

Towards Association Mapping of Drought Tolerance in Perennial Ryegrass

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Objective:

To identify candidate genes associated with drought tolerance traits in perennial ryegrass (*Lolium perenne* L.)

Rationale:

Association mapping, also known as linkage disequilibrium (LD) mapping, has recently been developed as an alternative and powerful tool for dissecting complex traits and identifying functional markers. Association mapping identifies marker and trait relationships using diverse natural populations. Compared to quantitative trait loci (QTL) mapping in traditional bi-parental populations, association mapping allows for easier fine mapping through exploitation of historical recombination events at the population level and tests large numbers of alleles rapidly. Candidate-gene association mapping relates to polymorphisms in selected candidate genes that have purported roles in controlling variations in specific traits.

Careful evaluation of drought tolerance traits is the key step to successful association mapping. Plants adapt to drought stress through various physiological and biochemical processes. However, under a natural environment, drought tolerance and susceptibility are even more complex due to the nature of drought stress and the large genotype by environment interactions. Therefore, exploring drought responses of natural plant populations in field conditions will provide insight into drought physiological mechanisms and dissection of the genetic network controlling drought tolerance. Selection of candidate genes is another critical step for association mapping. Research results from the model plant species provide a basis for candidate gene selection in the study of drought tolerance in turfgrass species.

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 on association mapping not only benefits grass breeders by providing molecular markers, but also improves our understanding of the genes underlying complex genetic traits.

Materials and methods:

The established 192 natural mapping populations were transferred into field plots at three different locations in Indiana: Turf Center in West Lafayette, IN (Figure 1), Pinney Agricultural Research Farm (North) in Wanatah, IN (Figure 2), and Southwest Agricultural Research Farm in Vincennes, IN (Figure 3). A total of 1728 individual grasses were planted. Each accession was propagated by tillers from the mother plant so that the plants for each individual accession used in different locations were genetically identical. Since the three locations differ in climate and soil type, screening of natural perennial ryegrass populations in these locations over two (or three) years will generate more reliable data for evaluating drought response and tolerance.



Figure 1. West Lafayette, IN
Soil type: Silt loam



Figure 2. Wanatah, IN
Soil type: sandy loam



Figure 3. Vincennes, IN
Soil type: Sandy loam

Results to date:

A total of 99 simple sequence repeat (SSR) markers were used to screen 192 populations of diploid perennial ryegrass for assessing genetic diversity. The cluster analysis by unweighted pair-group methods using arithmetic averages (UPGMA) and principal component analysis (PCA) showed that the perennial ryegrass accessions chosen for this study were diverse without forming major population groups, except for 6 commercial cultivars that clustered together, suggesting that the genetic diversity in commercial cultivars is limited. The first three principle components only explained 12.5 % (7.7 %, 2.6 %, and 2.2 %) of total variation. The pair-wise plots of the first three principle components exhibited some level of separation but not clearly identifiable groups. The results indicated that this perennial ryegrass collection would be an ideal population for further association mapping of candidate genes with drought tolerance traits.

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