

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: \$125,000

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

Cynodon was 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 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" reduces costs and leverages 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,



Researchers at the University of Georgia have established techniques for bermudagrass DNA analysis, determined the genome size of *C. dactylon* and *C. transvaalensis*, and produced genetic maps for *C. dactylon* x *C. transvaalensis* progeny.

together with our extensive repertoire of molecular tools, put us in a strong position to efficiently develop a *Cynodon* molecular map useful for turf improvement.

We established techniques for bermudagrass DNA analysis, determined the genome size of *C. dactylon* and *C. transvaalensis*, and produced genetic maps for *C. dactylon* x *C. transvaalensis* progeny totaling 449 loci (a minimum of 360 was the goal of our grant).

We have also sequenced about 100 *Cynodon* probes (which is beyond the goals of our proposal) and will be sequencing additional probes toward integration of the *Cynodon* map with the sequence of rice and the maps of sorghum, maize, and other major crops. The mapping cross to be used (T89 x T574) is sufficiently large that we will conduct some preliminary searches for QTLs (quantitative trait loci) with large phenotypic effects as fringe benefits that will come at no additional cost. We will complete data analysis and manuscript preparation.



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

Summary Points

- Researchers have established techniques for bermudagrass DNA analysis, determined the genome size of *C. dactylon* and *C. transvaalensis*, and produced genetic maps for *C. dactylon* x *C. transvaalensis* progeny totaling 449 loci.

- They have also sequenced about 100 *Cynodon* probes (which was beyond the goals of the proposal) and will be sequencing additional probes toward integration of the *Cynodon* map with the sequence of rice, and the maps of sorghum, maize, and other major crops.