

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

The creeping bentgrass mapping population (L93-10 x 7418-3) segregating for dollar spot resistance was evaluated for their variations in drought tolerance in 2008. A second bentgrass mapping population was evaluated for drought tolerance in a greenhouse in 2009. This is a hybrid population that was originally developed by crossing creeping (*Agrostis stolonifera* L.) and colonial bentgrass (*Agrostis capillaris* L.) by interspecific hybridization for the introgression of colonial genes for dollar spot resistance into creeping bentgrass and for development of colonial linkage map.

The F₂ population, progeny of a creeping/colonial (Hybrid 15) x creeping (9188) cross, was used for drought screening. The population was propagated and maintained in a greenhouse until establishment and exposed to drought treatment from 5/10-5/20/2009, during cool greenhouse temperatures to prevent additional heat stress. Soil volumetric water content (SWC) was monitored and was not significantly different among plants prior to drought treatment (approximately 25%). The duration of water being completely withheld for drought treatment was 10 days, when the SWC reached 8%. Measurements of drought tolerance characteristics included turf quality, relative water content, electrolyte leakage, and canopy temperature depression.

A field study was conducted in summer and fall of both 2008 and 2009 in a fully automated mobile shelter (35' x 60') at Rutgers University in North Brunswick. The shelter excludes unwanted rainfall from test plot areas, which allows the imposition of continuous drought stress without interruption from unwanted rainfall while retaining the advantages of natu-

ral field conditions.

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 4 replications.

From July to September, all plants were maintained under well-watered conditions to test 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. In both seasons, plants were evaluated for turf quality (TQ), canopy green leaf biomass, leaf area index, electrolyte leakage (EL), canopy temperature depression (CTD), relative water content (RWC), water use efficiency, and chlorophyll content.

The phenotypic traits associated with drought tolerance and the molecular marker data previously generated for the two mapping populations were subjected to QTL analysis. Molecular markers and chromosomal locations with significant LOD scores were identified as QTLs associated with the phenotypic traits of drought and heat tolerance.

Several possible QTLs associated with drought tolerance were identified in two bentgrass populations. Under drought stress of both the field and greenhouse studies, possible QTLs were identified on chromosomes 3, 5, 8, 11, and 13, of which two chromosomal locations on groups 3 and 11 overlapped for multiple traits. The QTL on group 3 was identified for both FvFm and for RWC whereas the QTL on group 11 was for TQ and carbon to nitrogen ratio.

QTL analysis of the data taken in the drought stress study in the greenhouse for the hybrid population resulted in highly significant QTLs on three different chromosomes, groups 4, 5 and 10. The

location of the QTL on group 5 overlapped for the two traits EL and CTD. TQ mapped to 3 locations, 2 on group 10, and 1 on group 4. This data is the result of only a single greenhouse study which will be repeated in the winter of 2010.

For heat tolerance QTLs, potentially important regions of the genome include chromosome groups 3, 6, 11, 12, and 13 identified for the traits including TQ, green leaf biomass, leaf area index, and FvFm. Groups 11 and 13 overlapped for both heat and drought data, indicating that these could also be important chromosomal locations for the combined heat and drought tolerance.

Markers associated with multiple traits and with both heat and drought tolerance are particularly important which will be further analyzed for future use in marker-assisted selection.

Summary Points

- Phenotypic variations in drought and heat tolerance exist in the creeping bentgrass and hybrid bentgrass mapping population developed for disease resistance.
- Significant QTLs were identified for various traits that were good indicators for stress tolerance and turf performance under below optimal conditions such as TQ, EL, and RWC.
- Important chromosomal locations for heat and drought tolerance may exist on 5 different linkage groups for the creeping bentgrass population and 3 different linkage groups in the hybrid population.
- Regions of the chromosome with significant overlap for both heat and drought tolerance and for multiple stress tolerance parameters such as CTD and EL may be the most useful in future studies for development of marker-assisted selection procedures.