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

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Project Description: 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.

How Ours is Different: 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 – realizing that we will only be able to detect those with large phenotypic effects – however these will come at no additional cost, so are unexpected fringe benefits.

Plans for Continuation: The focus of year 2 will be the scaleup 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 3 -- by the end of year 3, we expect to meet the formal goals proposed for the full 5 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.

A detailed summary of progress and supplemental materials discussed during the site visit is attached.

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A. Executive Summary – review basis for this project (copy attached).

B. Populations developed, and rationale for choice (table attached).

- tissue from mapping progeny is lyophilized and will be processed after we complete surveys and start labellings

C. DNA content of C. dactylon and C. transvaalensis (data attached) –

- Unexpected that it was so similar, as CD is tetraploid and CT is diploid – suggests that they may be quite divergent (consistent with RFLP data – below).
- Suggests that for longer-term goals (physical mapping and gene map assembly), there may be little gained by working with the diploid genome of CT, that it may be better to work with CD

D. DNA extraction procedures (not yet attached – still evolving).

E. Early results from pCD (Cynodon clones) (Erica to bring films)

- high level of DNA polymorphism, suggesting that mapping will be routine.
- ca. 40 surveys generated, aiming for 100.

F. Selection of comparative probes
- List of comparative probes used in sorghum and other taxa (attached) – sample 10 from each group, decide which groups to focus on
- Aim is to have a sufficient number of comparative probes that they represent all regions of all chromosomes of sorghum (and consequently other grasses)
- In addition, all of the ca. 200 pCD clones will be surveyed, and all of those detecting polymorphism will be mapped. Those that can be mapped in sorghum, will also be added to the sorghum map and become comparative probes.

G. Timetable
- Expect to have sufficient survey data by mid-2000
- largely-complete map by mid-2001 (2 years ahead of timetable)
- integrate with overall comparative genetic/physical map of grasses (figure attached).
- Probably will then explore for QTLs in mapping population – while it is a bit small, it may be adequate to find genes with largest effects.

H. Longer-term goal – 'comprehensive gene map' and 'physical map'
- Requires a BAC library (cost about $75,000 by taking advantage of our automation)
- May require generation of Cynodon EST database – which is also warranted for other reasons – cost of a comprehensive EST database and data archival/retrieval system would be about $2-3 million

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