

MEPS Student Travel Awards, Fall 2007

II. Abstracts of Presentations

Quantitative Trait Loci Mapping Heat Tolerance during Reproductive Development in Wheat (*Triticum aestivum*).

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High temperature stress during reproductive development is a major problem to wheat production and end-use quality in the Southern Great Plains and to wheat production in many environments worldwide. We have initiated a project to integrate genotypic (QTL), phenotypic, and transcript level data to identify genes controlling reproductive stage heat tolerance in heat tolerant genotypes of wheat as it relates to yield and end-use quality maintenance. Efforts have initially focused on building recombinant inbred lines (RILs), mapping of QTL linked to reproductive stage heat tolerance, and development of cDNA libraries enriched, through suppressive subtractive hybridization, for genes induced by the heat stress. RILs were derived from a cross between heat tolerant spring wheat cv Halberd, and a susceptible winter wheat cv Cutter or cv Karl92. These parents were used as models to define the two adaptive responses to heat stress (heat avoidance (susceptible) and heat tolerance). Major QTL controlling the maintenance of kernel weight, kernel number, grain filling duration, and seed abortion following a three-day heat treatment have been mapped, with some QTL being present in both susceptible backgrounds. The selected tissues for library construction included wheat heads and flag leaves isolated from plants subjected to heat stress at 10 days after pollination. Over 1920 unique ESTs have been sequenced. These genes include some potential regulatory proteins, heat shock proteins, lipid-transfer proteins as well as many novel genes that may belong to uncharacterized pathways involved in response to heat stress.

A *Saccharomyces cerevisiae* Type II Cation/H⁺ Antiporter- YNL321W

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Abstract

Cation/H⁺ antiporters (CAXs) are integral membrane proteins that transport Ca²⁺ and other cations out of the cytosol using the H⁺ gradient generated by primary transporters. Phylogenetic analysis of the CAX genes suggests there are three major types of CAXs: Type I (CAXs similar to *Arabidopsis thaliana* CAX1), Type II (CAXs with a long N-terminus hydrophilic region), and Type III (CAXs similar to *Escherichia coli* ChaA). Type II CAXs are present in fungi and some lower vertebrates but do not appear to be present in higher vertebrates, and plants. To date, no Type II CAX has been functionally characterized. A yeast putative transporter YNL321W belongs to the Type II CAXs and we have initiated characterization of this putative transporter. The YNL321W ORF was cloned, placed in yeast expression vectors, tagged with EGFP and HA. The *ynl321w* knock out yeast strain and various *ynl321w* double or triple yeast mutants were obtained. The YNL321W was localized on endoplasmic reticulum membrane and ionic analysis of *ynl321w* and other mutants suggested that *ynl321w* played a role in Ca²⁺ homeostasis. Additionally, *pmr1 ynl321w* mutants displayed an increased missorting of CpY over *pmr1* alone. Characterization of YNL321W should provide a platform to discern the function of Type II CAXs among various organisms.

Growth and Yield Responses of Southern US Rice (*Oryza sativa* L.) Cultivars to Supplemental Ultraviolet-B (UV-B) Radiation

A.R. Mohammed and L. Tarpley

Depletion of global stratospheric ozone could intensify ultraviolet-B radiation, which can alter rice crop productivity. The objective of these studies was to determine the effects of supplementary UV-B radiation on rice growth, development and physiology with special emphasis on screening for UV-B-tolerant rice cultivars. Eight popular southern U.S. rice cultivars were selected for the UV-B screening process. Plants received no natural UV-B radiation due to the UV-absorption characteristics of the greenhouse glass, hence UV-B was artificially supplied by supplemental UV-B lighting. Plants were grown in soil collected from research plots, and exposed to

UV-B radiation of 0, 8 (ambient) or 16 (high) $\text{kJ m}^{-2} \text{d}^{-1}$ for 90 days. Significant differences were observed among rice cultivars in sensitivity to increased UV-B radiation (16 kJ). For most of the cultivars, plants grown under a high UV-B treatment showed significant decreases in plant yield, photosynthesis, primary branches on the main-stem panicle, total number of grains and filled grain weight of the main-stem, compared to plants grown under UV-B-free environment. However, the magnitude of decrease in the above mentioned parameters varied among the cultivars. In our studies, the hybrids were less sensitive to high UV-B radiation (16 kJ) compared to conventional cultivars.

