Daniel W. Dewey

Department of Soil & Crop Sciences

Nature of the Problem

Quality water is a limited natural resource in Texas, the United States and throughout the world. In Texas, the majority of high quality water comes from groundwater and is used for municipal, industrial, and irrigation purposes. Demand on already over-taxed aquifers will only increase as population increases. As population increases and housing developments replace farmland, water conservation in landscape irrigation will become increasingly important. Water conservation is being addressed through improving irrigation system efficiency and public education concerning water efficient landscape issues. However, understanding how drought tolerant and non-drought tolerant landscape plants respond to water stress and using that understanding to improve the drought tolerance of non-drought tolerant plants should be an integral component of landscape water conservation. Turfgrass provides a unique opportunity in genetic research because little has been done concerning turfgrass biotechnology.

Turfgrass biotechnology is far behind biotechnology in other grass relatives (corn, barley, wheat, rice, etc.) [4]. However, advances in these turfgrass relatives can be used to accelerate understanding in turfgrass biotechnology. For example, wheat, barley, corn, and rice are all members of the Poaecaea family and all have group 3 late embryogenesis abundant (LEA) proteins that are produced in response to drought stress. These proteins are controlled by genes (pMA2005 in wheat [1], HVA1 in barley [2], MGL3 in corn [6], and wsi18 in rice [5]). A group 3 LEA gene in barley (HVA1) has been successfully transformed into rice and wheat respectively resulting in increased drought tolerance of both the transgenic rice and wheat [3,7]. Turfgrass research, such as this project, is needed to incorporate knowledge from previous research to enhance drought tolerance of commonly used turfgrass species.

Research Objectives

This study will address differences in gene expression of two varieties of Zoysia japonica and two varieties of Zoysia matrella. A drought tolerant and drought susceptible cultivar within each species will be compared.

The objectives of the study are: (i) to identify gene(s) that are up-regulated and correlate with physiological responses under drought conditions, (ii) to identify gene(s) that are differentially expressed in time or between varieties or species in response to drought conditions, and (iii) to show improved drought tolerance of transgenic lines.

There is a physiological and a laboratory section of this study. In the physiological study, samples of all four varieties will be grown together in one pot so that all plants are exposed to the same soil environment. An irrigation treatment (well-watered control and water-stressed treatment) will be applied to three replications of the four varieties. The

treatment will continue until severe leaf rolling occurs (about twenty days) and then the entire experiment will be repeated. During the treatment, all varieties in all pots will have measurements of leaf water potential taken every 2 days (12 noon each day) and samples from each variety in every pot will be frozen in liquid nitrogen for subsequent laboratory analysis. Water release curves for stressed and non-stressed plants will be developed to determine osmotic adjustment, relative water content at zero turgor and other water relations characteristics to quantify plant response to stress.

In the laboratory, total RNA will be isolated and subtracted cDNA libraries made and cloned into vectors (768 clones/ variety) which will then be sequenced. Control and drought stressed samples for each day will be hybridized to macroarrays containing the sequenced clones from the subtracted cDNA libraries to show a timeline of gene expression that can be correlated with results from the physiological study. Differentially expressed genes will be sequenced and compared to known drought tolerant genes and transformed into tobacco to assess whether the genes affect drought tolerance of the transgenic tobacco.

We expect to identify genes that are up regulated and correlate with physiological responses under drought conditions and increase the drought tolerance of transgenic plants. We also expect to see differential expression in time or between varieties or species in response to drought conditions.

This research should provide insight into the possibilities in turfgrass biotechnology to manipulate genes from drought tolerant varieties and use those genes to increase the drought tolerance of less drought tolerant species. This research should also provide a stronger physiological basis for development of drought tolerant turfgrass varieties that need less water in urban landscapes.

References

Curry, J., C.F. Morris and M.K. Walker-Simmons. Plant Molecular Biology 16:1073-1076 (1991).

Hong, B., S.J. Uknes and T.D. Ho. Plant Molecular Biology 11:495-506 (1998).

Sivamani, E., A. Bahieldin, J.M. Wraith, T. Al-Niemi, W.E. Dyer, T.D. Ho and R. Qu. Plant Science 155:1-9 (2000).

Sticklen, M.B. and M.P. Kenna. 1998. Turfgrass biotechnology : cell and molecular genetic approaches to turfgrass improvement. Ann Arbor Press, Chelsea MI.

Takahashi, R., N. Joshee and Y. Kitagawa. Plant Molecular Biology 26:339-352 (1994).

White, C.N. and C.J. Riven. Plant Physiology 108:1337-1338 (1995).

Xu, D., X. Duan, B. Wang, B. Hong, T.D. Ho and R. Wu. Plant Physiology 110:249-257

(1996).

Intended Career Path Statement

I intend to teach and conduct research in a university setting. I am interested in teaching undergraduate and graduate level courses in water conservation, genetics and plant physiology. My research interests are in genetic control of drought tolerance in turfgrass. This field interests me because I feel there is a research void to fill and the results can be directly applied to conserve water in landscapes and potentially in the production of other grasses used for food and feed.