

Identification of Quantitative Trait Loci (QTL) Associated with Drought and Heat Tolerance in Creeping Bentgrass

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Objectives:

1. To evaluate variations in drought and heat tolerance for two mapping populations of bentgrass segregating for disease resistance.
2. To identify phenotypic traits associated with drought and heat tolerance.
3. To identify QTL markers associated with drought and heat tolerance utilizing the available linkage maps.

Start Date: 2008

Project Duration: three years

Total Funding: \$89,912

A creeping bentgrass mapping population (L93-10 x 7418-3) segregating for dollar spot resistance was evaluated for variation in drought tolerance in this study. We examined both parents and 100 F₂ progenies. An intra-specific pseudo F₂ mapping population (180 individuals) was generated from a cross between a dollar spot resistant (L93-10) and a susceptible (7418-3) genotype in the spring of 2003. All individual clones (104 from L93-10 x 7418-3) were planted in one large plastic container (60 cm x 120 cm x 30 cm deep) filled with a mixture of sand and soil and replicated five times.

Plants were exposed to drought stress by withholding irrigation. During the dry-down period, several drought-stress indicators were evaluated to determine the genotypic variation and phenotypic traits for drought tolerance in these two mapping populations. Turf quality was rated visually based on the scale of 1-9 (9 = best) as the indicator of general turf performance. Several most commonly used parameters for phenotyping drought tolerance, including relative water content, osmotic adjustment, cell membrane stabil-

ity, and water use efficiency were analyzed.

The phenotypic data with the 'L-93' x 7418 population demonstrated that turf quality for two parents and 102 progenies exhibited large variation, with visual rating ranging from 3 to 6 following 7 days of drought stress. Leaf relative water content (RWC) and osmotic adjustment (OA), two commonly used stress indicators, are significantly correlated to turf quality under drought stress, with correlation coefficients being 0.73 and 0.68, respectively. Both traits exhibited a wide range of variation, with RWC varying from 33% to 94% and OA ranging from 0 to 0.50.

A field study was conducted in summer and fall 2008 in a fully automated mobile shelter (35' x 60') at Rutgers University in North Brunswick. The L93-10 x 7418-3 mapping population was established in a mowed spaced-plant evaluation trial in the rainout shelter in April 2008. The individual clones were arranged in a randomized complete block design with 3 replications.

From July to September, all plants were maintained under well-watered conditions and examined for turf quality, canopy green leaf biomass, leaf area index, and cell membrane stability to analyze for variation and phenotypic traits for heat tolerance. During October and November,

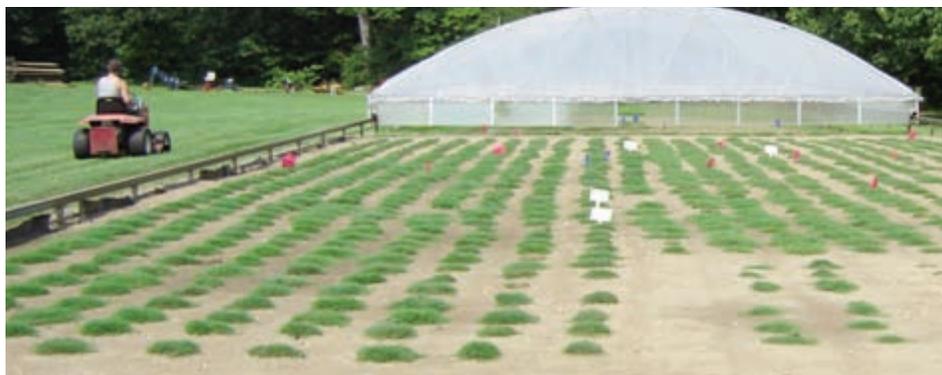
plants were exposed to drought stress by withholding irrigation to examine genetic variation in drought tolerance. Data for the field study will be analyzed and summarized in December.

QTL analysis was conducted on several phenotypic traits including electrolyte leakage (EL), relative water content (RWC), and osmotic adjustment in the 'L93' x 7418-3 mapping population. No significant QTLs were found on the more drought sensitive parent ('L-93'). Seven QTLs were found on the more drought tolerant parent (7418-3). Four significant QTLs (1 RWC; 2 EL; 1 TQ) and three suggestive QTLs (1 RWC; 1 WUE; 1 OA) were detected. These QTLs were found in four chromosome regions, with co-location of RWC and TQ, RWC and EL, and WUE and OA.

QTLs markers for TQ, RWC, and EL were highly correlated to drought tolerance. These initial QTLs from the greenhouse study will be compared to phenotypic traits associated with drought tolerance evaluated under field conditions.

Summary Points

- Phenotypic variations in drought tolerance exist in the creeping bentgrass mapping population developed for dollar spot resistance.
- Significant QTLs were identified for TQ, RWC, and EL, and those QTL markers are highly correlated to drought tolerance.
- QTL markers for drought tolerance were located in four regions of the genetic linkage map for the drought tolerant parent.
- Major QTLs located in the same chromosomal region for turf quality, relative water content, cell membrane stability, osmotic adjustment, and water use efficiency may be useful as molecular markers for marker-assisted selection.



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