

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

Stacy A. Bonos  
Rutgers University

## 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

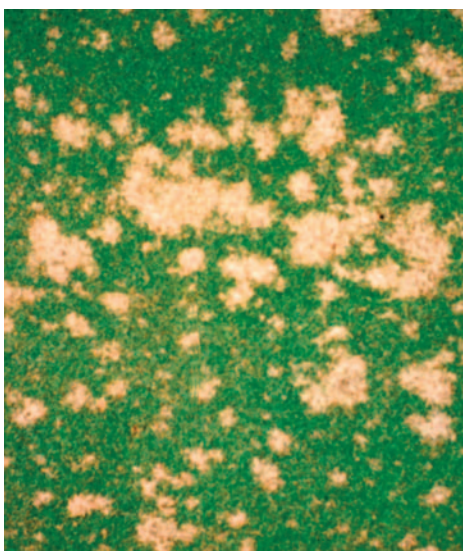
**Project Duration:** three years

**Total Funding:** \$89,820

Dollar spot disease, caused by the fungus *Sclerotinia homoeocarpa*, is one of the most important diseases of creeping bentgrass. 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.

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 then subsequently identify Quantitative Trait Loci (QTL) associated with dollar spot resistance.

Replicated, mowed spaced-plant



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

trials of the pseudo  $F_2$ , pseudo  $F_3$ , and backcross populations were inoculated with a virulent isolate of *S. homoeocarpa* on June 30, 2003. These spaced-plants were evaluated throughout the growing seasons (2003 and 2004) for dollar spot disease using a 1-9 rating scale. Although disease was less severe in 2004, similar observations were observed in both years. Significant mid-parent heterosis was observed in the backcross generations in both years indicating the presence of non-additive gene effects.

Approximately 3,000 sequences have been screened for SSR presence. Approximately 170 polymorphic microsatellite (SSR) loci were identified from those. 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 alleles, and also affect linkage map construction.

$F_2$ ,  $F_3$ , and backcross populations were evaluated for dollar spot resistance in 2003. Progeny distributions of pseudo  $F_2$  and  $F_3$  support our original findings that dollar spot resistance is quantitatively inherited. However, mid-parent heterosis data from backcross generations indicates that non-additive gene action may play a part in disease resistance.

Perhaps the most important accomplishment of this project is the opportunities that have evolved from conducting this research. USDA funding for a more in-depth study of the inheritance of allotetraploid creeping bentgrass was received. A Bentgrass Genomics Group was developed to coordinate bentgrass mapping projects at several institutions and



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to acquire additional funding from other sources.

## 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  $F_2$  and pseudo  $F_3$  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.