

# Scientists Unveil Bermudagrass Genetic Map

Growing legal and fiscal pressures could require genetic testing of sod for golf course construction and maintenance projects

By Andrew H. Paterson

**B**ermudagrass (*Cynodon* sp.) is a resilient perennial grass popular in the golf and turfgrass industries, owing to its ability to generate a variety of textures, its rapid recovery, and its low-growing nature that allows it to tolerate very close mowing. It is widely used in landscaping because of its ability to grow well in a wide range of soil conditions, as well as its fast growth rate. Seeded bermudagrass can spread to provide full coverage of 1,000 square feet within four to six weeks after planting, and it maintains active growth through the warm summer when many other grasses temporarily decline.

Despite its economic importance and the fact that the grass family (Poaceae) in general is one of the better-studied plant families, bermudagrass represents a subfamily (Chloridoideae) that is underexplored at the DNA level.

Moreover, many bermudagrass genotypes are polyploids, receiving not one but two or more sets of chromosomes from each parent. Polyploidy is thought to offer advantages such as the preservation of multiple alleles (slightly different versions of a gene) that provide adaptation to a broader range of environments or a wider range of pests than otherwise would be possible. However, polyploids also tend to hinder the rate at which breeders can make genetic changes in the crop.

Recently, the first detailed genetic maps of the bermudagrass genome were produced based on analysis of a cross between two bermudagrass species, *Cynodon dactylon* and *Cynodon transvaalensis* (Bethel et al. 2006). Other crosses between these species have generated most leading bermudagrass turf cultivars.

The map of *Cynodon dactylon*, a tetraploid (i.e. with four sets of chromosomes) is based on 189 DNA markers, or mileposts along the

roadmap of the genome. The map of *Cynodon transvaalensis*, a diploid (with just two sets of chromosomes) is based on 77 DNA markers. The present maps are thought to cover more than 60 percent of the bermudagrass genetic blueprint — additional markers are needed to cover the remainder.

The genetic maps provide bermudagrass researchers with the means to identify diagnostic DNA markers for important traits that differ among cultivars or breeding lines. For example, the identification under controlled conditions of DNA markers that are diagnostic of important traits, such as resistance to major diseases, using widely adopted approaches (Paterson et al. 1988) can reduce the need to screen for such diseases repeatedly in breeding programs. Similarly, diagnostic markers for stresses, such as drought, that might or might not occur during any one growing season, permit selections to be made even when the stress does not occur (Paterson et al. 1991).

It is important to note that the identification of a set of DNA markers that are diagnostic of a particular trait can take several years of careful research by skilled individuals. However, once established, the diagnostic marker has long-term value.

Its genetic map also will allow bermudagrass researchers to benefit from rapid advances in understanding the functions of specific genes in the genomes of fully-sequenced cereals, such as rice and sorghum. The fact that grasses largely share a common set of genes (Hulbert et al. 1990), many of which are in common order (Ahn and Tanksley 1993; Paterson et al. 1995), made it important to align the bermudagrass map to the sequences of leading cereal models.

By using fully sequenced genes from

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bermudagrass, rice and sorghum as reference points in the genome, it was possible to begin the alignment process.

Comparisons conducted using our framework map produce significant matches to regions of all 12 rice chromosomes and to regions of all 10 sorghum linkage groups. While some chromosomal re-arrangements have inverted blocks of genes in one taxon relative to another, a useful degree of predictive value appears to exist. This says that the completed rice and sorghum sequences will be of high value in predicting the locations of genes that serve corresponding functions in bermudagrass, accelerating progress in its study and improvement.

This will permit bermudagrass researchers to make increasingly educated guesses about which genes in bermudagrass are performing key functions, based on rapidly growing knowledge of the genes that perform corresponding functions in rice, sorghum or other grasses for which the genomes have been fully sequenced.

Indeed, the genetic map is a starting point for eventual sequencing of the genome of bermudagrass itself. A first step toward sequencing of a genome is the development of a framework of well-distributed DNA markers important to bridging the gap between the level of resolution at which DNA can be manipulated by molecular biology and the level by which it is reshuffled naturally by recombination. While comparison to the completed sequences of model grasses might teach us much about the common features that bermudagrass shares with other grasses, learning about its unique features likely will require more information about bermudagrass itself.

Building on technological improvements being pioneered in mammalian genomics, DNA sequencing continues to become more rapid and cost-effective. It is likely that in the next 10 to 20 years, the genomes of most plants and animals that are economically important, including bermudagrass, will be sequenced (Paterson 2006).

DNA markers from the bermudagrass map also provide the means to implement DNA fingerprinting to ascertain

the genetic identity of bermudagrass sod, assuring that both the industry and its customers reap the benefits of success in bermudagrass improvement.

In high-value markets such as the golf industry, the lack of molecular tools in the past has meant there was often far more control exercised over features such as the size of sand grains in the bunkers than the identity of grass planted on the fairways.

Recent cost trends and legal actions provide growing momentum for establishment of genetic quality-control testing of sod as a mandatory component of golf course construction and maintenance. DNA-based methods can fill these needs in much the same manner they have provided forensic tools for study of human populations.

In summary, DNA-based genetic maps contribute a new and important dimension to bermudagrass improvement. By taking greater advantage of rapidly advancing knowledge of gene functions in cereal models, such as rice and sorghum, bermudagrass improvement likely will be accelerated and empowered to tackle previously intractable problems.

Greater investments in bermudagrass improvement might be justified by DNA-based genetic quality-control testing, assuring that both the industry and its customers reap the expected benefits of accelerated genetic improvements.

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