

# Minnesota Wheat Research and Promotion Council

## RESEARCH PROPOSAL GRANT APPLICATION

<b>1. NAME AND ADDRESS OF ORGANIZATION TO WHICH AWARD SHOULD BE MADE</b>  <b>Name:</b> Regents of the University of Minnesota <b>Address:</b> Sponsored Projects Administration 450 McNamara Alumni Center, 200 Oak Street SE Minneapolis, MN 55455-2070		
<b>2. TITLE OF PROPOSAL</b> Exploiting Genetic Variation for Wheat Improvement in the Northern Great Plains		
<b>3. PRINCIPAL INVESTIGATOR(S)</b>  Brian Steffenson  PI# 2 Name: Gary Muehlbauer  PI# 3 Name: James Anderson	<b>4. PI #1 BUSINESS ADDRESS</b>  Department of Plant Pathology 495 Borlaug Hall 1991 Upper Buford Circle St. Paul, MN 55108	
<b>5. PROPOSED PROJECT DATES (calendar years)</b>  January 1, 2017 to December 31, 2017 Note: Research Reports are Due November 15th of Each Year	<b>6. TOTAL PROJECT COST</b>  \$44,107	<b>7. PI #1 PHONE NO.</b>  612-625-4735
<b>8. RESEARCH OBJECTIVES:</b> (List objectives to be accomplished by research grant)  Plant breeding and crop improvement are predicated on identifying and utilizing genetic variation. Our overall project goal is to improve regional wheat cultivars with unique alleles captured from diverse accessions of the primary <i>Triticum</i> gene pool, which includes landraces, breeding lines, and named varieties. This will be done through the development and characterization of the Minnesota Nested Association Mapping Population (MNAMP), which is ideally suited for identifying and characterizing these unique alleles and at the same time creating adapted lines with the desired alleles for immediate utilization in breeding programs. This research has a long-term horizon of about seven years, but the future payoff for growers in terms of enhanced wheat traits could be substantial. The MNAMP we developed for this project over the past four years with support from the Minnesota Wheat Research and Promotion Council shows great variation for many agronomic, quality, and disease reaction traits. However, we have only just begun to fully evaluate this valuable genetic resource for its potential in wheat improvement. Using molecular markers generated by genotype by sequencing (GBS), we will obtain valuable data on the number, chromosome location and effect of both qualitative genes and quantitative trait loci (QTL) controlling important wheat traits. Our objectives for year 5 of this five-year phase I project are as follows: 1) obtain a second year of field data on the MNAMP for select agronomic, quality and disease resistance traits; 2) characterize the number, chromosome location and effect of both qualitative genes and QTL controlling selected wheat traits; and 3) complete a final progress report for phase I of this project.  Attach a 2-page detailed discussion of importance of the proposal to wheat profitability; how study complements previous research in area; procedures to be used; and competency of the research group in achieving research objectives. (Please keep the proposal concise, only 2 pages will be provided reviewers).		
<b>Signature Of Principal Investigator</b>  	<b>Date</b>  January 6, 2017	<b>Phone Number</b>  612-625-4735
<b>Signature Of Authorized Representative</b>  	<b>Title Principal Grants &amp; Contracts Administrator</b>	<b>Date</b> 01/09/2017
<b>Address Of Authorized Representative</b>  Andrea Marshall, Principal Grants & Contracts Administrator, Office of Sponsored Projects Administration, 450 McNamara Alumni Center, 200 Oak Street SE, Minneapolis, MN 55455-2070		<b>Phone Number</b>  612-624-5599

