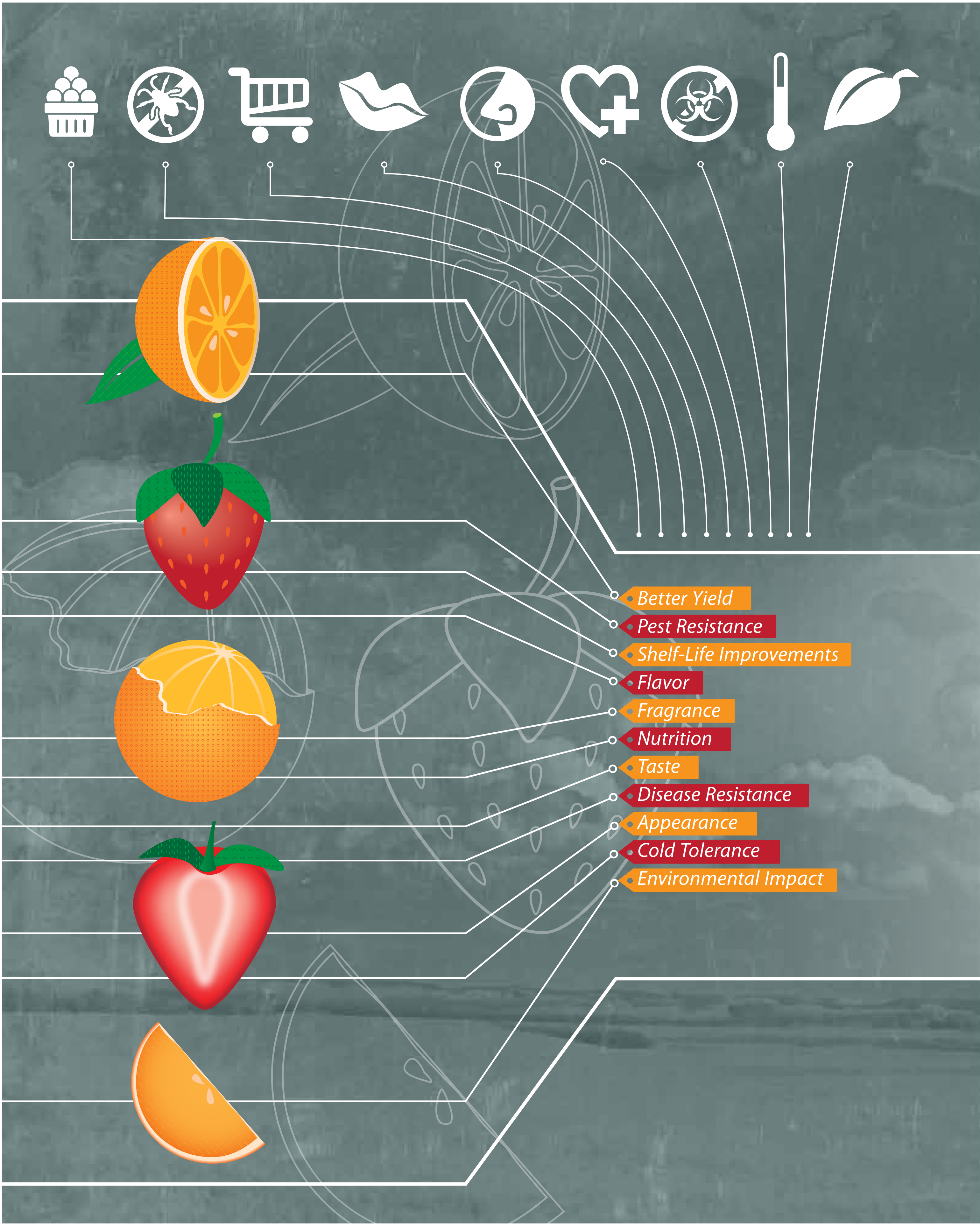


Illustrations by Paul Messal

Agricultural Assembly Line

By decoding the genomes for two fruits vital to Florida's economy, UF researchers are helping to write the agricultural instruction manual

By Mickie Anderson

Since the beginning of agriculture thousands of years ago, farmers have taken the seeds from the tastiest, hardiest fruits and vegetables and replanted them with the hope that the next generation would be even better.

Today, scientists are creating a genetic instruction manual that will allow them to program traits such as pest resistance, cold tolerance and taste directly into a plant's DNA.

