

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

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## Objectives:

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

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**Project Duration:** 3 years

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A creeping bentgrass mapping population (L93-10 x 7418-3) and a hybrid bentgrass population (creeping x colonial), both segregating for dollar spot resistance, were evaluated for variation in drought and heat tolerance and for QTL localization. The creeping population consisted of a pseudo F<sub>2</sub> mapping population (180 individuals) that was generated from the intraspecific cross of a dollar spot-resistant (L93-10) and a susceptible (7418-3) genotype in the spring of 2003. For all QTL analysis described here, a subset of the population (100 individuals, F<sub>2</sub> progeny) and the parents were evaluated for heat and drought tolerance. The population was evaluated four times for phenotypic variation in drought tolerance in three different environments (greenhouse, growth chamber, and field).

The hybrid bentgrass population was originally developed by crossing creeping (*Agrostis stolonifera* L.) and colonial bentgrass (*A. capillaris* L.) by interspecific hybridization for the introgression of colonial genes for dollar spot (*Sclerotinia homoeocarpa*) resistance into creeping bentgrass and for development of a colonial linkage map. The F<sub>2</sub> population, progeny of a creeping/colonial (Hybrid 15) x creeping (9188) cross, was used for drought screening.

Several drought-stress indicators were used to evaluate physiological responses to stress and to determine the genotypic variation and phenotypic traits in the mapping populations. Turf quality (TQ) was rated visually based on a scale of 1-9 (1 = desiccated, brown; 9 = healthy, green). Several commonly used parameters for phenotypic analysis of stress tolerance were measured, including relative

water content (RWC), electrolyte leakage (EL), osmotic adjustment (OA), photochemical efficiency (FvFm), carbon-to-nitrogen ratio, water-use efficiency (WUE), green leaf biomass (NDVI), and leaf area index (LAI) as determined by a multispectral radiometer (MSR).

In response to drought stress, both populations portrayed significant variation in most physiological parameters evaluated. The creeping population visual TQ ratings ranged from 3 to 6 following 7 days of drought. RWC varied from 60% to 94%, and OA ranged from 0 to 0.50. The hybrid population exhibited variation after 5 days of drought, ranging from 3 to 9 for TQ, 13% to 77% for RWC, and 0.4 to 0.8 for FvFm.

Several possible QTLs were identified during heat, drought, and recovery from stress within the creeping bentgrass population. Under drought stress, from the results of both the field and greenhouse studies, possible QTLs were identified on chromosomes 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, and 13. Of these, four chromosomes, groups 3, 5, 9, 10, 11, and 13, had multiple regions that could be possible QTLs or had overlapping regions for multiple traits. The QTL on group 3 was identified for both MSR and RWC in years 2007 and 2008.

The possible QTL region on group 11 was for TQ and carbon-to-nitrogen ratio, MSR, and TQ. TQ on this group mapped to the 70-80 cM region in both 2007 and 2008 during recovery from drought. Group 5 may be a location determining TQ characteristics under stress conditions, since the same region was consistent across all years. Groups 5, 11, and 12 may be the most important groups for drought-tolerance traits.

During heat stress analysis, potentially important regions of the genome include chromosome groups 2, 3, 6, 9, 10, 11, 12, and 13 identified for the traits TQ, NDVI, LAI, and FvFm. QTLs

on groups 2, 3, 9, 11, and 12 accounted for traits over multiple years, indicating that these could also be important chromosomal locations to look at for future use in marker-assisted selection. In the field studies of 2008 and 2009, groups 2, 9, 11, and 12 may have important regions controlling visual quality during heat stress as measured by TQ ratings and MSR readings.

Important linkage groups including possible QTLs for drought tolerance were chromosomes 3, 5, 9, 10, and 14. Greenhouse evaluation of variation in drought tolerance in 2009 resulted in 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 three locations, two on group 10 and one on group 4. In 2010, the greenhouse and growth chamber evaluations revealed possible QTLs on groups 1, 3, 5, 9, 10, and 14. Since the most consistent QTLs across years and environments were groups 5 and 10, traits in these regions may contribute greatly to the variation in drought tolerance seen within the hybrid population.

## Summary Points

- Phenotypic variation in drought and heat tolerance in both the creeping and hybrid bentgrass populations allowed for identification of potentially important QTL regions.
- QTL regions that were consistent across years and environments such as group 5 and 11 for the bentgrass population and 5 and 10 for the hybrid population may be important chromosomal regions governing stress tolerance traits.
- Regions of chromosomes groups 3 and 11 in the creeping population were significant for both heat and drought tolerance. The importance of these groups in tolerance to multiple stresses may be the most useful in future studies for development of marker-assisted selection procedures.