# Production, Maintenance, and Evaluation of Triploid Interspecific Bermudagrass Hybrids for QTL Analysis

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#### **Objectives:**

- 1. Increase the size of the T574 x T89 mapping population by 100 or more triploid interspecific hybrids.
- 2. Evaluate the hybrids for characteristics important in turf improvement and provide the information to Dr. Paterson for association to the molecular map.

### Start Date: 1999 Project Duration: ongoing Total Funding: \$90,000

Hand pollinations of the Cynodon

*transvaalensis*-T574 x *C. dactylon*-T89 cross were made in the spring of 2007. Crosses were harvested and the products of this cross were planted in the greenhouse in the spring of 2008.

Progeny were transplanted to 5cm pots, and single plants were established in 2m x 2m plots (methyl bromide fumigated soil) in the field in 2008. We were able to produce 20 new hybrids (confirmed with flow cytometry). Plant samples have been made available to A. Paterson for the molecular study.

The maintenance nursery for the triploid hybrids was re-established in 2008 in newly fumigated soil to maintain the purity of the stocks.

After analyzing the data on seed





The interspecifice triploid hybrids ranged in color from 1 to 3 ( $LSD_{0.05} = 1.5$ ), in turf quality from 4 to 8.5 ( $LSD_{0.05} = 1.8$ )

The products of the cross between C. tranvaalensis-T574 and C. dactylon-T89 are being propagated and established in field plots on 2- meter by 2-meter centers at the University of Georgia research facilities.

head formation, longest stolon, plant radius, texture, and vigor which we collected on the hybrids during the past three years and provided to Dr. Paterson, he found 105 (however, he indicated that this may be a little over-estimated) statistically significant QTL marker trait associations.

## **Summary Points**

• QTL molecular marker associations (105) were found for seed head formation, longest stolon, plant radius, plant texture, and vigor in the bermudagrass hybrids.

• New hybrids have been developed to add to the population for use in the genetic map.