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.

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Project Duration: three years
Total Funding: $30,000

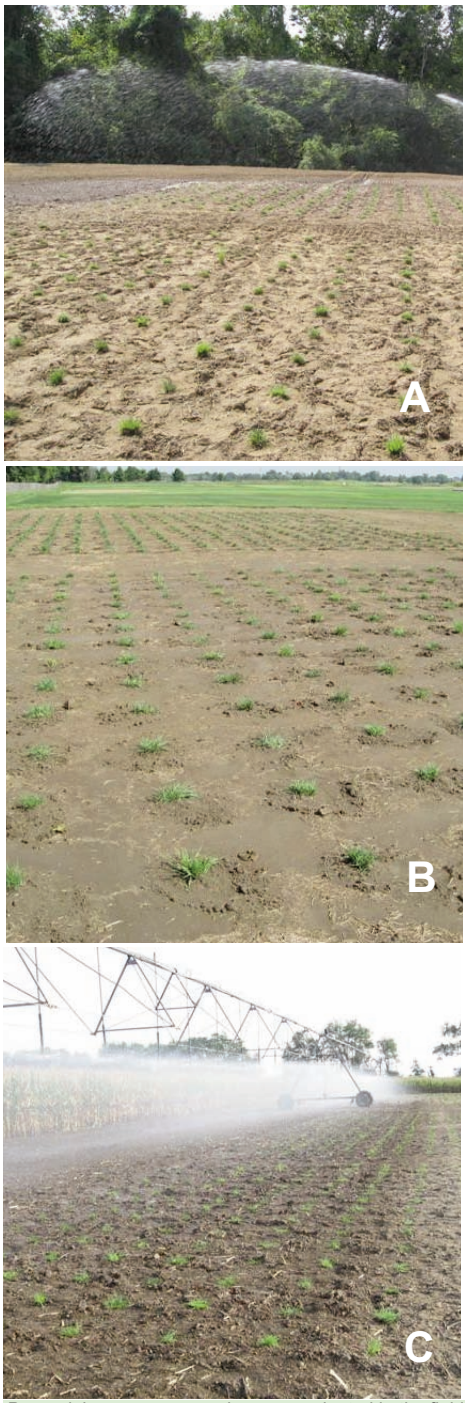
Production and utilization of drought tolerant turfgrass materials is an important approach for water conservation and for improving turfgrass performance in water-limited environments. However, the progress of breeding drought tolerant turfgrass can be restricted due to complex nature of drought stress, the large genotype by environment interactions, and 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 traits loci (QTL). Compared to linkage mapping in traditional bioparental populations, association mapping offers three main advantages: increased mapping resolution, reduced research time, and greater allele numbers.

A mapping population of 192 diploid perennial ryegrass accessions (*Lolium perenne* L.) was established. These grasses were selected from 43 countries and regions to maximize genetic diversity. The populations were planted in three different locations in Indiana: West Lafayette, Wanatah, and Vincennes.

Each accession was propagated by tillers from the mother plant so that plants for each individual accession used in different locations are genetically identical. Screening of perennial ryegrass populations in three locations over multiple years will generate more reliable data for evaluating drought response and tolerance.

A total of 105 simple sequence repeat (SSR) markers were used to screen 192 populations of diploid perennial ryegrass for assessing genetic diversity.



Perennial ryegrass accessions were planted in the field and drought tolerant traits will be evaluated at Vincennes (A), West Lafayette (B), and Wanatah (C).

The cluster analysis by unweighted pair-group methods using arithmetic averages (UPGMA) and principal component analysis (PCA) showed that perennial ryegrass accessions chosen for this study was diverse without forming the major population groups, except for 5 commercial cultivars that clustered together, suggesting that genetic diversity in commercial cultivars is limited.

The first three principle components only explained 11.4 % (7.0 %, 2.3 %, and 2.1 %) of total variation. The pair-wise plots of first three principle components exhibited some levels of separation, but not clearly identifiable groups. The result indicated that this perennial ryegrass collection would be an ideal population for further association mapping of candidate genes for drought tolerance.

Perennial ryegrass is a self-incompatible species that can potentially provide high-resolution association mapping. The project will sample natural diverse populations to evaluate the physiological adaptations of perennial ryegrass to drought stress and to identify, through the association mapping approach, genes that play an important role in drought tolerance and adaptation.

Summary Points

- The diploid perennial ryegrass was planted and drought tolerance traits will be evaluated.
- The mapping population showed a large genetic diversity.
- Genetic population structure will be estimated and candidate genes will be continuously chosen for future association analysis.