

# 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.

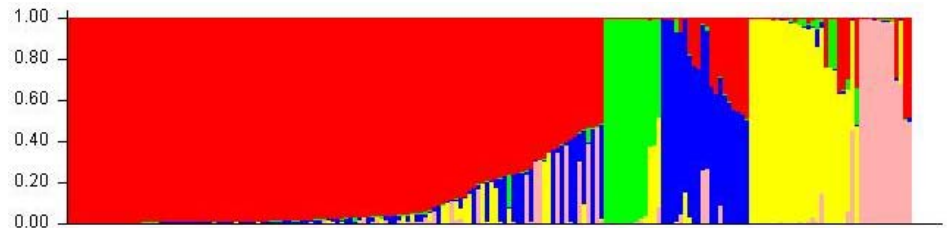
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**Project Duration:** three years

**Total Funding:** \$30,000

**T**urfgrass improvement for drought tolerance requires a comprehensive, integrated understanding of the physiological traits and genetic basis underlying trait variations in diverse natural populations. In recent years, association mapping has been developed as a novel and more powerful mapping technique. This technique uses a natural plant population to collate genes 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 resolution, reduced research time, and greater allele numbers.

Phenotypic traits were evaluated in the natural population of perennial ryegrass (*Lolium perenne* L.) established in three locations varying in soil texture in



Five subpopulations were identified among the natural mapping population by STRUCTURE analysis (G1, red; G2, green; G3, blue; G4, yellow; G5, pink)

Indiana for the first year. Across all population, leaf wilting ranged from 1 (no wilting) to 9 (severely wilted), leaf water content ranged from 60 % to 82 %, canopy temperature ranged from 29°C to 38°C, and chlorophyll fluorescence ranged from 0.69 to 0.85 under drought stress, respectively. Other traits associated with plant metabolisms are being characterized. Large variations in drought tolerance across the mapping population provide a good basis for future gene and trait association analysis.

A total of 109 simple sequence repeat (SSR) markers were used to screen 192 diploid perennial ryegrasses for assessing genetic diversity, population structure, and molecular variance among

and within populations. The overall genetic diversity and polymorphic information content of mapping population was 0.80 and 0.79, respectively.

The STRUCTURE identified five subpopulations (G1 to G5). The genetic diversity was 0.76, 0.75, 0.74, 0.79, and 0.75 for G1, G2, G3, G4, and G5, respectively. Genetic distance was the largest between G2 and G3 (0.69) and the smallest between G1 and G3 (0.21), and the results were consistent with population pair-wise Fst test.

The Molecular Variance Analysis indicated that genetic variation among and within populations were 8.6 % and 91.4 %, respectively. As population structure (associated with local adaptation or diversifying selection) or familial relatedness (from recent co-ancestry) can result in spurious associations of genes with traits, it is necessary to examine population structure to enhance accuracy of association mapping.



Drought responses of perennial ryegrass natural populations in Indiana. Soil at the site is 59% sand.

## Summary Points

- The natural mapping population showed large variations in drought tolerance.
- The overall genetic diversity of mapping population was 0.80.
- Five subpopulations were identified among the natural mapping population.
- Genetic variation among and within populations were 8.6 % and 91.4 %, respectively.