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

Andrew H. Paterson
University of Georgia

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.

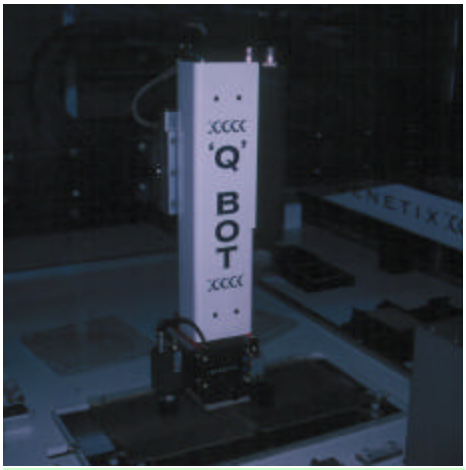
Start Date: 1999
Project Duration: 5 years
Total Funding: $135,000

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

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 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.



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.

We have established techniques for bermudagrass DNA analysis, determined the genome size of *C. dactylon* and *C. transvaalensis*, identified DNA polymorphism between *C. dactylon* and *C. transvaalensis*, and begun to identify diagnostic DNA markers. We have also sequenced about 100 *Cynodon* probes to be mapped, providing the largest amount of *Cynodon* DNA sequence available to date (which is beyond the goals of our proposal).

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 - realizing that we will only be able to detect those with large phenotypic effects.

The focus of year five will be genetic linkage mapping, using about 150 *Cynodon* probes (prepared) together with a sampling of mapped probes from other taxa. Recently, we decided that we would need more *Cynodon* DNA markers in addition to comparative probes from other taxa, so we have made a small *Cynodon* genomic library and begun to characterize about 1000 additional candidate markers.

We expect to complete the map this year, and will then proceed to apply the map to identification of QTLs, and DNA markers. We also plan to development of a small BAC library for bermudagrass.

Summary Points

- DNA analysis techniques were developed for bermudagrass and have been used to demonstrate ample polymorphism.
- Produced DNA sequence for the *Cynodon* probes to be used in the mapping efforts.
- A mapping cross with 126 individuals will be used to conduct some preliminary searches for quantitatively inherited traits (QTLs).