DROUGHT TOLERANCE TURFGRASS CULTIVARS FOR MICHIGAN

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The Michigan Agricultural Statistics Service (MASS) showed that over 1.9 million acres of turfgrass were maintained throughout the state during 2002-2003. Over 84% of this acreage was in the residential sector, while 96,000 acres were intensively managed by golf course superintendents. In addition, 1.8 million acres were used as forage grasses in the state of Michigan. The contribution of the turfgrass industry to Michigan's state economy exceeded $1.8 billion annually and created jobs for over 30,000 full-time employees. Furthermore, the turfgrass industry depends primarily on Michigan State University for research to determine the best grass cultivars and management practices for the State of Michigan. Our ultimate goal is to develop efficient drought tolerant cultivars by combining modern molecular and conventional breeding technology to transfer valuable traits from fescue in which new and improved drought tolerant cultivars will be released. The newly developed drought tolerant cultivars will ultimately save the turfgrass industry millions of dollars by reducing the irrigation rate, energy input, and more importantly conserving water resources, as it becomes exceedingly limited throughout the USA and the world. With regions experiencing increased drought conditions, along with cities and municipalities declaring water emergencies, the watering of landscapes will be severely restricted.

Festuca mairei St. Yves is a tetraploid (2n=4x=28, $M_1M_1M_2M_2$) species, commonly known as Atlas fescue. It shares the M_1M_2 genomes with *F. arundinacea* var. *atlantigena* ($G_1G_1G_2G_2M_1M_1M_2M_2$), which is only found near the Atlas Mountain ranges of northwest Africa. The M genome in *Festuca* is associated with a xeriphytic adaptation allowing the plant to survive long summers under drought stress (Marlatt et al., 1997). Very little is known about the involvement of the major morphological, physiological, and biochemical characteristics, and the genes associated with drought tolerance. This limited knowledge-base hinders and prevents successful breeding efforts. Identifying the corresponding genes to drought tolerance in *Festuca mairei* would facilitate breeding programs in developing drought tolerant cultivars.

Response of plants to drought stress is manifested by various changes in the physiological and metabolical processes. Physiological changes are reflected at the molecular level. Genes involved in many different pathways are expressed in response to drought stress in Arabidopsis, which has been extensively studied as a model plant that tolerates moderate water deficits. The molecular complexity of the process was illustrated by recent microarray experiments (Seki et al., 2001). It has become obvious that a network of signal transduction pathways allows the plant to adjust its metabolism to the demands imposed by a water deficit (Shinozaki and Yamaguchi-Shinozaki, 2000; Kirch et al., 2001). Several hundred genes are differentially expressed in response to dehydration, as evidenced by transcript profiling (Bockel et al., 1998). The identified genes can

be assigned to diverse metabolic pathways. Although precise function of these genes has not yet been demonstrated, five main groups have been summarized by Bartels and Salamini (2001) as genes encoding (a) proteins with protective properties, (b) membrane proteins involved in transport processes, (c) enzymes related to carbohydrate metabolism, (d) regulatory molecules, such as transcription factors, kinases, or other putative signaling molecules, and (e) open reading frames that show no homologies to known sequences.

Although a large number of drought induced genes have been identified in a wide range of species, the molecular basis still remains far from being completely understood (Ingram and Bartels, 1996). With turfgrasses, molecular genetic mechanism conditioning of the expression of drought tolerance is also an unknown field. Investigating genes correlated with drought tolerance is essential to breeding programs. Genes governing specific components of the resistance mechanism must be identified and cloned if molecular breeding and the associated research is to advance. The advent of whole genomic-related technology for differential gene expression provides the necessary tools to identify key genes in the networks that respond to drought stress, also relating their regulation to adaptive events occurring during stress. cDNA amplified fragment length polymorphism (cDNA-AFLP) is an extremely efficient method for isolating differentially expressed genes or transcript derived fragments (TDFs) (Bachem et al. 1996). cDNA-AFLP shows high reproducibility and sensitivity, good correlation with northern blot analysis and low set-up cost, even though it requires a comprehensive reference database (Donson, et al., 2002).

