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 microstellite loci to develop a genomic 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. Utilize the genomic linkage map and/or DNA markers to identify other traits such as environmental stress tolerance.

Start Date: 2003
Project Duration: three years
Total Funding: $89,820

The goal of the project is to create a genetic linkage of creeping bentgrass for the identification of DNA markers linked to 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 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.

Once QTL markers are identified, marker-assisted selection can be utilized to quickly and efficiently screen germplasm for resistance to dollar spot. Furthermore, the development of a genetic linkage map in tetraploid creeping bentgrass will be a major contribution to the advancement of turfgrass breeding and genetics.

Approximately 2,330 plasmids (330 GCT, 1000 GA, 1000 GT) from the enriched library have been sequenced for SSR presence. From those sequences, we have identified 100 polymorphic microsatellite (SSR) loci that will be used to create the preliminary linkage map. The genotypes of all 180 F_1 mapping population individuals for all 100 SSR loci have been completed.

Differences in dollar spot disease between the dollar spot resistant parent, L93-10, planted in a clonal row (below) and the dollar spot susceptible parent (7418-3) planted in a clonal row (above)

Profiles have been built for each of the 100 loci. These profiles contain genotypes of each individual in the mapping population, peak heights, and copy numbers of the specific alleles. These 100 completed profiles were sent to Dr. Rongling Wu (our collaborator at the University of Florida), to begin analysis of the specific preferential paring behavior for creeping bentgrass.

Once the specific pairing behavior of creeping bentgrass is determined, these 100 loci will be used to develop an initial linkage map of creeping bentgrass. From this data, we hope to obtain the number of linkage groups present, as well as the number of additional SSR loci that will be needed to complete the map.

Initial analysis of the SSR loci indicates that several loci may be undergoing double reduction. Double reduction can occur when tetrads (quadrivalents) form at meiosis. This indicates that at some loci, tetrasomic inheritance may be occurring. All previous literature has indicated strict disomic (bivalent) inheritance in this species.

Replicated, mowed spaced-plant trials of the F_1, F_2 and backcross populations were inoculated with a virulent isolate of *Sclerotinia homoeocarpa* (the causal organism of dollar spot disease) on June 30, 2003. These 700 replicated spaced plants were evaluated throughout the growing season (2003) for dollar spot disease. These current data being analyzed along with another year of disease evaluation (2004) will used to determine the phenotype of each individual progeny making up the mapping population. This will be used to identify QTLs associated with dollar spot resistance in creeping bentgrass.

Differences in dollar spot resistance among progeny of the mapping population from a cross between a resistant and susceptible creeping bentgrass parent

Vegetative clones of each of these 700 individuals making up the F_1, F_2 and BC mapping populations were also established in a spaced-plant nursery at the Plant Biology and Pathology Research and Extension Farm, Adelphia, NJ to maintain the population for future DNA isolation.

Summary Points

- Approximately 2,330 plasmids (330 GCT, 1000 GA, 1000 GT) from the enriched library have been sequenced for SSR presence.
- 100 polymorphic microsatellite (SSR) loci have been identified that will be used to create the preliminary linkage map.
- Genotypes of all 180 F_1 mapping population individuals for all 100 SSR loci have been completed. Profiles have been built for each of the 100 loci.
- Vegetative clones of each of these 700 individuals making up the F_1, F_2 and BC mapping populations were established.