# Minnesota Wheat Research and Promotion Council

## RESEARCH PROJECT PROPOSAL

### (2-pages maximum)

#### **Project Title:**

Exploiting Genetic Variation for Wheat Improvement in the Northern Great Plains

#### **Importance of this project to the profitability of wheat producers:**

Crop improvement is predicated on exploiting genetic variation. Without this variation, breeders cannot advance germplasm for any of the important traits of interest to growers. A recent example is with the African stem rust (*Puccinia graminis* f. sp. *tritici*) isolate Ug99. Soon after this highly virulent isolate was first discovered, research revealed that all widely grown wheat cultivars in the region were highly susceptible. To identify effective resistance to this pathogen, an extensive search had to be made across a wide genepool of wheat accessions, and ultimately non-adapted parental sources had to be used in breeding. The germplasm enhancement project described here is very broad in its scope and will provide a rich source of allelic diversity for many traits in a genetic background that can be readily utilized in breeding programs. These traits include, but are not limited to: yield, protein content, milling and baking quality, root growth, stand establishment, nitrogen use efficiency, water use efficiency, and disease and insect resistance. The Minnesota Nested Association Mapping Population (MNAMP) we developed for this project (2,240 lines in total) shows great variation for the agronomic traits of heading date, plant height, spike length, number of kernels/spike, and lodging; quality traits of flour weight, extraction weight, protein content, and water absorption; and disease reactions to stem rust, leaf rust, stripe rust and bacterial leaf streak. Significantly, we identified desirable transgressive segregants (i.e. progeny lines exhibiting extreme phenotypes that exceed those of the parents) for most of these traits. Use of select, agronomically advanced transgressive segregants will allow breeders to enhance a particular trait in their program more efficiently--whether higher protein content or disease resistance. Cultivars bred with one or more of these enhanced traits will increase profitability for wheat producers in the region.

#### **Procedures:**

*Summary of population development activities.* Over the past four years, we have been developing a diverse population (the MNAMP) to enhance important traits in regional wheat breeding programs. The source germplasm for the MNAMP parents was the ~4,500 accession Spring Wheat Core Collection held by the USDA-ARS National Small Grains Collection. Based on genetic diversity as assayed by single nucleotide polymorphism (SNP) markers, desirable phenotypes in field nurseries and diversity for geographic origin, we narrowed this collection down to a workable number of 25 accessions for crossing to the Minnesota cultivar RB07. The final number of lines in the MNAMP, now at the BC<sub>1</sub>F<sub>6</sub> generation, is 2,240. In the fall greenhouse 2016, BC<sub>1</sub>F<sub>6</sub> seed was planted for increase. The derived BC<sub>1</sub>F<sub>7</sub> generation seed will be planted and evaluated for various agronomic and disease reaction traits in the field in 2017. For the field trials, the MNAMP will be planted at the Northwest Research and Outreach Center in Crookston and possibly at the University of Minnesota St. Paul campus if sufficient seed is available. During the course of the season, data will be collected on the following agronomic traits: days to heading, plant height, spike length, and number of kernels per spike. Natural infections of several important wheat diseases occur often in these nurseries. Thus, we will score the reaction of all lines to prevalent diseases. In August, we will hand harvest the MNAMP using a sickle and then thresh the grain with a threshing machine. After additional seed cleaning, we will assess the population for test weight, 1000-kernel weight, etc. In 2018, we hope to identify specific families of the MNAMP for assessing milling quality with Senay Simsek at North Dakota State University.

To elucidate the number, chromosome location and effect of genes/QTL controlling target traits of interest, we will subject the MNAMP to genotype by sequencing (GBS). This assay will generate sufficient numbers of molecular markers (>35,000) to construct a saturated map and perform these genetic mapping analyses. The genotyping work will be performed by the USDA-ARS Regional Genotyping Laboratory in Raleigh, NC under the direction of Gina Brown-Guedira. We have already collected tissue from BC<sub>1</sub>F<sub>6</sub> plants and sent them to North Carolina.

#### *Timetable of activities*

##### **2017 Winter Greenhouse:**

- Analyze genotype by sequencing data for the MNAMP.
- Plant families (and parents) of the MNAMP segregating for various rust resistance traits and obtain phenotype data from the greenhouse.

##### **2017 Spring-Summer Field:**

- Plant MNAMP (and parents) at Crookston and obtain year 2 phenotype data from the field.
- Collate all data collected on the MNAMP parents by our cooperators and by us.

**2017 Fall-2018 Winter Greenhouse and Laboratory:**

- Analyze data.
- Identify and distribute advanced lines with enhanced traits to regional breeders for crossing in their programs.
- Write up manuscript for publication.
- Continue evaluations of derived materials until variety candidates are identified.

**Regional linkage to other research activities:**

Our project will create strong linkages with many other research programs in the region because it developed a unique population with a high level of genetic diversity from the primary gene pool of wheat. A number of wheat scientists in the region (Walid Sadok, Ruth Dill-Macky and Madeleine Smith at the University of Minnesota; Andrew Green, Francois Marais, Shaobin Zhong & Senay Simsek at North Dakota State University and Karl Glover and Shaukat Ali at South Dakota State University) have agreed to participate in this project by phenotyping the MNAMP for traits of their interest. We will also make the germplasm available to other interested researchers. All of the data generated from this study will be deposited in the publicly available T3 website maintained by the USDA-ARS. Additionally, all lines from the MNAMP will be deposited in the USDA-ARS National Small Grains Collection for long-term storage.