In summary this research shows that:

1) *Festuca mairie* in the greenhouse can maintain living green turf under sub-optimal water supply compared with other fescue species (Fig. 1).
2) The F_1 hybrid and their backcrosses between *Festuca mairie* and perennial ryegrass were successfully obtained.
3) DNA molecular marker assessment indicated that the *Festuca mairie* genome has been successfully introduced into drought susceptible perennial ryegrass (Fig. 2).
4) Evaluation of the chromosome pairing and pollen viability of the F_1 hybrid and its backcross lines indicates that some lines have the potential to release as new drought tolerant cultivars (Fig. 3).
5) By using high throughput transcript profiling techniques, cDNA-AFLP and 464 differentially expressed fragments were identified in Fm during the drought stress. In total, 434 (94%) were recovered from acrylymide gel and 179 gene fragments responding to drought stress were confirmed by using macro-array (reverse northern hybridization) techniques.

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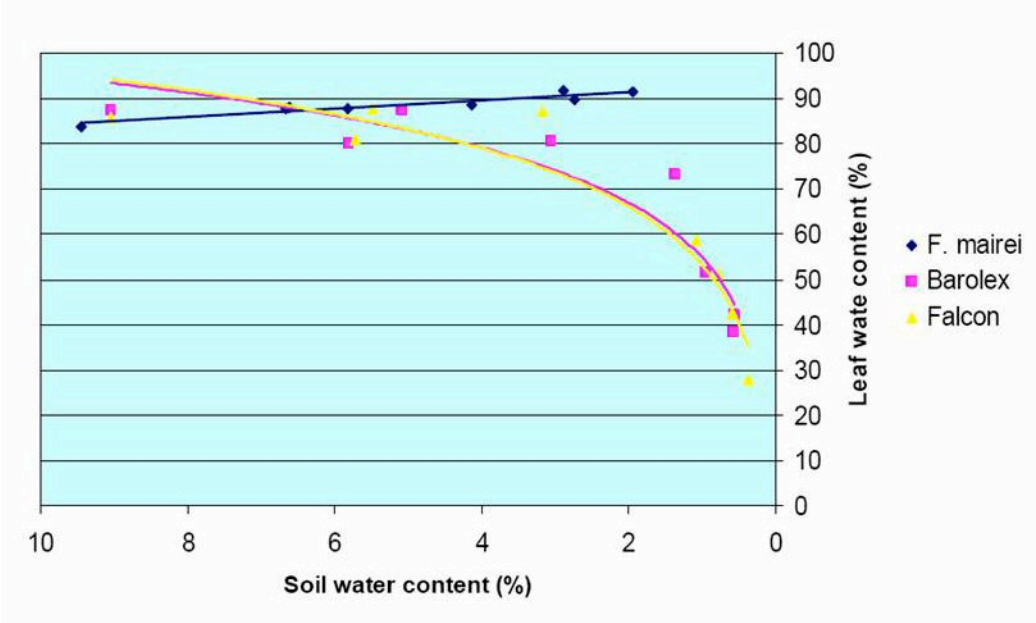

Figure 1. The relationship between leaf water content and soil moisture content of *F. mairei* compared with tall fescue cultivars. Falcon Borolex.

