

Confirmation of QTL Markers for Dollar Spot Resistance in Creeping Bentgrass

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Objectives:

1. Genotype backcross and pseudo F₃ generations for the 180 SSR markers identified to date.
2. Evaluate the populations for dollar spot resistance to a different isolate of *Sclerotinia homoeocarpa* than previously evaluated.
3. Confirm QTLs in the backcross and pseudo F₃ generations to provide definitive SSR QTL markers that can be directly utilized for marker-assisted selection in turfgrass breeding programs.

Start Date: 2007

Project Duration: two years

Total Funding: \$50,000

Previous research projects have identified QTL (Quantitative Trait Loci) for important traits in mapping populations of creeping bentgrass. However, all initial QTL experiments have several limitations. They may detect ghost QTLs, fail to detect a real QTL, and may over- or underestimate the true effects of QTLs. Furthermore, QTLs can vary in different environments and different genetic backgrounds, and QTLs may not be linked to the quantitative trait after further rounds of recombination.

The confirmation of initial QTLs is necessary to successfully utilize QTL markers in marker-assisted selection breeding programs. Almost every QTL confirmation study finds some discrepancy with initial QTL experiments. The goal of this project is to confirm putative QTL for dollar spot resistance identified in a previous study (funded by the USGA, OJ Noer Foundation, and USDA) by evaluating the QTL markers in three subsequent mapping populations (two backcross populations and a second generation [pseudo F₃] population) developed from the initial mapping population.



A replicated, mowed spaced-plant trial of the pseudo F₂, pseudo F₃ and backcross populations was planted in the spring of 2008 to reevaluate the population to different virulent isolate of *S. homoeocarpa*.



Host resistance for plant diseases is an important part of improving turfgrass cultivars. Researchers at Rutgers University are using molecular techniques to identify genetic components that are responsible for resistance to dollar spot caused by *Sclerotinia homoeocarpa*, prevalent on golf course turf.

This confirmation step is necessary because it is important to determine if the QTLs remain linked to dollar spot resistance after further rounds of recombination. This project will result in easily useable, reproducible, SSR QTL markers for dollar spot resistance that will be publicly available to turfgrass breeding programs interested in using them for marker-assisted selection.

We have identified approximately 200 unique SSR markers. Approximately two-thirds of the markers have been genotyped in the backcross and pseudo F₃ generations. Initial genetic linkage maps of each original parents based on approximately 200 SSR markers were developed. Three putative QTL markers have been identified for the 'Crenshaw' isolate and one different putative QTL marker was identified for the perennial ryegrass isolate.

We analyzed the backcross and second generation populations for these putative QTLs and are in the process of scoring the markers and genotyping the progeny for presence or absence of the QTLs. This data will be compared to the phenotype data to determine whether the QTL remains linked to dollar spot resistance in these populations.

A replicated, mowed spaced-plant

trial of the pseudo F₂, pseudo F₃ and backcross populations was planted in the spring of 2008 to reevaluate the population to a different virulent isolate of *S. homoeocarpa* than was previously evaluated. We will inoculate the plants next spring and evaluate the populations for two years for dollar spot resistance.

Summary Points

- Three putative SSR QTL markers were identified in the initial population for the 'Crenshaw' isolate. One was identified in the susceptible parent and three were identified in the resistant parent. One QTL has been identified in the resistant parent for the perennial ryegrass isolate.
- Two of the three QTLs for the 'Crenshaw' isolate show evidence of dominance for susceptibility and only one exhibits dominance for resistance. This is consistent with gene number estimations (2-5 genes).
- Selection for a combination of markers identified genotypes with good dollar spot resistance. These markers may be useful in marker-assisted selection breeding programs to develop new cultivars with improved dollar spot resistance.
- Classical genetics and molecular markers support evidence for dominant genes for susceptibility.