Last winter, University of Florida plant researchers released genome sequences for a strawberry and two citrus varieties that ushered in a new era of plant genome research.

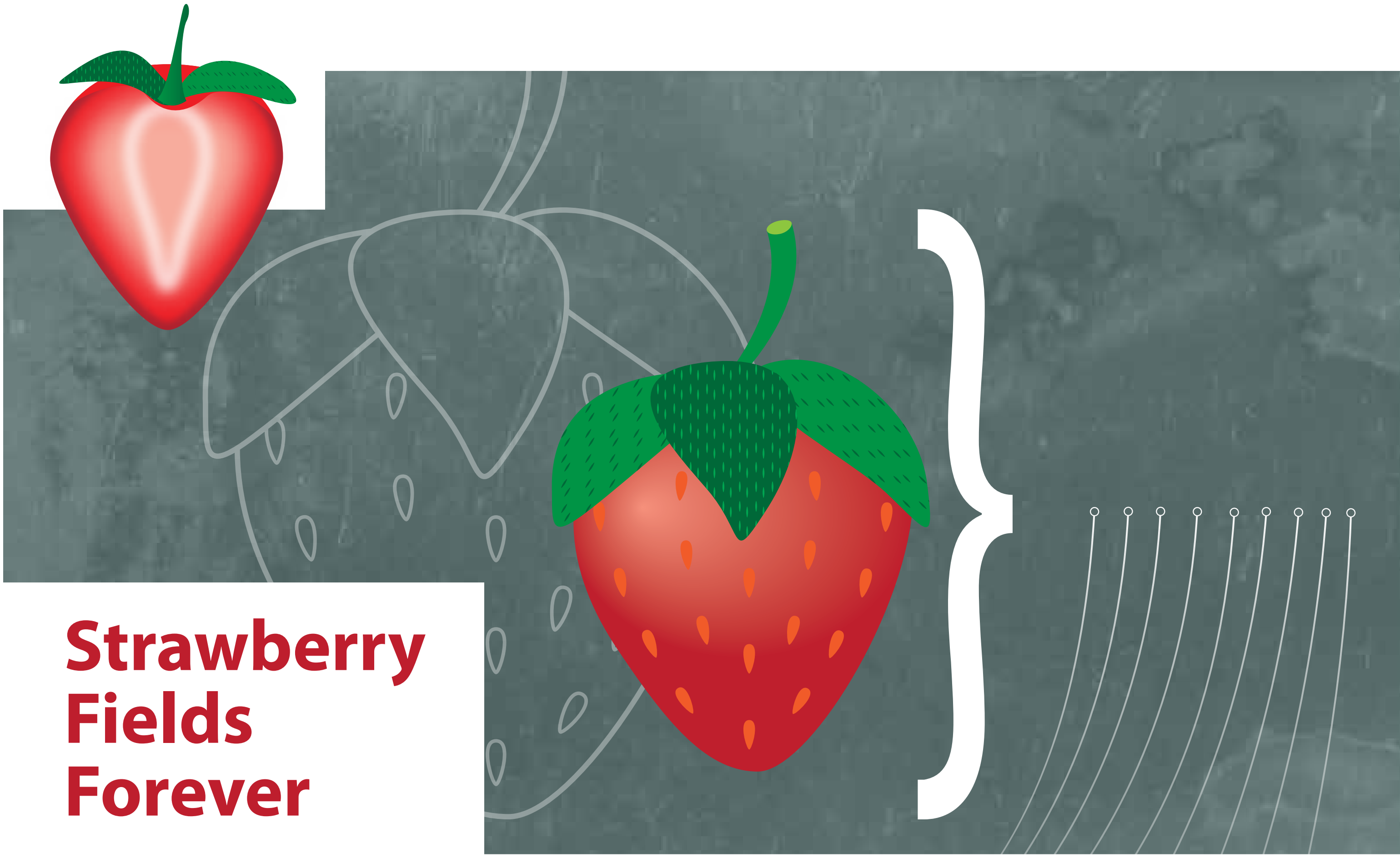
In late December 2010, an international team of 75 researchers from 38 institutions around the world led by UF's Kevin Folta published the DNA sequence for the woodland strawberry in the journal Nature Genetics.

"We've created the strawberry parts list," says Folta, an associate professor of horticultural sciences. "For every organism on the planet, if you're going to try any advanced research, such as molecular-assisted breeding, a parts list is really helpful. In the old days, we had to go out and figure out what the parts were. Now we know the molecular nuts and bolts that make up the strawberry plant."

