

# A Turfgrass Genome Project: Integration of *Cynodon* Chromosomes with Molecular Maps of the Cereals

**University of Georgia**

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Start Date: 1999

Number of Years: 5

Total Funding: \$125,000

Objectives:

1. *Establish a primary molecular map for the chromosomes of Cynodon.*
2. *Align the chromosomes of Cynodon with those of the major cereals, gaining access to much genetic information.*

We are integrating new DNA probes for *Cynodon*, with tools that have been previously mapped in other Poaceae, to develop a primary molecular map of the *Cynodon* chromosomes. The map will be useful for investigating many aspects of turfgrass population biology and genetics, and a molecular conduit for turf improvement to benefit from the large body of genetic information now accumulated about cereals and other grasses. *Cynodon* is chosen as a focal point for turf genome analysis due to its importance across the southern USA, and abundance of phenotypic variation. Dr Wayne Hanna has assisted in population development and maintenance.

To our knowledge, this project is the first effort to enable turf improvement to benefit from extensive genetic data for well-studied grains such as maize and rice. The "comparative approach" will reduce costs, and leverage much existing information and tools. Our experience in molecular analysis of complex populations such as sugarcane and buffelgrass, as well as grain crops such as rice, maize, and sorghum, together with our extensive repertoire of molecular tools, puts us in a strong position to efficiently develop a *Cynodon* molecular map useful for turf improvement.

**Progress to Date.** We have established techniques for bermudagrass DNA analysis, determined the genome size of *C. dactylon* and *C. transvaalensis*, demonstrated that there is ample DNA polymorphism between *C. dactylon* and *C. transvaalensis*, and begun to identify diagnostic DNA markers. We expect to have identified all the DNA differences needed by late 2000, and largely completed the map by late 2001, two years ahead of schedule. The mapping cross to be used (T89 x T574) is sufficiently large (126 individuals) that we will conduct some preliminary searches for QTLs directly in this cross.

**Plans for Continuation.** The focus of year 2 will be the scale-up of identifying DNA polymorphisms, and the beginning of genetic linkage mapping, using about 150 *Cynodon* probes (prepared) together with a sampling, of mapped probes from other taxa. Full-scale genetic mapping, will be done in year three. By the end of year three, we expect to meet the formal goals proposed for the full five years (data analysis may continue into year 4). We will then proceed to applying the map to identification of QTLs, and DNA markers diagnostic of agriculturally important traits, and also to development of a small BAC library for bermuda.