

Genomic Linkage Map Construction and Identification of Quantitative Trait Loci Associated with Dollar Spot Resistance in Creeping Bentgrass

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Objectives:

1. Isolate GA/GT, and GTC microsatellite loci to develop a genetic linkage map of the creeping bentgrass genome.
2. Evaluate dollar spot resistance in a mapping population to identify creeping bentgrass germplasm with improved dollar spot resistance.
3. Identify QTL markers associated with dollar spot resistance to use as a selection tool for resistant germplasm.

Start Date: 2003

Project Duration: three years

Total Funding: \$89,820

One of the major challenges in breeding creeping bentgrass is improving disease resistance. Dollar spot disease, caused by the fungus *Sclerotinia homoeocarpa* F.T. Bennett, is one of the most important diseases of creeping bentgrass because it accounts for a majority of the fungicides applied to golf courses in temperate areas.

The goal of this research project is to create a genetic linkage map of creeping bentgrass and identify Quantitative Trait Loci (QTL) associated with dollar spot disease resistance. Once these QTLs are identified, these markers have the potential to identify favorable gene combinations which can enhance traditional plant breeding methods, reduce the evalua-



Spaced-plants were evaluated throughout the growing seasons (2003 and 2004) for dollar spot disease using a 1-9 rating scale.

tion time associated with identifying dollar spot resistant germplasm, and increase the efficiency of breeding disease-resistant cultivars.

A mapping population of creeping bentgrass generated from a cross between a dollar spot resistant and susceptible genotype is being analyzed for dollar spot disease resistance and DNA marker polymorphism. These DNA markers will be used to develop a genetic linkage map of creeping bentgrass and to subsequently identify Quantitative Trait Loci (QTL) associated with dollar spot resistance.

Replicated, mowed spaced-plant trials of the pseudo F₂, pseudo F₃ and backcross populations (700 replicated genotypes) were inoculated with a virulent isolate of *S. homoeocarpa* on June 30, 2003 and are in the second year of evaluation for dollar spot disease resistance. These spaced-plants were evaluated throughout the growing seasons (2003 and 2004) for dollar spot disease using a 1-9 rating scale.

Progeny distributions of the pseudo F₂ population were normally distributed and represented a range of phenotypes from low to high. No progeny were completely resistant to dollar spot disease. The pseudo F₃ population was slightly skewed towards resistance, while both backcross populations were skewed toward the original parent. Transgressive segregants were observed in all populations. These data support our original findings that dollar spot resistance is quantitatively inherited. These data will help us further identify the inheritance of dollar spot resistance in creeping bentgrass

We have identified approximately 170 of the 200 SSR markers proposed.

The initial genetic linkage maps of each parent based 112 SSR loci is currently underway. This initial map will give us an idea of how many additional markers will be needed to saturate the map. Initial analysis of the SSR loci indicates some complex inheritance patterns at several loci. Double reduction, segregation distortion, and the presence of null and multiple copy alleles have been observed.

These complexities affect recombination frequencies and segregation ratios of particular alleles, and also affect linkage map construction. Once the specific pairing behavior of creeping bentgrass is determined, these models will be incorporated to develop an accurate linkage map of creeping bentgrass.

Summary Points

- A mapping population of creeping bentgrass generated from a cross between a dollar spot resistant and susceptible genotype is being analyzed for dollar spot disease resistance and DNA marker polymorphism
- Data from F₂ and pseudo F₃ populations support our original findings that dollar spot resistance is quantitatively inherited. These data will help us further identify the inheritance of dollar spot resistance in creeping bentgrass
- Initial analysis of the SSR loci indicates some complex inheritance patterns at several loci. Double reduction, segregation distortion, and the presence of null and multiple copy alleles have been observed.
- A Bentgrass Genomics Group was developed to coordinate bentgrass mapping projects at several institutions and is being used to try to acquire additional funding from other sources.