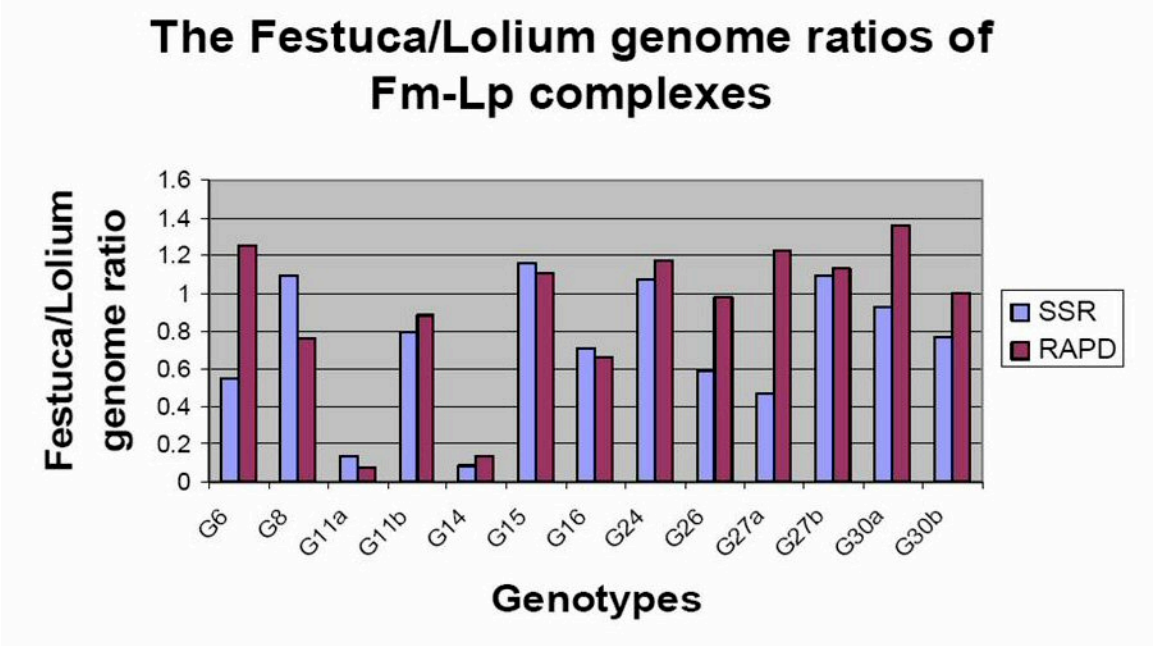

Figure 2. *Festuca/Lolium* genome ratios of backcross progenies from *Festuca mairei* and perennial ryegrass assessed by using SSR and RAPD marker.

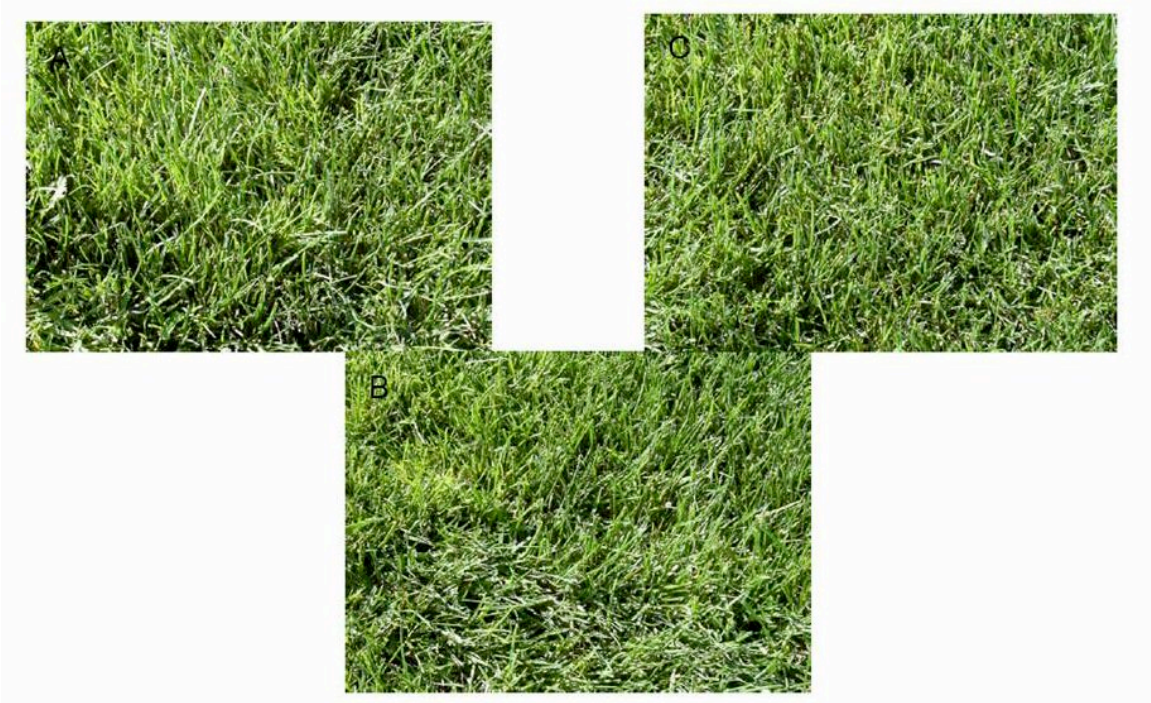

Figure 3. The plots in the field for evaluation of turf quality and seed production. A is backcross progeny G11. B is backcross G14. C is backcross progeny G16.