Linking Drought Tolerance Traits and Candidate Genes in Perennial Ryegrass through Association Mapping

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Objectives:
1. Evaluate the natural diversity of drought tolerance traits in perennial ryegrass.
2. Estimate the genetic population structure of perennial ryegrass.
3. Choose candidate genes involved in drought tolerance and genotyping the population for candidate genes.
4. Identify the correlation between the candidate gene and plant performance for target traits.

Start Date: 2007
Project Duration: one year
Total Funding: $10,000

Water conservation is a long-term concern in turfgrass management and will have an increasing impact on the turfgrass industry in the future. Production and utilization of drought tolerant turfgrass materials is an important approach for water conservation and for improving turfgrass performance in water-limiting environments. However, the progress of breeding to improve drought tolerance in turfgrass can be restricted by the lack of drought-tolerant germplasm and by the limited knowledge of the genes or traits linked to drought tolerance.

In recent years, association mapping has been developed as a novel and more powerful mapping technique. It uses a natural plant population to provide molecular markers associated with a phenotypic trait of interest and serves as an alternative method for mapping quantitative trait loci (QTL). Compared to linkage mapping in traditional bioparental populations, association mapping offers three main advantages: increased mapping reso-

Natural perennial ryegrass accessions were planted in the field and drought tolerance traits will be evaluated.

The preliminary trial in the greenhouse showed large variations in drought tolerance among natural perennial ryegrass accessions.

lution, reduced research time, and greater allele numbers. The genome-wide approach to association mapping requires an excessive number of molecular markers. Therefore, a candidate gene approach to association mapping could also be successful for identifying useful markers linked to the traits.

A careful evaluation of phenotypic traits is the key step to successful association mapping. We have initially chosen 200 natural populations of perennial ryegrass (*Lolium perenne* L.) from the USDA National Plant Germplasm System based on geographical location (43 countries). A preliminary trial conducted in the greenhouse in the spring of 2007 showed large variations in growth and drought tolerance among these accessions. Grasses were transferred to the field in the fall of 2007, and field evaluations for drought tolerance traits will be conducted in the summers of 2008 and 2009.

We have been screening the ploidy level for these 200 accessions using flow cytometry techniques to ensure that only diploid materials will be used for the association mapping. DNA extraction from leaves is being conducted and used for microsatellite (SSR) analysis to estimate the genetic population structure in selected germplasm. A selection of candidate genes involved in plant adaptation to water limi-

tation will be continued. Future research will include candidate gene sequencing and identification of polymorphisms and association mapping between phenotype and genotype.

Perennial ryegrass is a self-incompatible species that can potentially provide high-resolution association mapping. The use of natural populations may be particularly beneficial in perennial ryegrass since many potentially useful variations are still unexplored. Research in association mapping not only benefits turfgrass breeders by providing molecular markers, but also improves our understanding of the genes underlying complex genetic traits such as drought tolerance.

Summary Points

● Preliminary greenhouse trial demonstrated large variations in drought tolerance in natural populations of perennial ryegrass. Field evaluations of drought tolerance traits will continue.

● Ploidy level is being examined to ensure the selection of diploid germplasms.

● The genetic background of the germplasm is being tested using SSR markers.

● Candidate genes will be continuously chosen for future association analysis.