

Minnesota Wheat Research and Promotion Council
RESEARCH PROJECT PROGRESS REPORT
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Exploiting Genetic Variation for Wheat Improvement in the Northern Great Plains

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Introduction: 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. The germplasm enhancement project initiated in 2013 is a long-term and broad-based program that will provide a rich source of genetic diversity for many traits that are or may become important to wheat growers in the region. This includes, but is 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: First, we will assemble a germplasm collection that captures as much genetic variation as possible in the primary (i.e. unadapted wheats and landraces) genepool of wheat and then develop populations to exploit this variation. The collections and populations will be evaluated for traits of immediate priority to wheat producers and then genotyped with the latest genomics technology, if not already done. 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. This project will lead to the utilization of genetic variation useful to all wheat improvement programs in the region. 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 objective for year 1 is as follows:

Objective 1. Assemble, increase, and characterize genetic and phenotypic variation in a diverse collection of wheat germplasm. Nearly 2,200 accessions of the Spring Wheat Core Collection were genotyped with over 90,000 single nucleotide polymorphic (SNP) markers by the TCAP and analyzed for their genetic relatedness using Principal Coordinate Analysis (PCA) (Figure 1). The

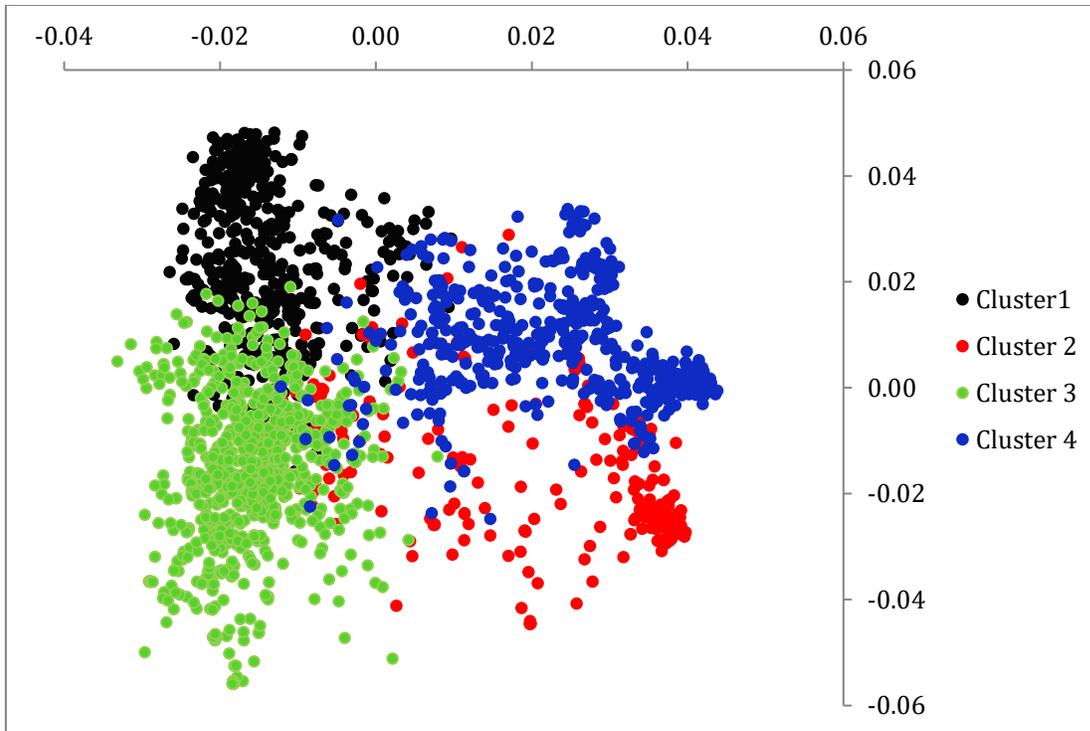


Figure 1. Principal coordinate analysis of 2,195 accessions from the Spring Wheat Core Collection (SWCC) based on 90,000 SNP markers (Data courtesy of Shiaoman Chao, USDA-ARS).

Spring Wheat Core Collection showed an extraordinary level of diversity and was grouped into four subpopulations (represented by the four different colors) based on their degree of relatedness. We then selected 409 accessions that represent the greatest genetic and geographic diversity in the Spring Wheat Core Collection (Figure 2). These 409 accessions were designated as the “Spring Wheat Diversity Collection” (SWDC) and evaluated in the field for various traits.

The SWDC was planted at St. Paul (May 9th) and Crookston (May 15th) in 2013. Also included in the nursery as checks were the Minnesota wheat varieties Linkert, Norden, Rollag, Sabin, Marshall and RB07. Data were collected on the SWDC and checks for the agronomic traits of heading date, height, awn length and lodging as well as 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 (e.g. heading date and height given in Table 1, Figure 3). Wheat breeder James Anderson selected 16 accessions from the St. Paul nursery exhibiting superior phenotypes, i.e. normal heading date, short-statured, good straw strength, disease resistance, etc.

