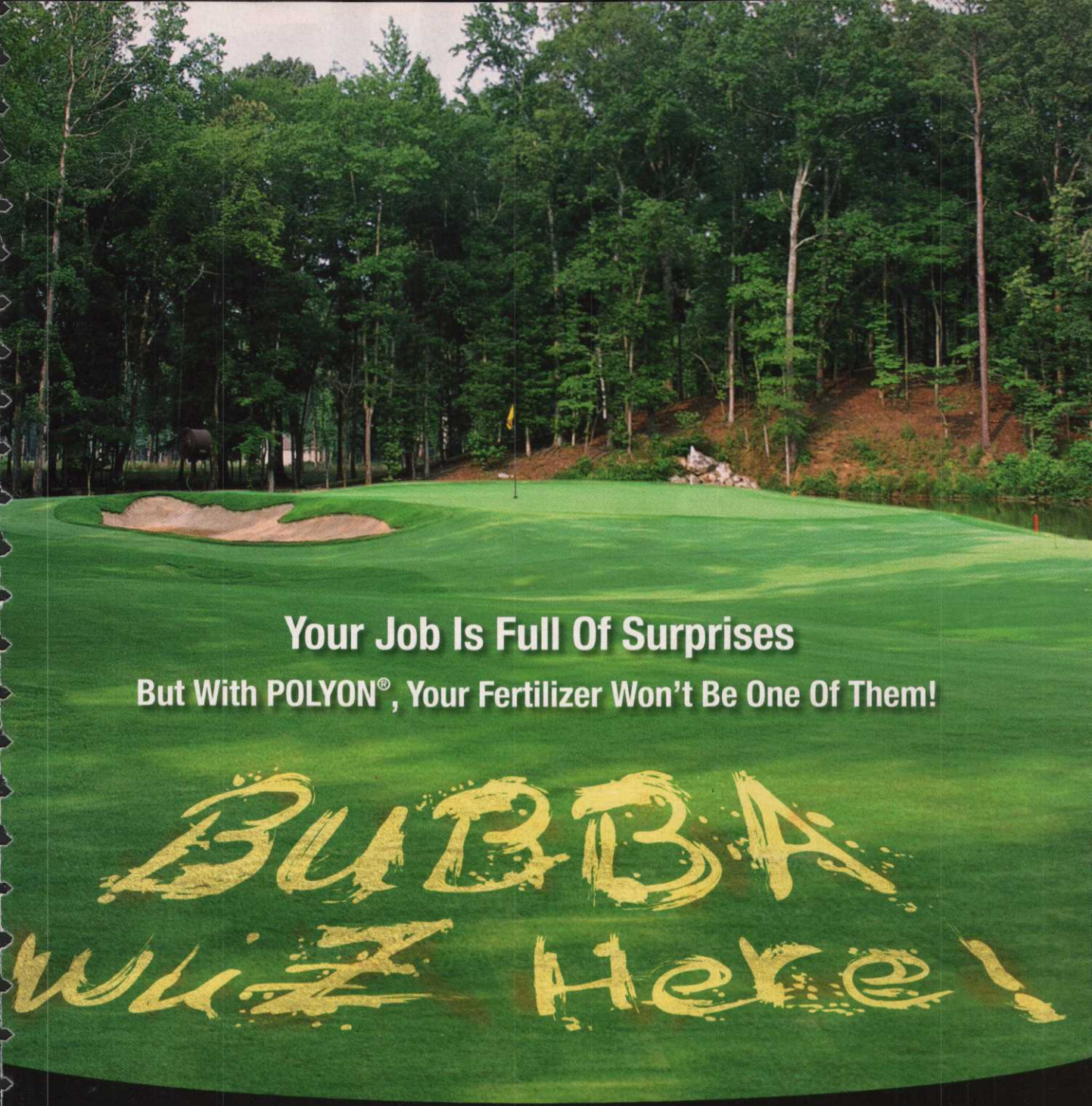

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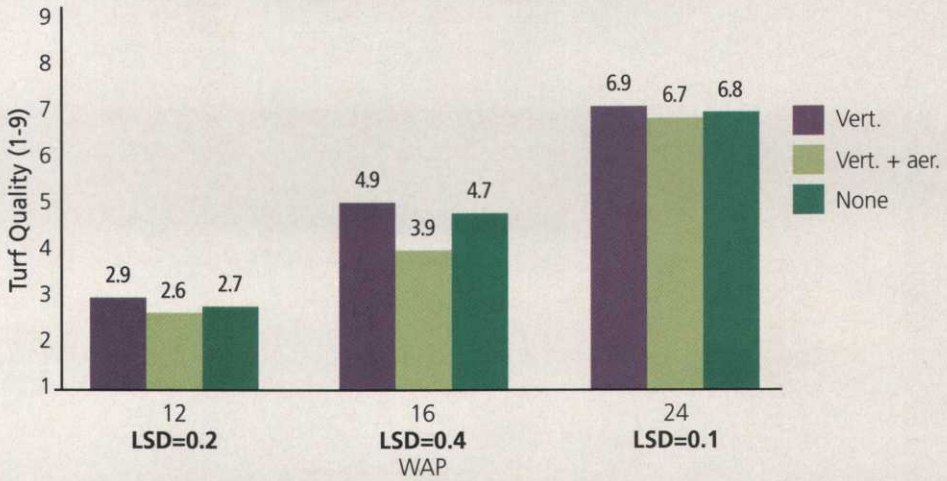
TABLE 2

Effect of Seedbed Preparation Techniques on Turf Quality



DAP: days after planting, WAP: weeks after planting, LSD: least significant difference (P=0.05).

Continued from page 50

tion, and no seedbed preparation resulted in an acceptable playing surface at 24 WAP, indicating the seedbed preparation might not be required.

At one year after treatment, which was one month after the 128 fl oz/a Roundup application, the previously treated plots exhibited no phytotoxicity. But the nontreated areas, which received seedbed preparation and were seeded but received no Roundup until 11 MAP, were completely desiccated (100 percent phytotoxicity), regardless of seedbed preparation technique. These data indicate Roundup applications during establishment are critical as no RRCB were present in previously nontreated plots, although initial Roundup application timing may range from at seeding to two weeks after seeding. The broader implication of this treatment indicates that interseeding new and improved cultivars into existing bentgrass can be an unsuccessful practice. Also, in the previously treated plots, it demonstrates RRCB was tolerant of postemergent Roundup applications totaling 352 fl oz/a in nine applications in 12 months.

In additional research trials, RRCB was seeded into a conventionally prepared seedbed to compare the establishment and maintenance of RRCB compared to several nontransgenic creeping bentgrass cultivars, including Crenshaw, Penncross, Penneagle, Providence, Backspin, A4 and L93. Data from these trials indicate RRCB responds similarly to conventional nontransgenic bentgrass cultivars grown under fairway conditions with the exception of tolerance to Roundup. Additionally, RRCB established from seed grew in similarly to nontransgenic bentgrass cultivars, indicating seeding RRCB is a viable option for RRCB establishment. Other significant differences in growth habits or characteristics were not noted during the trial period.

The authors would like to thank Hennen Cummings, Jason Hinton, Scott McElroy, Walt Pierce, Leon Warren and Bill Whaley for their efforts initiating the research trials. USGA and The Scotts Co. funded this research.

Travis W. Gannon, research associate at North Carolina State University, Department of Crop Science, can be reached at travis_gannon@ncsu.edu.

Fred H. Yelverton, PhD., professor and co-director of the Center for Turfgrass Environmental Research and Education at NC State, can be reached at fred_yelverton@ncsu.edu.