Abstract title: Screening of rice cultivars for grain Arsenic concentration and speciation

Tushara Raghvan, Wengui Yan, Hesham A. Agrama, William D. James, Terry J. Gentry, Richard H. Loeppert

Recently, there has been growing interest in the concentration and speciation of arsenic in rice (*Oryza sativa* L.) grain because of concerns with food quality and interest in minimizing any potential risk from dietary exposure. Our objective was to screen a range of rice varieties from the USDA world collection for tolerance to soil arsenic and determine their relative arsenic concentration and speciation in the rice grain. Based on known or suspected rice tolerance to arsenic in soil that is associated with the physiological disease called straighthead, thirty-seven indica and japonica cultivars were chosen and grown in a replicated trial at Stuttgart, AR using native soil and test plots amended with very high levels of As (i.e. MSMA). Total arsenic concentration of milled rice grain was determined by ICP-MS following digestion by $\text{HNO}_3/\text{H}_2\text{O}_2$. Arsenic species were determined by HPLC-ICP-MS following extraction with 1M TFA. In the MSMA-amended soil, the grain As concentration was 2-6 times higher compared to that in the native soil. A few cultivars had especially low levels of grain arsenic in the native soil as well as in the MSMA-amended soil. Cultivar tolerance to straighthead, as induced by high As in the soil, was not related to total grain arsenic content. The dominant species of grain arsenic were DMA and As (III), but these were found at varying levels in different cultivars. These results demonstrate the potential for selection of rice cultivars that yield lower grain arsenic concentrations and lower ratios of inorganic to organic arsenic.

AN ELECTRON MICROSCOPY STUDY OF THE SALT GLANDS IN *ZOYSIA MATRELLA*

SHEETAL RAO, E. ANN ELLIS* and MARLA BINZEL

Salt tolerant plants are characterized by the presence of functional salt glands on their leaves. Salt glands are modified trichomes through which these plants excrete excess salt. This research focuses on studying the mechanism of salt tolerance in *Zoysia matrella* (Manila grass), a warm-season, highly salt-tolerant, turf grass. Scanning electron microscopy (SEM) and transmission electron microscopy (TEM) studies of functional salt glands were done on plants grown in the greenhouse and watered with either deionized water (control) or high concentrations of sodium chloride (300 mM NaCl).

SEM was used to visualize salt glands on both the adaxial and abaxial leaf surfaces, located in rows parallel to stomata. In the leaves harvested from salinized (300mM NaCl) plants, salt crystals

were deposited next to the salt glands indicating active salt secretion from glands on the adaxial side. There were no salt crystals on leaves of control plants or on the abaxial side of salinized leaves. An opening near the tip of the salt gland is assumed to be the salt gland pore through which excess salt is excreted onto the leaf surface. Energy dispersive spectroscopy (EDS) analysis of the leaf surface confirmed the presence of sodium and chlorine around the secreting salt gland.

Title: Mapping of QTLs for heat tolerance of wheat (*Triticum aestivum*) in response to high temperature

Jung Hwa Do¹, Dirk B. Hays¹
Abstract

In cereals heat stress during seed formation is critical factor in lowering yield. This study was conducted to identify and map QTLs for heat tolerance in wheat in response to two heat treatments (short term- and long term-) during seed formation using recombinant inbred lines derived from a cross of '7C'(heat resistant) and 'SERIM 82'(heat susceptible). Yield components such kernel number, kernel weight, and grain filling duration were used as an indicator of heat susceptibility. The phenotypic variation of yield components were normally distributed, suggesting that the yield components have quantitative heritability over high temperature. Transgressive segregation compared to parents was also observed, suggesting that genetic variation from an optimal recombination of favorable loci from both occurred in the progeny population. 113 SSRs markers among 320 SSRs markers polymorphic between the two parents '7C ' and 'SERIM 82' with a linkage coverage of 2609cM and average interval map distance of 25 cM throughout the whole genome. QTLs for heat tolerance and their genetic effects were analyzed by association of % reduction of each phenotypic trait of yield components with polymorphism in the 62 RILs. 11 QTLs and 22QTLs for heat tolerance under short- term and long- term heat stress, respectively were detected from each of the phenotypic trait of yield component, showing phenotypic variation of 93 % and 86%, respectively.