Phenotype data collected on the SWDC from the field were collated and analyzed. Twelve of the 16 accessions selected by Dr. Anderson, plus 18

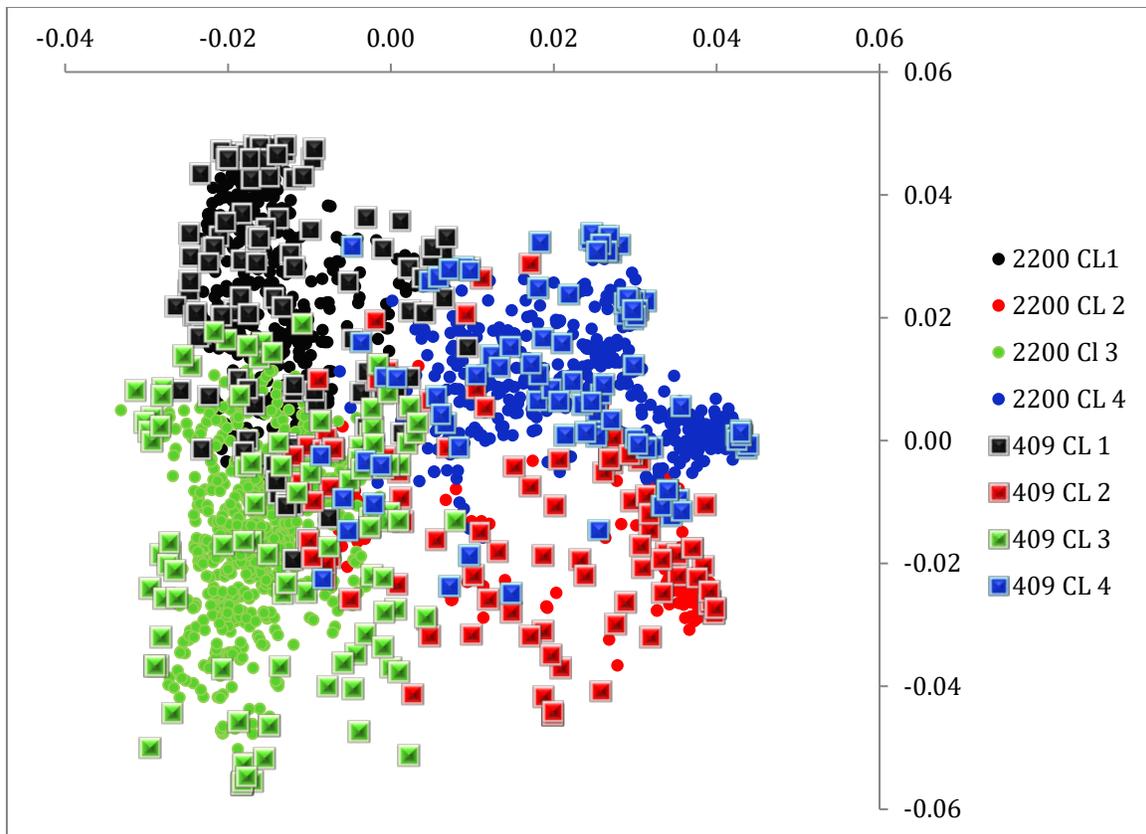


Figure 2. Accessions of the Spring Wheat Diversity Collection (SWDC) (411 in total depicted as raised square “buttons”) selected from the four subpopulations of the Spring Wheat Core Collection based on genetic diversity as assayed by 90,000 SNP markers and also geographic origin.

additional ones selected based on a) genetic diversity as assayed by SNP markers, b) phenotype data collected from the field, and c) geographic origin comprised the final set of select germplasm for development of nested association mapping populations (Figure 4). These 30 Nested Association Mapping Parental Selects (NAMPS) were sown in the fall greenhouse for crossing with cultivar RB07, selected by Dr. Anderson as the recurrent parent. The first crosses will be completed in December. F₁ seed derived from the initial cross will be backcrossed to RB07 in the spring greenhouse for the second step in NAM population development. All proposed objectives were completed according to schedule.

Table 1. Range and mean data for heading date of the Spring Wheat Diversity Collection (SWDC) planted in St. Paul and Crookston in 2013.

Checks	Days to heading	
	St. Paul	Crookston
Linkert	51	52
Marshall	55	54
Norden	51	52
RB07	50	49
Sabin	55	55
Rollag	51	53
SWDC MEAN (range)	55 (44-69)	53 (42-63)



Figure 3. Diversity of phenotypes observed in accessions of the Spring Wheat Diversity Collection (SWDC) planted in Crookston in 2013.

