

Identification of the Colonial Bentgrass Contribution to Dollar Spot Resistance in Colonial x Creeping Bentgrass Interspecific Hybrids

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Objectives:

1. To construct a genetic linkage map for colonial bentgrass.
2. To identify the regions of the colonial bentgrass genome that confer dollar spot resistance to the colonial x creeping bentgrass interspecific hybrids.

Start Date: 2006

Project Duration: three years

Total Funding: \$90,000

Dollar spot disease is one of the major management problems encountered with creeping bentgrass. The related species colonial bentgrass has good resistance to dollar spot. We have found that some interspecific hybrids between colonial bentgrass and creeping bentgrass exhibited excellent dollar spot resistance. When one of the resistant hybrids was crossed with another creeping bentgrass plant, some of the progeny also exhibited good resistance.

In 2006, these plants were evaluated in a replicated field test where they were inoculated with the fungal pathogen. At the end of the rating period, about 15% of the individuals showed good resistance. Interspecific hybridization between the colonial and creeping bentgrass may thus be a useful new approach to improving the dollar spot resistance of creeping bentgrass.

In order to ultimately discover the genes in colonial bentgrass that are responsible for the dollar spot resistance, we are developing a genetic linkage map of colonial bentgrass. We are using the backcross individuals as our mapping population. For our linkage map we are focused on mapping genes. To support this effort, we were participants in a multi-investigator EST sequencing project. Through this project, we generated 7,528 colonial bentgrass ESTs and 8,479 creeping bentgrass ESTs. The sequences have been deposited in the NCBI dbEST and can also be searched on the Belanger lab website at <http://aesop.rutgers.edu/~belangerlab/research.htm>.

These ESTs provide a valuable resource for gene-based marker development for genetic mapping. Linkage mapping is based on identifying polymorphisms between the parents that are segregating in the progeny.



2006 field test of the mapping population

Identification of such polymorphisms is actually the most difficult aspect of gene-based linkage mapping. In an effort to improve the efficiency of polymorphism detection, we have developed a new approach to identification of useful markers, termed dideoxy polymorphism scanning. This is the method that we are currently using to map genes.

Our current colonial bentgrass genetic linkage map covers 753 cM and consists of 15 linkage groups. Additional markers should resolve the linkage groups into the expected 14. AFLP markers were generated by Scott Warnke at the USDA to quickly establish some linkage groups and provide a framework for placement of gene-based markers. We now have a total of 104 linked markers (43 gene-based and 61 AFLP) and 37 unlinked markers (18 gene-based and 19 AFLP).

We are using a comparative genomics approach to guide our current mapping efforts. The DNA sequence of rice has been determined and there is considerable genomic information available for wheat. Bentgrasses are more closely related to wheat than to rice and share the same base chromosome number of 7. Detailed comparisons of the rice and wheat chromosomes have been reported and the wheat chromosomes are largely derived from specific rice chromosomal regions.

We have found that there is considerable conservation of gene composition of linkage groups between colonial bentgrass and wheat.

We are therefore using the rice chromosomal location of specific genes and the relationship of rice to the wheat chromosomes to target the regions of the colonial bentgrass map that need additional markers. We expect that such a targeted approach to gene mapping will be an efficient way to fill out our current linkage groups.

Summary Points

- We are using a population generated from a cross between a dollar spot resistant colonial bentgrass x creeping bentgrass hybrid and another creeping bentgrass plant to develop a colonial bentgrass genetic linkage map.
- The mapping population was evaluated in a field test in 2006, and about 15% of the individuals exhibited good dollar spot resistance.
- We participated in a multi-investigator bentgrass EST project. We have also developed a new approach to gene-based polymorphism detection, termed dideoxy polymorphism scanning.
- Our current colonial bentgrass linkage map covers 753 cM and we have identified a total of 61 gene-based markers. We are utilizing the wealth of genomic information available from rice and wheat to guide our current mapping efforts.