

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

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Objectives:

1. Establish a primary molecular map for the chromosomes of *Cynodon* (bermudagrass).
2. Align the chromosomes of *Cynodon* with those of the major cereals.

Start Date: 1999

Project Duration: 5 years

Total Funding: \$135,000

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. It will also serve as a molecular conduit for turf improvement to benefit from the large body of genetic information now accumulated about cereals and other grasses.

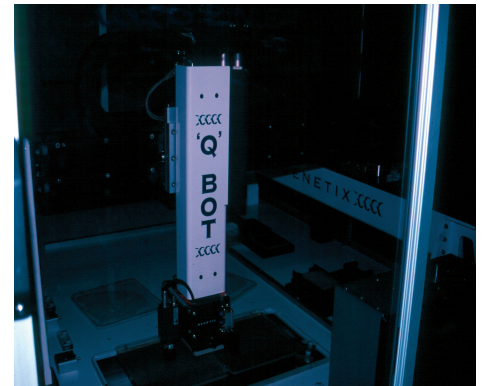
Cynodon is chosen as a focal point for turf genome analysis due to its importance across the southern USA and abundance of phenotypic variation. Dr Wayne Hanna will assist in population development and maintenance.

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.

We have established techniques for bermudagrass DNA analysis, determined the genome size of *C. dactylon* and *C. transvaalensis*, surveyed >740 DNA probes to identify an estimated 222 probes suitable for genetic mapping in *C. dactylon* x *C. transvaalensis*. We have mapped about 80 to date, detecting an estimated 160 loci. Based on this average of two informative loci per probe, the 222 probes are expected to yield more than 400 loci, including about 300 in *C. dactylon* and 100 in *C. transvaalensis*, providing initial genetic maps of each of these important species.

We have also sequenced about 100 *Cynodon* probes, providing the largest amount of *Cynodon* DNA sequence available to date (which is beyond the goals of our proposal). The mapping cross to be



At University of Georgia, Dr. Andrew Patterson uses new robot technology to perform some of the mundane tasks required to create a genetic map of bermudagrass chromosomes.

used (T89 x T574) is sufficiently large (n=126) that we will conduct some preliminary searches for quantitative trait loci with large phenotypic effects.

The focus of year five will be genetic linkage mapping of the remainder of the informative probes identified. This is expected to permit us to complete the "first draft", and permit initial exploration for QTLs and DNA markers diagnostic of agriculturally-important traits.

Summary Points

□ We have established techniques for bermudagrass DNA analysis, determined the genome size of *C. dactylon* and *C. transvaalensis*, surveyed >740 DNA probes to identify an estimated 222 probes suitable for genetic mapping in *C. dactylon* x *C. transvaalensis*.

□ We have also sequenced about 100 *Cynodon* probes, providing the largest amount of *Cynodon* DNA sequence available to date.

□ The focus of year five will be genetic linkage mapping of the remainder of the informative probes identified.



At University of Georgia, Dr. Andrew Paterson explains to research committee members how the genetic map of bermudagrass will be developed.