Production and Maintenance of Triploid Interspecific Bermudagrass Hybrids for QTL Analysis

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Objectives:

1. *To evaluate the B17 F_1 mapping population in replicated tests at Tifton, GA and Griffin, GA for turfgrass performance characteristics with the goal of identifying quantitative trait loci (QTL) for these traits.*
2. *To increase the size of the B17 F_1 mapping population to 200 or more individuals.*

A framework genetic map was created using single dose restriction fragments (SDRF) by Bethel, Sciara, Estill, Bowers, Hanna, and Paterson in 2006. In 2010, seventy-five simple sequence repeat (SSR) and 70 expressed sequence tag (EST) markers were identified to assess genetic diversity, identify cultivars of bermudagrass including those cultivars derived from 'Tifgreen', confirm pedigrees, and differentiate contaminants from cultivars. In the field, two replicated field trials of the B17 F1 mapping population were planted in Tifton and Griffin, GA to assess the phenotypic variation of these bermudagrass plants as observed in two distinct environments.

Summary

- **During 2014:** Much of our time was spent going through the development of the diploid African bermudagrass map and the tetraploid common bermudagrass map, separately. The SSR markers screened by the Paterson lab were added to the previous maps published that used AFLP markers. Considering the previous publication, many SSRs were thrown out to avoid inflating any linkage group while maintaining the base chromosome count found in the bermudagrass species. Prior to the visit, initial analysis of phenotypic data collected in the field over multiple years and locations was conducted to perform preliminary QTL identification.
- **To Date:** Both of the maps have been finalized and attempts were made to join the maps together to find homologous linkage groups between the two species. In addition, each of the phenotypic traits (16 traits total; both quantitative and qualitative) have been analyzed across locations and years for genotype means, genotype × location interaction means, genotype × year interaction means, and the three way interaction between genotype, location and year for a complete QTL identification search. Furthermore, the qualitative traits were evaluated for expected genotypic ratios corresponding to monogenic or polygenic characteristics.
- **Future Work:** Analyses to identify QTL using the finalized maps and the means obtained from the phenotypic, quantitative means still remain. These processes will hopefully detect associations between tightly linked markers and the genes controlling the trait. The qualitative traits that segregate in a dominant ratio (3:1) will be treated as a dominant marker and can be added to each map based on presence/absence. The position of each pseudo marker may be tightly linked to an existing genetic marker. In either case, quantitative and qualitative, each marker associated with the traits of interest can be used in breeding programs for selection.