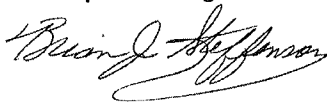



## Minnesota Wheat Research and Promotion Council

### RESEARCH PROPOSAL GRANT APPLICATION

<b>1. NAME AND ADDRESS OF ORGANIZATION TO WHICH AWARD SHOULD BE MADE</b>  Regents of the University of Minnesota Office of Sponsored Projects Administration 200 Oak Street SE, Suite 450 Minneapolis, MN 55455		
<b>2. TITLE OF PROPOSAL</b> <b>Exploiting Genetic Variation for Wheat Improvement in the Northern Great Plains</b>		
<b>3. PRINCIPAL INVESTIGATOR(S)</b> <b>Brian Steffenson</b>	<b>4. PI #1 BUSINESS ADDRESS</b>  Department of Plant Pathology 495 Borlaug Hall 1991 Upper Buford Circle St. Paul, MN 55108	
PI# 2 Name: <b>Gary Muehlbauer</b>		
PI# 3 Name: <b>James Anderson</b>		
<b>5. PROPOSED PROJECT DATES (calendar years)</b> <b>January 1, 2014 to December 31, 2014</b>  <small>Note: Research Reports are Due November 15th of Each Year</small>	<b>6. TOTAL PROJECT COST</b> <b>\$36,355</b>	<b>7. PI #1 PHONE NO.</b> <b>612-625-4735</b>
<b>8. RESEARCH OBJECTIVES: (List objectives to be accomplished by research grant)</b>  Plant breeding and crop improvement are predicated on identifying and utilizing genetic variation. Our overall project goal is to improve wheat with unique alleles captured from diverse accessions in the primary genepool. This will be done by developing nested association mapping populations, which are ideally suited for identifying and characterizing these unique alleles and at the same time creating adapted lines with the alleles for utilization in breeding program. This research has a long-term horizon of about five years, but the future payoff for growers in terms of enhanced wheat traits could be substantial. Our year 2 objectives are: 1) make backcrosses with the 30 different F <sub>1</sub> plants created in the first crossing block; 2) plant resulting BC <sub>1</sub> crossed seed of each hybrid combination in the field and record phenotype data; and 3) harvest BC <sub>1</sub> F <sub>1</sub> 's from the field and plant for increase in the 2014 fall greenhouse.  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> <b>November 18, 2013</b>	<b>Phone Number</b> <b>612-625-4735</b>
<b>Signature Of Authorized Representative</b>  	<b>Title</b> Kevin McKoskey Senior Associate Director	<b>Date</b> 11/18/13
<b>Address Of Authorized Representative</b>  Kevin McKoskey, Sr. Associate Director, 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 race Ug99. Soon after this highly virulent race was first discovered, research revealed that all widely grown wheat cultivars in the region were highly susceptible. To identify effective resistance genes to this pathogen, an extensive search had to be made across a wide gene pool of wheat accessions, and ultimately non-adapted parental sources had to be used in breeding. The germplasm enhancement project proposed 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. Cultivars bred with one or more of these enhanced traits will increase profitability for wheat producers in the region.

**Procedures:** This proposal covers the second year activities of a five-year research project. The first year's activities, which will be completed in late 2013, involved the analysis of 90,000 single nucleotide polymorphism (SNP) markers in nearly 2,200 accessions of the USDA Spring Wheat Core Collection. This collection exhibited an extraordinary level of diversity and was grouped into four subpopulations based on their degree of genotypic relatedness. Within each of the four subpopulations, we selected 98 to 106 accessions that captured the greatest diversity with respect to the SNP markers while also considering their geographic origin. In total, 409 highly diverse accessions (designated as the Spring Wheat Diversity Collection or SWDC) were selected for phenotypic evaluation at St. Paul and Crookston in 2013. Data were collected for the agronomic traits of heading date, height, awn length and lodging as well as for general disease reactions to stem rust, leaf rust, bacterial leaf streak, and Fusarium head blight. As expected, a wide range of phenotypic diversity was observed for many of the traits in the SWDC. In the final selection process, 30 wheat accessions from 24 countries were chosen based on: a) various phenotypic traits assessed in the field, b) genetic diversity as assayed by SNP markers, and c) geographic origin. These 30 accessions were designated as the Nested Association Mapping Parental Selects (NAMPS) and were sown in the fall greenhouse for crossing to Minnesota wheat cultivar RB07, selected as the recurrent parent because of its wide adaptation to the spring wheat growing areas in Minnesota, North Dakota, and South Dakota. The first of these 30 crosses will be completed by December. All objectives from the 2013 proposal will be completed according to schedule.