Having that "parts list" in hand will enable strawberry breeders to bring new varieties to market faster, creating plants that can be grown with less environmental impact, better nutritional profiles and larger yields.

"All of those dividends are probably at least a decade off, but they are definitely realities on the horticultural radar screen," says Folta, a member of the UF Genetics Institute.

In January, UF's Fred Gmitter announced the genome sequences for two citrus varieties, sweet orange and Clementine mandarin, at a genome conference in California. Those discoveries could have more immediate impact on growers' efforts to thwart industry-threatening diseases like citrus greening.



Strawberry Fields Forever

The strawberry genome sequence has implications far beyond the tasty red fruit. That's because the woodland strawberry is part of the Rosaceae family of flowering plants, which includes many important agricultural and ornamental crops such as apples, peaches, plums, cherries, raspberries, almonds and roses.

Having a fully mapped strawberry genome may mean quicker breeding advances for all of those crops, Folta says. For the strawberry itself, the sequence could lead to breeding advances such as firmer fruit that can better withstand shipping. As with citrus, more nutritious fruit with greater yields and stronger disease resistance are also possible outcomes.

Folta says the strawberry could also become a workhorse in the laboratory.

Strawberry is an excellent crop for scientists to use in genetic and physiological studies, Folta says, because it takes so little space to grow and is a quick-turnaround crop, unlike some others in the Rosaceae family, such as peach, which can take several years to bear fruit.

Folta says he believes strawberry has many factors that make it ideal for genetics research.

"Already in the six years I've been working with strawberries, there's been a real upsurge in interest in the system," he says. "Arabidopsis (a fast-growing mustard plant) was an excellent model and still is. I still use it all the time. But strawberry offers an inroad into specialty crops with tremendous economic value. So this is a system where you can study gene function in a relevant background — and that makes it extremely attractive."

"I think in 10 years you'll see many, many laboratories using strawberries as a system to study their biological questions."

Another unique thing about the strawberry project is that it was the first plant analyzed entirely through short-read sequencing, meaning that smaller fragments of DNA were contributed by various teams, and later put together into one longer stream by software designed for that purpose.

Folta explains it like this: "If you had the alphabet from A to Z, and someone gave you a piece that was A-B-C, and another piece was C-D-E-F, and another piece that was E-F-G-H, you could align all those using the common letters, and eventually develop the whole alphabet."

Ted Campbell, executive director of the Florida Strawberry Growers Association, calls the genome sequencing a "very significant milestone" for growers around the world — including those in Florida, where strawberries are a $338 million-a-year commodity.

Todd Mockler, an Oregon State University associate professor and member of the genome-sequencing team, says it may be a few years before the discovery is noticeable to consumers — but positive changes will come.

"For fruit crops, and strawberry in particular, it will matter to farmers and, ultimately, to consumers," he says. "It may mean better yields or pest resistance, improvements in shelf life and things like flavor, fragrance, taste and appearance. Having the genome sequence will enable all of that."

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>
> ↳ **KEVIN FOLTA**

Orange Crush

While the strawberry scientists are still figuring out all the ways they'd like to apply their new-found knowledge, citrus researchers had a much more immediate reason for sequencing the genomes for sweet orange and Clementines.

Growers have high hopes the knowledge will bring breakthroughs in scientific research aimed at understanding and fighting the bacterial disease citrus greening. Since greening's presence was first confirmed in Florida in 2005, it has been found in 34 counties, making it a major threat to Florida's $9.1 billion citrus industry, says Gmitter, a horticultural sciences professor at UF's Citrus Research and Education Center at Lake Alfred southwest of Orlando.

Greening slowly weakens and kills most types of citrus trees, while leaving fruit malformed and discolored. It has decimated some citrus crops in Asia, Africa, the Arabian Peninsula and Brazil. Two international teams worked to obtain citrus gene sequences. The Clementine mandarin team included scientists from UF, Italy, Brazil, France, Spain and the U.S. Department of Energy's Joint Genome Institute (JGI). The sweet orange sequence was completed by scientists from UF, JGI, Georgia Tech and the Roche Company 454 Life Sciences.

Florida citrus industry officials says they were thrilled, and relieved, by the news that the genome sequences had been complete.

"The publication of the sweet orange and Clementine mandarin genomes will accelerate the discovery of innovative solutions to a myriad of pest and disease problems that threaten citrus production," says Dan Gunter, chief operating officer of the Citrus Research and Development Foundation Inc.

