

## Genomics—A New Gene Pool of Potential

*Genomics.* It is one of the hottest buzzwords in science today. But it's far from being simply a new toy for making genetic improvements.

Genomics refers to mapping and sequencing of the genetic material of a particular species and then associating the genes with the traits they express. "Genomic libraries" are constructed for each species to decipher the genetic information and associate it with traits.

Such genomics libraries are either being built or are essentially complete for many important agronomic species. ARS has been a leader in developing genomic libraries for several animal and plant species. The agency is also working on genomic databases for insects like the honey bee (see story on page 14) and for microorganisms like the foodborne pathogen *Listeria*. For some species, the goal is to map the entire genome; with others, the aim is to concentrate on locating traits most important to breeders and producers.

As genomics data accumulates for a species from a wide range of production environments, scientists will not only understand how a trait operates in the real world, they will also know which specific genes control that trait.

With genomics, a whole new horizon is opening up for conventional breeding, especially for complex traits previously beyond breeders' abilities to manipulate. The new genomics data is allowing researchers and breeders to identify genes that can add or improve a specific trait.

Before, in conventional crosses, breeders have had to depend on finding parents that exhibited the sought-after trait. But often the parent not only passes on the genes of interest, but also other, sometimes undesirable, genes.

Genomics data allows breeders to locate a specific gene sequence whether it is expressed or not. The precise genes can be moved directly into high-quality progeny without the need for many generations of backcrossing to produce consistent offspring that have the new trait. And there's no addition of undesirable genes.

This will greatly speed up breeding. It will also allow breeders to tackle complex traits they haven't been able to introduce, amplify traits that are only faintly expressed, or suppress undesirable traits, and often without having to reach outside the species for new genes that would then create a transgenic organism.

And when the source of the genes is a member of the same species, or a sexually compatible relative, the gene pool of the offspring would not be altered. This eliminates concerns that arise when genes are taken from wildly disparate species to achieve a new trait.

Of course, genomics helps to make genetic engineering from unrelated sources more precise. By narrowing the amount of genetic material to just those genes that need to be moved, potential problems and risks from unintended and unneeded gene transfer are minimized.

Scientists have even taken advantage of information from well-characterized species to develop tools for less well-characterized crops and animals. For example, rice genome data recently enabled an ARS team to design DNA markers to pinpoint an important rye gene for resistance to high levels of soil aluminum in progeny from rye/wheat hybrids.

Similarly, continued refinement of the genetic map of the Hessian fly is now enabling research on the evolution of virulence when new resistance genes are deployed in wheat cultivars. (See story on page 4.)

ARS has been a lead partner in creating genetic maps of chickens. Almost overnight, researchers went from having only about 2,000 genetic markers for traits to having potentially more than 3 million, which will help scientists make improvements that result in healthier, more nutritious, even tastier chickens.

ARS scientists working with researchers from around the world have developed a physical, bacterial artificial chromosome—or BAC—map of the cow and are participating in the international effort to sequence the entire cow genome. Traits that are being targeted for improvement include feed efficiency, reduced mastitis in dairy cows, and reduced susceptibility to diseases such as bovine spongiform encephalopathy, or mad cow disease. (See story on page 15.)

One result from the cow genome work has been development of a test for genes that code for the enzyme  $\mu$ -calpain, which is a major reason for tenderness in beef. Breeding for tenderness will take a giant, but more precise, leap forward with the guidance of this DNA test.

Compared to other animal genomes under study, the pig's has farthest to go. But ARS is contributing to efforts to sequence the swine genome. (See story on page 12.)

Genomics research will markedly improve our ability to mine useful genes to enhance crops, livestock, insects, and microorganisms. A whole new pool of genetic potential for research and breeding is opening up.

**Judith B. St. John**  
Deputy Administrator  
Crop Production and Protection

**Steven M. Kappes**  
Deputy Administrator  
Animal Production and Protection