PROGRESS REPORT

PROJECT NO: BJKW69, BJKW70

TITLE: Genomics-Accelerated Breeding for Abiotic Stress Resistance in Wheat

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The ultimate goal of this research project is to deploy current genomics tools to efficiently identify and characterize drought stress tolerance and lay the groundwork for development and release of winter and spring wheat cultivars with improved drought stress tolerance to security grain production under drought conditions. Specific objectives are: 1) Identify drought-related traits, QTL and markers that significantly associated with grain yield under drought conditions in adapted cultivars, breeding lines, and mapping populations; 2) Create novel germplasm and develop new drought tolerant varieties using chemical mutagenesis.

ACCOMPLISHMENTS:

In order to identify drought-related traits, we established a drought screening nursery with drip irrigation system in Aberdeen and evaluated 30 spring wheat cultivars from PNW breeding programs for grain yield, heading date (HD), height (HT), and three physiological traits flag leaf senescence (FLS), canopy temperature (CT), chlorophyll content (CPC), and carbon isotope discrimination (CID) in two years of 2009 and 2010. Five of the 30 lines showed good tolerant to water stress, which have lower yield loss; late senescent flag leaf, higher CID value, and lower canopy temperature.

One RIL mapping population derived from RioBlanco x IDO444 (RB444) was evaluated for GY, HT, HD, test weight (TW), and kernel weight (KW) in six location-years from 2006 to 2010; for FLS, CT, CPC, and CID in three field trials of two years (2009 and 2010). A total of 40 QTLs with R^2 ranging from 6% to 42% were identified and located on 13 chromosomes (1A, 1B, 2B, 2D, 3A, 3B, 4A, 4B, 5A, 5B, 6A, 6B, 6D, 7A, and 7D). QTLs on 1B, 2B, 4B and 7D have pleiotrophic effect that simultaneously affect grain yield and the other related traits. Our results demonstrated that the simultaneously selection on multiple genomic regions that affecting GY and GY-related traits could significantly improve grain yield of wheat. Two manuscripts derived from the mapping project are in processing of submission for publication.

Two mapping populations, RB444 and a spring wheat DH population derived from ND495 x TA6150-60 (NT60) were used to map thirteen candidate genes (CGs) that showed important role in drought tolerance in other plant species. The 13 CGs were mapped in ten chromosomal regions in NT60 population and 3 CGs were mapped in RB444 population. One manuscript derived from this study is in processing of re-submission for publication.

Out of 3000 Alturas mutant lines, we selected some mutants with contrast traits of root biomass, peduncle length, kernel weight, number of tillers, plant height, protein content, grain hardness, and amylose content. These lines will be further evaluated under both GH and field conditions in 2011.

In collaboration with other 25 scientists, we obtained a new grant (T-CAP) from USDA-NIFA to evaluate WUE and NUE in NSGC materials from 2011 to 2015. We have completed a seed increase and evaluated height and heading date for over 5000 spring wheat and barley materials this summer and have planted over 2000 winter wheat and barley lines for seeds increase in fall 2010. A total of 1800 wheat and 1200 barley lines will be selected for WUE and NUE evaluation in 2011 - 2015.

PROJECTIONS:

Identification and genetic mapping of genes controlling WUE and NUE can lead to the deployment of improved wheat varieties to help maintain the viability of Idaho and PNW wheat on the global market. Genetic improvement of WUE and NUE would be aided by the identification of markers associated with genes responsible for physiological characteristics and biochemical processes under drought and low nitrogen stresses. Identification of new tolerant genes and sources would accelerate the breeding of tolerant varieties that increase grain yield significantly in stressed environments. In 2011 we are going to evaluate WUE for RB444 population under drip irrigation; evaluate WUE for chemical mutagenesized lines derived from Alturas (M3), Moreland (M2), and IDO621 (M2) in Aberdeen under terminate water stress; evaluate WUE and NUE for 600 spring NSGC materials under drip irrigation. Most of work proposed here will be supported by T-CAP in coming five years.

PUBLICATIONS:

Manuscripts in preparation:

Hu, G., **J.Chen**, Ch. Chu, and Y. Wu. 2009. Genetic mapping of drought tolerance candidate genes in wheat (T. *aestivum*).

Zhang, J., **J. Chen**, P. Li, W. Zhao, Ch. Chu, E. Souza, and R. Zemetra. Quantitative trait loci for grain yield, plant height, heading date, kernel and test weight of bread wheat (*Triticum aestivum* L.) identified in six diverse environments.

Li, P., P. Wu, **J. Chen**, J. Zhang, Ch. Chu, D. See, and G. Brown-Guedira. Mapping of quantitative trait loci for coleoptile and root growth in a winter wheat germplasm IDO444 (*Triticum aestivum* L.).