The next step in Nested Association Mapping (NAM) population development will be the backcrossing of the 30 different  $F_1$  plants to RB07. Since the NAMPS are mostly unadapted to Upper Midwest conditions, the backcross will serve to convert more of the genome in the derived lines to the genetic constitution of RB07. Simply stated, we will be assessing the effect of "alien" chromosomal fragments contributed by the NAMPS within the elite genetic background of the adapted Minnesota wheat cultivar RB07. After the backcrosses have been made, the  $BC_1F_1$ 's will be selfed for four generations to achieve greater homozygosity in the NAM populations and also increase seed amounts for subsequent phenotypic evaluations (yield, quality, and other agronomic traits) by researchers in the region. Our goal is to develop at least 100 lines from each of ~20 selected populations, resulting in a total of about 2,000 NAM lines that can be used in the search for novel allelic variation within the elite hard red spring genetic background of RB07. Since the developed NAM populations involve a backcross and four generations of selfing, they should be fairly well adapted to Upper Midwest conditions, and therefore lines with the desired phenotypes can be used directly as parents in the breeding program as part of this pre-breeding and allelic mining effort. Thus, for regional breeding projects, this wide-ranging research will develop advanced breeding lines with new or enhanced traits of economic importance to growers. Moreover, molecular markers closely linked to the causal gene(s) will be identified, thereby facilitating the efficient transfer of these traits in breeding.

NAM populations are also ideally suited for identifying and characterizing quantitative trait loci (QTL) (i.e. the continuously varying trait type most often faced in breeding) because they capture both historic (i.e. occurring throughout the life history of the NAMPS) and recent (i.e. occurring after crossing with RB07) recombination events. NAM populations are superior to other methods of QTL analysis (i.e. conventional biparental linkage mapping and association mapping) having low marker density requirements, high allele richness, high mapping resolution, and enhanced statistical power—all without the drawbacks of the other two methods. With advances in genotyping (e.g. the 90K SNP chip) and targeted sequencing of gene-rich genomic regions (e.g. exome capture technology), it will be possible to precisely map and eventually clone the genes controlling target traits in these NAM populations. To leverage existing intellectual, resource, and infrastructure

strengths, the proposed project will ultimately involve a large cohort of scientists (from breeders and geneticists to cereal scientists and pathologists) from the University of Minnesota, North Dakota State University, and South Dakota State University. Additionally, this project will leverage the substantial resources of the Triticeae Coordinated Agricultural Project (TCAP) as well as wide-ranging international efforts in wheat genetics and genomics.

Our objectives for year 2 of this five-year project for developing and evaluating diverse NAM populations are as follows:

1) make backcrosses with the 30 different  $F_1$  plants created in the first crossing block; 2) plant resulting  $BC_1$  crossed seed of each hybrid combination in the field and record phenotype data; and 3) harvest  $BC_1F_1$ 's from the field and plant for increase in the 2014 fall greenhouse.

Details of experimental plan. For year 2 of this project, we will cross the 30  $F_1$  plants developed in year 1 back to the recurrent parent cultivar RB07 in the 2014 winter greenhouse. About 100  $BC_1$  crossed seed from each cross combination will be planted in the field at Crookston and/or St. Paul where phenotype data for various agronomic traits (heading date, height, disease reactions, etc.) will be recorded.  $BC_1F_1$ 's will be harvested from the field and 100 arbitrarily selected seeds (for single seed descent) from each cross combination will be increased in the 2014 fall greenhouse (1st selfed generation), where a stem rust evaluation (a non-lethal assay) will be made. In year 3, additional selfing and seed increase generations will be made. Beginning in year 4, we will have sufficient seed stocks to share with members of the regional wheat improvement community who have an interest in evaluating the germplasm for traits of immediate priority to wheat producers. At the University of Minnesota, this will include evaluations for agronomic performance (yield, quality, and reaction to major diseases (the rusts, Fusarium head blight, bacterial leaf streak, etc.).

