21st-Century Sugar Beet Breeding

A sugar beet can be likened to a factory. To uncover the blueprint for the factory, ARS started a sugar beet genome project 5 years ago. You could say that proteins—coded by genes—are the workers. By understanding the proteins—through unraveling the codes for the library of genes that produce them—we will one day learn what the sugar beet factory has to do to make a beet that is profitable to both farmers and industry.

The sugar beet genome consists of the complete set of chromosomes that are in the nucleus of every cell of a sugar beet. Genomics, the relatively new science of genome analysis, uses the latest genetic methods to extend traditional breeding. But it does not require use of genetic engineering. Genomics makes it possible to breed plants that possess a desired combination of genes selected from the entire sugar beet genome.

As the story on page 4 shows, we at ARS—with substantial funding from the Beet Sugar Development Foundation—have begun a revolution in the United States that will change sugar beet breeding from traditional trait-based to gene-based selection. This means that farmers and the rest of the industry will be able to order custom sugar beet varieties selected for the genes they contain. An understanding of the genes and proteins will make breeding faster than ever, because we will be able to predict outcomes of crosses and choose the most efficient routes to achieve desired ends.

All this means that better sugar beet varieties are on the way—and fast!

To unravel the code the sugar beet blueprint is written in, we need what Mitch McGrath—a geneticist at the ARS Sugar Beet and Bean Research Unit at East Lansing, Michigan—calls an "alphabet soup" of genetic tools, such as ESTs (expressed sequence tags), BACs (bacterial artificial chromosomes), and RILs (recombinant inbred lines). We have to build these tools for sugar beets because very few members of its plant family have been mapped.

Though we are in our first decade of this revolution, there are already more than 20,000 ESTs; 5,000 RILs are on the way; and a BAC library is in hand that covers the sugar beet genome 5 times over.

The East Lansing group and two independent groups in Germany deposited the ESTs into the National Center for Biotechnology Information's GenBank site (www.ncbi.nlm.nih.gov). The sequence tags identify probably one-third to one-half of the 30,000 genes thought to make up the operational blueprint for the sugar beet factory.

The RILs are specially bred to breed true, allowing us to separate the effects of genes from the effects of disease, drought, or other environmental factors. The BAC library has been built in collaboration with ARS scientists at Fargo, North Dakota; Fort Collins, Colorado; and Salinas, California.

These tools have helped McGrath and his team develop possible genetic markers for the genes that control the proteins that enable sugar beet seeds to sprout and the seedlings to survive the critical month when they're at their weakest stage. This is the top concern of farmers.

McGrath has also found a possible marker for high sugar levels in beets. Along with yield, sugar content is the second major area of concern to farmers and the industry. And McGrath's team is on the trail of the genes for resistance to two major seedling disease agents: *Aphanomyces* and *Rhizoctonia.* Disease is the main threat to a seedling's survival its first month.

The way genetics is advancing today, undoubtedly by the next decade we'll be working with tools that don't exist today, adding still more to this highly productive mix of technologies.

The BAC library is the first step toward creating order in these early days of sugar beet genome mapping. We don't even have a common language for any of the sugar beet's nine chromosomes. But we at ARS work very closely with university and industry scientists around the world to build advanced tools.

Thanks to ESTs, BACs, and RILs, we are already gaining insights into solving problems once thought to be unsolvable. And progress is likely to accelerate as these investments in genomics are leveraged with scientific expertise from inside and outside the sugar beet community.

Just as the work of genetic researchers mapping the genomes of other plants, such as rice, has given us a head start on sugar beet mapping, we expect that our work will be useful to future efforts.

Genomics has made it possible to use the same basic tools to decode the blueprint for plant factories that make widely different products. Lessons learned in building genetic deciphering tools for one crop can save a lot of time and money in building them for others.

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