

# 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 454 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	<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: Gary Muehlbauer		
PI# 3 Name: James Anderson		
<b>5. PROPOSED PROJECT DATES (calendar years)</b> January 1, 2015 to December 31, 2015  Note: Research Reports are Due November 15th of Each Year	<b>6. TOTAL PROJECT COST</b> \$34,624	<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 by developing nested association mapping (NAM) populations, which are ideally suited for identifying and characterizing these unique alleles and at the same time creating adapted lines with the alleles for immediate utilization in breeding programs. 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 objectives for year 3 of this five-year project for developing and evaluating diverse NAM populations are as follows: 1) self ~2,500 BC <sub>1</sub> F <sub>2</sub> plants three successive times in the greenhouse to achieve greater homozygosity; and 2) increase the Nested Association Mapping Parental Selects (NAMPS) and distribute seed to cooperators for trait evaluation.  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 16, 2015	<b>Phone Number</b> 612-625-4735
<b>Signature Of Authorized Representative</b> 	<b>Title</b> Andrea Marshall Principal Grants and Contracts Admin. Sponsored Projects Administration	<b>Date</b> January 20, 2015
<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 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. Cultivars bred with one or more of these enhanced traits will increase profitability for wheat producers in the region.

**Procedures:** This proposal covers the third year of activities for a five-year research project. The first two years of activities involved the analysis of 90,000 single nucleotide polymorphism (SNP) markers in nearly 2,200 accessions of the USDA Spring Wheat Core Collection. Based on these data, 409 highly diverse accessions were selected for phenotypic evaluation at St. Paul and Crookston in 2013. As expected, these accessions showed a wide range of phenotypic diversity for traits such as heading date, height, disease reaction, etc. 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 2013 greenhouse and crossed to Minnesota wheat cultivar RB07, selected as the recurrent parent because of its wide adaptation to the spring wheat growing region. All but five of these crosses were successful; thus, we will be advancing a Nested Association Mapping (NAM) population based on 25 different parents all crossed to RB07. Crossed seed from these hybridizations were planted in the 2014 winter greenhouse and backcrossed to RB07. This backcross served to convert more of the genome of the derived progeny lines to the genetic constitution of RB07 since many of the NAMPS are not fully adapted to the Upper Midwest environment. About 100 BC<sub>1</sub>F<sub>1</sub> seed from each cross was planted in the 2014 fall greenhouse and harvested in December (producing BC<sub>1</sub>F<sub>2</sub> seed representing the 1st selfed generation). One arbitrarily selected BC<sub>1</sub>F<sub>2</sub> seed (for single seed descent) from each of ~2,500 BC<sub>1</sub>F<sub>1</sub> plants was sown in the 2015 winter greenhouse and will be harvested in March 2015 (producing BC<sub>1</sub>F<sub>3</sub> seed representing the 2nd selfed generation). BC<sub>1</sub>F<sub>3</sub> seed will be sown in the greenhouse in April and harvested in June (producing BC<sub>1</sub>F<sub>4</sub> seed representing the 3rd selfed generation). We will self the NAM population two more times in the 2015 fall and 2016 winter greenhouse seasons to ultimately produce the 5<sup>th</sup> selfed generation, which will have a high level of homozygosity. In 2015, seed of the NAMPS will be distributed to other wheat scientists in the region for various trait evaluations (i.e. yield, disease resistance, etc.). We will ultimately develop 100 Recombinant Inbred Lines (RILs) from each of the 25 NAM populations. The output from this process will be 2,500 RILs 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 population involves a backcross and five 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 breeding programs 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 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 genotype by sequencing) 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 this NAM population. 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 3 of this five-year project for developing and evaluating this diverse NAM population are as follows: 1) self ~2,500 BC<sub>1</sub>F<sub>1</sub> plants three successive times in the greenhouse to achieve greater homozygosity; and 2) increase NAMPS and distribute seed to cooperators for trait evaluation.

Details of experimental plan. In year 3 of this project, one arbitrarily selected BC<sub>1</sub>F<sub>2</sub> seed from each of 2,500 BC<sub>1</sub>F<sub>1</sub> plants was sown in the 2015 winter greenhouse and harvested in March 2015 (producing BC<sub>1</sub>F<sub>3</sub> seed representing the 2<sup>nd</sup> selfed generation). BC<sub>1</sub>F<sub>3</sub> seed will be sown in the greenhouse in April and harvested in June (producing BC<sub>1</sub>F<sub>4</sub> seed representing the 3<sup>rd</sup> selfed generation). We will self the NAM populations two more times in the 2015 fall and 2016 winter greenhouse seasons to produce the 5<sup>th</sup> selfed generation, which will have a high level of homozygosity. In spring 2015, seed of the NAMPS will be distributed to other wheat scientists in the region for various trait evaluations (e.g. yield, heading date, height, disease reactions, etc.). Beginning in year 4 (fiscal year 2016), we will have sufficient seed stocks of the NAM population 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.)).

The data generated from this research 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 USDA-NIFA funded 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 genepool of wheat. A number of regional wheat scientists have expressed a strong interest in utilizing this germplasm.

**List current or potential other funding sources for this project:** Professors Steffenson and Muehlbauer will dedicate a portion of their recurring endowment funds towards this project. Professor Anderson has some available funds from his breeding project to assist in the phenotyping of NAM populations.

**Research Group:** A number of prominent wheat scientists in the region (Ruth Dill-Macky and Madeleine Smith at the University of Minnesota; Mohamed Mergoum, Francois Marais, Shaobin Zhong & Senay Simsek at North Dakota State University and Karl Glover, Shaukat Ali, and Bill Berzonsky at South Dakota State University) have agreed to participate in this project by phenotyping germplasm.

**Relationship to past projects:** This is the third 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 second year involved the crossing and backcrossing of the 30 diverse landraces to RB07, the widely adapted Minnesota cultivar. The third year activities described here involve the selfing of ~2,500 NAM progeny for several generations to achieve greater homozygosity and the phenotyping of the NAMPS for disease resistance.

**Estimate the budget requirements:** The total budget requested is \$34,624, which includes a 50% time technician (\$30,374 base and fringe), prebaccalaureate student (\$3,000), greenhouse supplies (\$500) and rental fees (\$750).

**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

<b>PROJECT TITLE:</b>			
<b>Exploiting Genetic Variation for Wheat Improvement in the Northern Great Plains</b>			
<b>Principal Investigator(s) / Project Directors(s)</b> <b>Brian Steffenson, Lead PI</b> <b>Gary Muehlbauer</b> <b>James Anderson</b>	<u>Funds Requested For</u>		
	Year 1 (2015)	Year 2 (2016)	Year 3 (2017)
<b>A. Salaries and Wages</b>	\$	\$	\$
1. Co-principal Investigator(s)			
2. Senior Associates			
3. Research Associates - Post Doctorate			
4. Other Professionals	24,049		
5. Graduate Students			
6. Prebaccalaureate Students	3,000		
7. Secretarial - Clerical			
8. Technical, Shop and Other			
<b>B. Fringe Benefits</b>	6,325		
<b>C. Nonexpendable Equipment (Planting and harvesting equipment use)</b>			
<b>D. Materials and Supplies</b>	1,250		
<b>E. Travel</b>			
<b>F. Publication Costs</b>			
<b>G. Computer Costs</b>			
<b>H. All Other Direct Costs (Attach supporting data)</b>			
<b>TOTAL AMOUNT OF THIS REQUEST (per year)</b>	<b>\$ 34,624</b>	<b>\$</b>	<b>\$</b>