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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

Bermudagrass (*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

Continued on page 56

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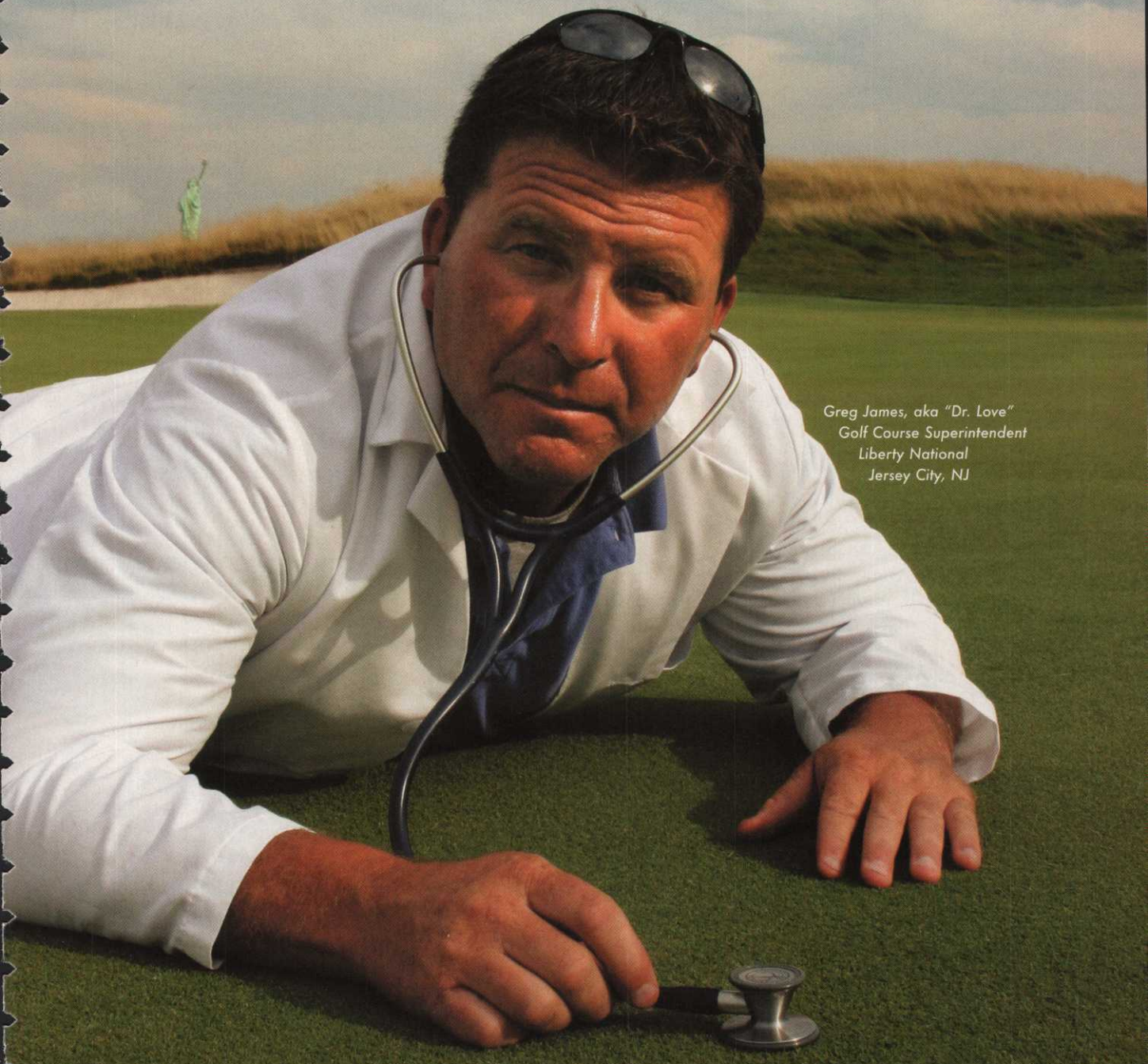

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Continued from page 54

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 successes 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.

Andrew H. Paterson is a distinguished research professor at the University of Georgia Plant Genome Mapping Laboratory.