Michael W. Sparks, executive vice president and CEO of Florida Citrus Mutual, a trade organization comprised of 8,000 members, called genomics "the future of not only Florida citrus but the entire global citrus industry."

"It is exciting to see breakthroughs such as the release of these (genome) assemblies, and I am confident the talented scientists working on this project will eventually propagate a citrus cultivar that withstands disease pressure and allows consumers worldwide to continue enjoying nutritious citrus products," he says.

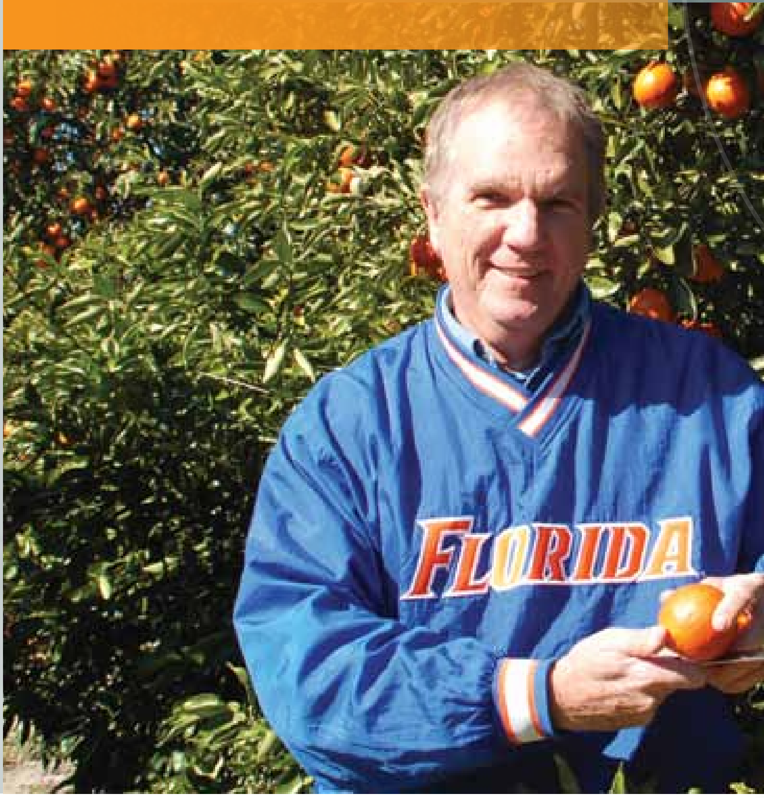
Potential applications for the citrus genome sequences are nearly endless, Gmitter says. For example, researchers have long known that some types of citrus tolerate the greening pathogen better than others.

"There's no kind of citrus that's absolutely resistant, but there are some that are more tolerant and the question is why? Why, if a lemon tree is infected with huanglongbing (HLB), does it look terrible and then grow lush in the spring and have loads of fruit, and then start declining again and then come back, when oranges just collapse and die? What's going on?"

Having the genome lets the citrus scientists play detective and find out specifically what the differences are and how they're being expressed, he says, "and we can put this huge puzzle together a whole lot better."

The Clementine mandarin genome came from a haploid, meaning it has a single set of chromosomes. The scientists used a more detailed method of obtaining its genome sequence, which was more expensive, but provides longer strings of DNA, Gmitter says.

> *"Potential applications for the citrus genome sequences are nearly endless."*
>
> ↳ **FRED GMITTER**



"It gives you longer reads, longer pieces — so that you're assembling a jigsaw puzzle out of a million pieces, instead of out of 25 million smaller pieces," Gmitter says. "What's most important is to have this high-quality, original haploid reference sequence. And we did that."

Beyond the immediate disease worries, Gmitter's lab is focused on improving the health benefits of citrus fruit as well as its flavor and other qualities. Having citrus genome sequences makes such goals more approachable, he says, not only by gaining a better understanding of the genetics and the metabolism behind citrus fruit qualities but also by translating that information into tools to speed up the breeding process to develop those traits.

But while the two new genome sequences may provide just the tool scientists need to help them solve the greening crisis, Gmitter says having them is "really much, much, bigger than that."

Some of the possibilities, he says, include citrus trees with more beautiful fruit, better disease resistance, more phytonutrients, and tolerance for salt, bad soil or extreme temperatures.

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Related websites
http://www.strawberrygenomics.com/
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