987. The relationship between HWM glutenin subunit composition and the bread-making quality of British grown wheat varieties. *J Sci Food Agric* 40:51-65
- 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
- Varshney et al., 2006. *Trends in Biotechnology* (24) 11: 490-499.

# **IDAHO WHEAT COMMISSION - BUDGET FORM**

|              |                        |                |    |         |
|--------------|------------------------|----------------|----|---------|
| Allocated by | Idaho Wheat Commission | during FY 2015 | \$ | 166,254 |
| Allocated by | Idaho Wheat Commission | during FY 2016 | \$ | 117,307 |

## **REQUESTED FY 2016 SUPPORT:**

|                        | Salary*   | Temporary Help** | Fringe*** | Travel**** | OE*****   | Graduate Tuition/Fees | TOTALS     |
|------------------------|-----------|------------------|-----------|------------|-----------|-----------------------|------------|
| Idaho Wheat Commission | \$ 10,752 | \$ 60,279        | \$ 27,027 | \$ 15,000  | \$ 40,000 | \$ -                  | \$ 153,058 |

## **OTHER RESOURCES (not considered cost sharing or match):**

|                                          |           |                |
|------------------------------------------|-----------|----------------|
| a) Industry (BASF)                       | \$        | 10,000         |
| b) UI (salaries, operating, July - June) | \$        | 138,000        |
| <b>TOTAL OTHER RESOURCES</b>             | <b>\$</b> | <b>148,000</b> |

|                                            |                    |                   |           |                |
|--------------------------------------------|--------------------|-------------------|-----------|----------------|
| <b>TOTAL PROJECT ESTIMATE FOR FY 2017:</b> | <b>\$ 153,058</b>  | <b>\$ 148,000</b> | <b>\$</b> | <b>301,058</b> |
|                                            | <i>(Requested)</i> | <i>(Other)</i>    |           | <i>(Total)</i> |

## **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 | \$ -        | \$ -        | \$ -        | \$ -        |
| <b>TOTALS</b>                 | <b>\$ -</b> | <b>\$ -</b> | <b>\$ -</b> | <b>\$ -</b> |
| <b>Total Sub-budgets</b>      |             |             |             | <b>\$ -</b> |

\* 25% of salary for a post doc continuing the second year appointment.

\*\* Wage for four full time IH working for 6 to 8 months, two IH working for two months, and one college student working for four months in summer

\*\*\* Benefit for TH and student based on suggested rates.

\*\*\*\*Attend PNW QC and growers conferences and travel to field nurseries.

\*\*\*\*\*Budget for land charges, maintainance and rental of transportation vehicles, rental of greenhouse, purchase field supplies, and produce 200 DH lines.

## ANNUAL REPORT

**PROJECT NO:** BJKV32

**TITLE:** Developing Wheat Cultivars for Idaho and World Markets

**PERSONNEL:** J. Chen, J. Wheeler, N. Klassen, W. Zhao, B. Bowman, S. Nayak, J. Wu

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

### ACCOMPLISHMENT:

After licensed UI Stone and UI Platinum our pipeline for potential releases showed promising outcomes. We are in the process of releasing hard white winter line IDO1101 and soft white winter line IDO1108DH. Foundation seed of the two lines were planted in Aberdeen in the fall of 2015. We also planted breeder seed for a new short hard white winter line IDO1506 this fall and will plant breeder seed for additional two short hard white spring lines (IDO1602 and IDO1604) in the spring of 2016. In addition, we harvested breeder seed for hard white winter line IDO1209DH, two soft white winter lines IDO1004 and IDO1005, two hard white spring lines IDO1202S and IDO1203S-A, and one hard red spring wheat line IDO862E. These lines are pending to release upon additional testing and when a licensed partner identified.

**Breeding using wheat x maize system.** Wheat by maize doubled haploid system has been used in the program and generated six breeding and mapping populations since 2008. Following by IDO1108DH, we selected two hard red winter DH lines IDO1607DH and IDO1609DH derived from the cross IDO835 x Moreland. The two lines are being evaluated on the second year in the Western Regional trials and in the seed increase in the breeding program. One hard white winter DH population derived from UI Silver x Shaan89150 (135 lines) and the other hard white spring DH population derived from UI Platinum x SY Capstone (122 lines) showed very good agronomic performance in 2015. These DH lines are being evaluated for bread baking quality in Idaho Wheat Lab in Aberdeen, ID. The two DH populations will result in not only elite lines but also molecular markers that can be used to select excellent bread baking quality of UI Silver and UI Platinum. Molecular markers associated with resistance genes to dwarf bunt and stripe rust will also be identified in the three DH populations in 2016. Furthermore, we are in the production of two additional DH populations from UI Platinum x LCS Star and UI Platinum from LCS Atomo to accelerate low Cadmium (Cd) wheat development and molecular markers associated with Cd content.

**Breeding using molecular marker assisted selection.** Using molecular marker assisted selection we pyramided three disease resistance genes *FHB1*, *H25*, and *Yr36* and advanced 640 lines in 2014. The 640 lines were evaluated in yield trials in two locations this year. These lines were also evaluated for stripe rust resistance in a field nursery in Pullman, WA, for Hessian Fly

are selected based on uniformity and disease resistance if occurs. The selected B1 headrows are individually harvested and tested for protein and test weight and some of headrows with low test weight will be discarded. The final selected headrows are planted in yield plots in the second year breeder seed production (B2), simultaneously, a tea-spoon grain of each B2 plots are tested in disease nurseries (stripe rust, dwarf bunt, FHB). The B2 plots are selected based on uniformity and disease resistance and composited to form final breeder seed for foundation seed production in the following year.

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**DURATION:** Third of five years (2013-2018)

#### **COOPERATION:**

University of Idaho: J. Marshall, K. O'Brien, D. Fu, Y. Wang, C. Schroeder, N. Bosque-Perez, D. Strawn, J. Kuhl.

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#### **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.

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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.

#### REFERENCES:

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