

Title: The integration of quantitative trait locus mapping and transcriptome studies reveals candidate genes for water stress response in St. Augustinegrass

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Interpretive Summary: St. Augustinegrass is one of the major warm-season grasses that can be found in various spaces where turfgrasses are like in consumers yards as well as golf courses and sports fields. An important aspect of a grass is how it can tolerate heat as well as experiencing lack of water or drought. In this study we were able to utilize greenhouses to water a variety of different types of St. Augustinegrass with different amounts of water to experience varying levels of drought conditions. Through this we were

able to measure different traits that indicate the way the different types handle the water stress like leaf wilting and how green a plant is. We were able to capture genetic information about the genes that were turned on at different times to identify a number of genes which may be responsible for giving these beneficial types their desirable traits. We can further study these genes in the future which can help us to develop drought tolerant St. Augustinegrass varieties.

Technical Abstract: Background: Drought resistance is an increasingly important trait for many plants—including St. Augustinegrass, a major warm-season turfgrass—as more municipalities impose restrictions on frequency and amount of irrigation. Breeding efforts have focused on breeding for drought resistance, and several drought-related quantitative trait loci (QTL) have been identified for St. Augustinegrass in previous studies. However, the molecular basis of this trait remains poorly understood, posing a significant roadblock to the genetic improvement of the species. Results: This study sought to validate those QTL regions in an independent biparental population developed from two sibling lines, XSA10098 and XSA10127. The drought evaluation in two greenhouse trials showed significant genotype variation for drought stress traits including leaf wilting, percent green cover, relative water content, percent recovery, and the area under the leaf wilting-, percent green cover-, and percent recovery- curves. A linkage map was constructed using 12,269 SNPs, representing the densest St. Augustinegrass linkage map to date. A multiple QTL mapping approach identified 24 QTL including overlapping regions on linkage groups 3, 4, 6, and 9 between this study and previous St. Augustinegrass drought resistance studies. At the transcriptome level, 1965 and 1005 differentially expressed genes were identified in the drought sensitive and tolerant genotypes, respectively. Gene Ontology and KEGG analysis found different mechanisms adopted by the two genotypes in response to drought stress. Integrating QTL and transcriptomics analyses revealed several candidate genes which are involved in processes including cell wall organization, photorespiration, zinc ion transport, regulation of reactive oxygen species, channel activity, and regulation in response to abiotic stress. Conclusions: By innovatively integrating QTL and transcriptomics, our study advances the understanding of the genetic control of water stress response in St. Augustinegrass, providing a foundation for targeted drought resistance breeding.