

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*.
2. Align the chromosomes of *Cynodon* with those of the major cereals.

Start Date: 1999

Project Duration: 5 years

Total Funding: \$125,000

Over the past decade, genome mapping has advanced from an expensive high-risk venture to a routinely-used tool in genetic improvement of many plants and animals. Genome mapping tools find routine use in DNA fingerprinting, genetic distance analysis of breeding materials, monitoring the behavior of genes in populations, DNA-marker accelerated transfer of agriculturally important genes, and molecular cloning of high-value genes.

A turfgrass genome project is timely, permitting turf improvement to benefit from extensive genetic information from the cultivated cereals. By "riding the coat-tails" of cereal genome analysis, we can quickly bring the opportunities and efficiencies of genome mapping to turf improvement at minimal cost.

We are integrating new DNA probes for *Cynodon* with tool's that have been previously mapped in other species of the 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. Development of this map will 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 United States and abundance of phenotypic variation. Dr. Wayne Hanna is assisting 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 buffalograss, 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*, demonstrated that there is ample DNA polymorphism between *C. dactylon* and *C. transvaalensis*, and begun to identify diagnostic DNA markers.

We have identified most of the DNA differences needed and are shifting our emphasis to preparation of DNA and blots to make the map of the segregating progenies. We have also sequenced the majority of *Cynodon* probes to be mapped and provided the largest amount of *Cynodon* DNA sequence available to date.

The mapping cross to be used (T89 x T574) is sufficiently large (126 individuals) that we will conduct some preliminary searches for quantitatively inherited



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

traits directly in this cross, realizing that we will only be able to detect those with large phenotypic effects.

The focus of year three will be genetic linkage mapping, using approximately 150 *Cynodon* probes (prepared) together with a sampling of mapped probes from other taxa. By the end of year 3, we expect to be near the formal goals proposed for the full 5 years (some mapping and data analysis may continue into year four).

We will then proceed to applying the map to identification of quantitatively inherited traits (QTLs), and DNA markers diagnostic of agriculturally-important traits, and also 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).



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.