These datasets will allow us to identify novel variation for important traits and molecular markers linked to genes governing such traits. These marker-trait associations can be used to accelerate the development of new wheat cultivars with enhanced yield, quality and value-added characteristics. All data from the project will be deposited in a publically available database called The Triticeae Toolbox (T3), which is supported by TCAP. This will provide all interested researchers public access to data collected from the project. Germplasm developed during the course of the project will be distributed to all breeders and other interested researchers for investigating specific traits of their interest.

**Regional linkage to other research activities:** This project will create strong linkages with many other research projects in the region because it will develop unique populations with a high level of genetic diversity from the primary gene pool of wheat. A number of regional wheat scientists have expressed a strong interest in evaluating this germplasm.

**List current or potential other funding sources for this project:** Professor Steffenson holds the Lieberman-Okinow Endowed Chair whose primary mission is to identify, characterize, and utilize genes from unadapted germplasm (wild species and landraces) for the enhancement and improvement of wheat, barley, oat, and rye. He will dedicate a portion of his recurring endowment funds towards this project. Professor Muehlbauer, who studies the molecular genetics of cereal crop improvement, will contribute a portion of his endowment toward the project. Professor Anderson has some available funds from his breeding project to assist in the phenotyping of NAM populations.

**Research Group:** Wheat scientists in the region (Mohamed Mergoum, Francois Marais, Shaobin Zhong & Senay Simsek at North Dakota State University and Karl Glover & Shaukat Ali, South Dakota State University) have agreed to participate in this project by phenotyping germplasm.

**Relationship to past projects:** This is the second year of a five-year project to develop genetically diverse populations for use in regional wheat breeding programs. The first year involved genotype analysis and phenotyping of a large wheat collection as a basis for selecting the final set of 30 diverse landraces for NAM population development. The first crosses of these NAMPS to RB07 were made in November-December 2013.

**Estimate the budget requirements:** To complete the next phase of NAM population development in the greenhouse and field, funding is requested for a 60% time technician (base: \$23,462 + fringe: \$8,642@36.8%) and an undergraduate student (\$3,000 + \$216 fringe). Funding is also requested for greenhouse and field rental costs (\$750) and for general supplies (envelopes, stakes, etc.) (\$500). The total budget for the second year phase of this project is \$36,355.

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

# Minnesota Wheat Research and Promotion Council

## RESEARCH PROJECT PROPOSAL BUDGET

PROJECT TITLE <b>Exploiting Genetic Variation for Wheat Improvement in the Northern Great Plains</b>			
Principal Investigator(s) / Project Directors(s)	Funds Requested For		
<b>Brian Steffenson Gary Muehlbauer James Anderson</b>	Year 1 (2014)	Year 2 (2015)	Year 3 (2016)
A. Salaries and Wages		\$	\$
1. Co-principal Investigator(s)			
2. Senior Associates			
3. Research Associates - Post Doctorate			
4. Other Professionals (Tamas Szinyei)	\$23,462		
5. Graduate Students			
6. Prebaccalaureate Students	\$3,000		
7. Secretarial - Clerical			
8. Technical, Shop and Other			
B. Fringe Benefits	\$8,643		
C. Nonexpendable Equipment (Planting and harvesting equipment use)			
D. Materials and Supplies	\$500		
E. Travel			
F. Publication Costs			
G. Computer Costs			
H. All Other Direct Costs (Attach supporting data) greenhouse and field rental fees	\$750		
<b>TOTAL AMOUNT OF THIS REQUEST (per year)</b>	<b>\$36,355</b>	<b>\$</b>	<b>\$</b>