**List current or potential other funding sources for this project:**

For this research project, the PI (Steffenson) secured a grant of \$100,000 from USAID to support M.S. student Fazal Manan from Pakistan. Steffenson will provide up to \$6,000 additional in-kind personnel support and supplies in 2017.

**Research Group:**

This research project is the M.S. thesis of my graduate student Fazal Manan, who will graduate in August 2017. Other members of the Steffenson project (graduate students, technicians and a post-doctoral research associate) will assist Fazal in various aspects of this research, especially the harvest and threshing of 2,240 lines from the field as was done in 2016. Co-PIs Jim Anderson and Gary Muehlbauer advise us on the breeding and molecular mapping aspects of the research, respectively.

**Relationship to past projects:**

This is the fifth year of a five-year phase I project to develop and characterize the MNAMP for use in regional wheat breeding programs. Year 1 involved genotype analysis and phenotyping of a large wheat collection as a basis for selecting diverse cultivars/landraces for population development; Year 2 involved the crossing and backcrossing of the final 25 diverse cultivar/landrace selections to Minnesota cultivar RB07; Year 3 involved the selfing of ~2,500 MNAMP progeny for several generations to achieve greater homozygosity; and Year 4 involved the first phenotyping experiment of the MNAMP in the field at Crookston.

**Estimate the budget requirements:**

The total budget requested is \$44,107. The breakdown for this budget is as follows: 35% time for research specialist 2 (\$15,426 base and \$4,103 fringe), 5% time for post-doctoral research associate (\$2,626 base and \$857 fringe) and 800 total hours for two prebaccalaureate students (\$11.00 x 800 hours = \$8,800). Travel costs of \$2,820 (\$708 vehicle rental; \$1,232 for per diem with 4 people x 4 trips x 2 days; and \$880 hotel) will be needed to make four separate trips to Crookston for planting, trait assessment and harvest. Service charges for greenhouse rental needed for the population grow-out will be \$5,474 (\$0.0274 sq/ft/day x 270 days x 740 sq/ft) and for the 2-acre field plots \$1,500 (\$750/acre). For general operating supplies (envelopes, stakes, bags, labels, etc.), the costs will be \$2,500. Grand total for 2017 is \$44,107.

**References:**

McMullen, MD, et al. (2009). Genetic Properties of the Maize Nested Association Mapping Population. *Science* 325:737–740.

Bajgain, P. 2014. Using next-gen sequencing in genetic mapping of stem rust resistance genes in hard red spring wheat populations. Ph.D. diss. University of Minnesota, St. Paul.

# Minnesota Wheat Research and Promotion Council

## RESEARCH PROJECT PROPOSAL BUDGET

<b>PROJECT TITLE:</b>			
Exploiting Genetic Variation for Wheat Improvement in the Northern Great Plains			
<b>Principal Investigator(s) / Project Directors(s)</b>  Brian Steffenson	Funds Requested For		
	Year 1 (2017)	Year 2 (2018)	Year 3 (2019)
<b>A. Salaries and Wages</b>	\$	\$	\$
1. Co-principal Investigator(s)			
2. Senior Associates			
3. Research Associates - Post Doctorate	\$2,626		
4. Other Professionals	\$15,426		
5. Graduate Students			
6. Prebaccalaureate Students	\$8,800		
7. Secretarial - Clerical			
8. Technical, Shop and Other			
<b>B. Fringe Benefits</b>	\$4,961		
<b>C. Nonexpendable Equipment (Planting and harvesting equipment use)</b>			
<b>D. Materials and Supplies</b>	\$2,500		
<b>E. Travel</b>	\$2,820		
<b>F. Publication Costs</b>			
<b>G. Computer Costs</b>			
<b>H. All Other Direct Costs (Attach supporting data)</b> Greenhouse and field charges, see budget paragraph above	\$6,974		
<b>TOTAL AMOUNT OF THIS REQUEST (per year)</b>	<b>\$44,107</b>	<b>\$</b>	<b>\$</b>