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TURFGRASS TRENDS

SECTION STAFF

Managing Editor
Curt Harler
440-238-4556; 440-238-4116 (fax)
curt@curtharler.com

Graphic Designer
Kristen Morabito
216-706-3776; 216-706-3712 (fax)
kmorabito@questex.com

Golfdom Staff Contact
David Frabotta
216-706-3758; 216-706-3712 (fax)
dfrabotta@questex.com

INDUSTRY ADVISORS

Bill Byrnes
Floratine

Jeff Higgins
Pursell Technologies

Jerry Quinn
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Scott Welge
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CONTACT US:

Web site: *www.turfgrasstrends.com*
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Golfdom Sales Staff

Pat Roberts
Publisher
600 Superior Avenue, East, Suite 1100
Cleveland, OH 44114
Phone: 216-706-3736
Fax: 216-706-3712
E-mail: *proberts@questex.com*

Kevin Stoltman
Group Publisher
Phone: 216-706-3740
Fax: 216-706-3712
E-mail: *kstoltman@questex.com*

George Casey
National Account Manager
Phone: 216-706-3752
Fax: 216-706-3712
E-mail: *gcasey@questex.com*

Dave Huisman
Regional Sales Manager
Phone: 732-493-4951
Fax: 732-493-4951
E-mail: *dhuisman@questex.com*

Brian Olesinski
Account Executive, Classified
Phone: 216-706-3757
Fax: 216-706-3712
E-mail: *bolesinski@questex.com*

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CONFECTIONS CAN CELEBRATE THE SEASON AND PROVE GREAT JOY CAN COME IN LITTLE PACKAGES

BY MARK LUCE

One doesn't normally admit to crimes in public. However, in this case, my gut tells me that you've been in the same place. The scene: A grocery store. Alone. You pass the by-the-piece candy display. Suddenly, the caramel seductively coos, "You want me. You want me." Well, yes, I do. But not a pound of you. Sly fingers nab two or three, transferring them effortlessly into a closed fist. You flee to the next aisle to unwrap, and the sweetness envelops your mouth.

The ethics of such a discount? Slippery, at best. I got into the habit of confessing my behavior to the checkout clerk. Mostly, they grinned with familiarity. Occasionally, they charged me nine cents.

While we all know what scarfing down caramels by the fistful will do to your waistline and tooth enamel, it seems to me that October should be a caramel celebration month. Think of it this way: If the leaves on trees (any of them, anywhere) are the color of caramel, you remain free to chew the sugary ambrosia until your heart's content.

Further, because October tends toward raucous behavior anyway — Oktoberfest with its brats and beers, and Halloween with its tricks and treats — commemorating the goodness

perfected by Arabs in the 11th century makes all the more sense.

Best of all, there's a great rationalization for skipping down the caramel path: caramel apples, which bring together the best of October worlds.

Fresh apples give us mega doses of fiber, a heap of potassium and vitamin C, contain no fat and can aid in the prevention of cancer and heart disease. Caramels possess a smidgen of calcium, and they taste good. When twirled together it's almost healthy … sort of.

So when those leaves begin to turn, gather up the following and get to spinning. First, you need four apples that match your palate, whether Granny Smith (green and tart), Macintosh (juicy and tender) or Red Delicious (crispy and sweet). Next, pick up a 14-ounce package of caramels from the store, along with some popsicle sticks. It is possible to make your own caramel (there are plenty of recipes online), but it will take much more trial and error.

Twist off the stems of the apples and shove the popsicle sticks in far enough to provide a sturdy base. Then set out either a lightly greased cookie sheet or some wax paper.

Testing your will power, unwrap the little morsels and drop them into a deep, microwave-safe bowl with about two tablespoons of water. Nuke on high for about three minutes, stirring after each minute until the mixture is smooth.

Dip the apples fully into the caramel, spinning them to coat the apple. Then, with care, transfer them to the cookie sheet or wax paper. Once completed, put the apples in the refrigerator for about 15 to 20 minutes to let the caramel set.

Pour yourself a glass of milk or some hot cider and enjoy this match made in October heaven.

Mark Luce is a freelance writer based in Kansas City, Mo., where he's increasingly tempted to concoct a caramel-apple martini.

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