Towards a genetic map in creeping bentgrass based on SSRs, AFLPs and RFLPs

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Introduction Creeping bentgrass (*Agrostis palustris*) (2n=4x=28) is commonly used in golf course, putting green, tees and fairways. In spite of the importance of the species in turfgrass industry, the genetic study of the creeping bentgrass has received relatively little attention. Genetic mapping, as a new tool, helps traditional turfgrass breeding methods through the construction of linkage, identification of quantitative trait loci linked to traits of interest, and application of marker assisted selection program. Molecular markers such as AFLPs, SSRs and RFLPs have been used extensively for the preparation of linkage maps of a number of crop species. The objective of this study is to construct a genetic linkage map of creeping bentgrass.

Materials and methods A two-way pseudo-testcross F_1 population is being used to produce a map based on AFLPs (*Pst*I/*Eco*RI and *Mse*I/*Eco*RI), SSRs and RFLPs (anchor probes), to estimate the degree of orthology and colinearity between creeping bentgrass and the Triticeae genomes for all linkage groups, and to investigate the association with genetic markers of several potential quantitative traits: leaf width, flower time, gray snow mold and dollar spot resistance.

Results and discussion An F_1 progeny set comprising 184 individuals, derived from a cross between snow mold resistance and susceptibility clones, was obtained and confirmed by a physiological marker to eliminate any progeny from selfing. The data set included three different segregation patterns: 1:1 for heterozygous markers in one parent and homozygous or null in the other, 3:1 for dominant markers heterozygous in both parents, 1:1:1:1 for co-dominant multiallelic markers. For each marker, a chi-square test ($p<0.05$) was used to identify deviations from the expected Mendelian ratios. Linkage analysis was carried out using JoinMap v3.0 software with a minimal LOD of 4.0 and a maximum recombination fraction of 3.0 as the group criteria. A composite interval-mapping approach was used for estimate the number of QTLs, the amount of variation explained by each of them, and their position on the genetic linkage maps.