

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

Faith C. Belanger
Rutgers University

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 and may be a source of novel genes or alleles that could be used in the improvement of creeping bentgrass. Despite the dollar spot resistance of colonial bentgrass, creeping bentgrass is generally preferred because colonial bentgrass does not have the desirable aggressive stoloniferous growth habit of creeping bentgrass, which aids in repair of the turf from the damage incurred during play.

Interspecific hybridization has been used by breeders of many crops to introduce beneficial traits from related species into crop species. However, it has not yet been used in bentgrass breeding and so presents a great opportunity for creeping bentgrass improvement. The ultimate goal of such an approach would be to develop bentgrass cultivars with the stoloniferous growth habit of creeping bentgrass combined with the dollar spot resistance of colonial bentgrass.

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 backcross progeny also exhibited good resistance. The backcross progeny were evaluated in field tests over several years and 11-18% of the individuals exhibited excellent dollar spot resistance, suggesting three colonial bentgrass genes may be required for the observed 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 combining amplified fragment length polymorphisms (AFLP) and gene-based markers. The AFLP markers were generated by Scott Warnke at the USDA. We are using colonial bentgrass EST sequences for the development of the gene-based markers. We are using three different methods for polymorphism detection. One method is to identify +/- polymorphisms or length polymorphisms in PCR fragments generated from the 3' ends of the genes. We have also developed single nucleotide polymorphism (SNP) markers that are detected by minisequencing. We have also developed a new method for marker development called dideoxy polymorphism scanning, which can reveal SNPs and indels without prior knowledge of a sequence polymorphism.

Using gene-based markers for the mapping allows us to take advantage of the wealth of genomic resources developed for other crops, particularly the cereal grains. Similarities in chromosomal organization are found among the grass species. Detailed comparisons of the rice and wheat chromosomes have been reported. Rice is a diploid species with 12 chromosomes and wheat is a hexaploid species with a base chromosome number of 7. Although there are numerous exceptions, the wheat chromosomes are largely derived from specific rice chromosomal regions.

Colonial bentgrass is more closely related to wheat than to rice and also has a base chromosome number of 7. We are

using the rice-wheat chromosomal relationships to make linkage group assignments of our colonial bentgrass linkage groups, using the wheat chromosome nomenclature. We are using the rice chromosomal location of specific genes and the relationship of rice to the wheat chromosomes to guide our mapping.

Colonial bentgrass is an allotraploid composed of two subgenomes, designated A1 and A2, each with 7 chromosomes. We therefore expect a total of 14 linkage groups. From sequence comparisons of the bentgrass ESTs, we can often make predictions of the subgenome of a linkage group, since the colonial and creeping bentgrass A2 subgenomes are quite similar to each other. Our current colonial bentgrass genetic linkage map covers 1160 cM and consists of the expected seven A1 and seven A2 linkage groups.

Summary Points

- Colonial bentgrass is resistant to dollar spot disease. Hybridization with creeping bentgrass may be a way to improve the dollar spot resistance of creeping bentgrass.
- Field evaluations of the backcross progeny from a cross of an interspecific hybrid with creeping bentgrass suggest that three colonial bentgrass genes may be required for the observed dollar spot resistance.
- We are developing a genetic linkage map of colonial bentgrass in order to develop molecular markers that could be used for marker-assisted selection for introgression of colonial bentgrass dollar spot resistance genes into creeping bentgrass.
- Our current colonial bentgrass linkage map covers 1160 cM and consists of the expected seven A1 and seven A2 subgenome linkage groups. Our data suggests the colonial bentgrass dollar spot resistance genes may reside on linkage groups 2A1 and 3A1.



Graduate student David Rotter next to a dollar spot resistant backcross plant.