Poster 4. Differential gene expression in wheat under long-term, post-anthesis heat stress using microarray and real-time PCR techniques.

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Long-term, post-anthesis, high temperature stress is one of the major limiting factors for wheat production globally, including the southern Great Plains areas in U.S. The objectives of the research were to study the differential gene expression in heat-tolerant and heat-sensitive wheat lines at long-term, high temperature stress. The plants were grown in optimum conditions in a growth chamber. In the expression study, the plants were exposed to stress after flowering by gradually increasing the temperature from 20/15°C to 36/30°C day/night in 4 days with 80% relative humidity and 16/8 hours daylight to simulate natural conditions. Leaf tissue was collected from both heat-treated and control plants at 4, 7, and 10 days. The microarray gene expression study was performed by using an Affymetrix gene chip array at only the 4- and 7-day sampling dates. A total of 337 and 228 genes were up-regulated at day 4 and day 7, respectively. In tolerant lines, 41 genes were up-regulated at both dates, whereas in the sensitive lines, 917 and 1,045 genes were up-regulated at day 4 and day 7, respectively, with a common expression of 236 genes. The putative functions of the ESTs were predicted by BLASTX. The differentially expressed genes were broadly classified according to their function. In the tolerant lines, protein synthesis-, transcription factor-, cell wall synthesis-, signaling-, photosynthesis-, and oxyreductase genes were expressed higher under stress conditions. On the other hand, genes related to cell wall degradation, senescence, metabolism, and stress had higher expression in the heat-sensitive lines. The differential expression of 14 selected transcripts was studied by real-time PCR of tolerant and sensitive lines and their parents under stress and optimum conditions. Results from real-time PCR confirmed their differential expression. The differential expression of those genes may be attributed to genotypic variations in response to heat stress.

Poster 5. Single nucleotide polymorphism markers for Fusarium head blight resistance in wheat.

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Fusarium head blight (FHB) is a devastating disease in humid and semihumid wheat-growing regions of the world. The quantitative trait locus (QTL) on 3BS (*Fhb1*) of Sumai 3 and Ning 7840 has been identified to have the largest effect on FHB resistance. Simple-sequence repeat (SSR) markers flanking the *Fhb1* are identified. These SSR markers have been widely used for marker-assisted screening of *Fhb1*. However, the SSR markers flank a relatively large chromosome region of the QTL and more closely linked markers to the QTL may improve selection efficiency. The rich sources of wheat expressed-sequence tags (ESTs) and the abundance of single nucleotide polymorphism (SNP) markers makes SNPs ideal markers for fine mapping. We developed SNP markers based on wheat ESTs that mapped to the 3BS QTL region. A total of 15 SNPs were identified between Ning 7840 and Clark (FHB-susceptible) based on sequence analysis of three different ESTs. SNP primers were designed and the single-base extension method was used to analyze the SNPs in 125 'Ning 7840/Clark' recombinant inbred lines. Three SNP markers mapped between *Xgwm533* and *Xgwm493*. Two of them, *Xsnp-21-1* and *Xsnp–20-1a*, have higher coefficient of determination (R^2) than *Xgwm533* and should be good markers for marker-assisted selection of the *Fhb1* QTL in breeding programs.