

Constructing the Cattle Genome:

What Will It Mean for Angus Producers?

by Barb Baylor Anderson

That pie-in-the-sky cattle genome discussion you've been reading about isn't so hocus-pocus anymore. An international consortium of scientists, including animal researchers from the University of Illinois and the U.S. Department of Agriculture (USDA) Agricultural Research Service (ARS), is working toward producing a draft sequence of the cattle genome.

What does this mean to the average Angus producer? In the next few years, scientists from around the world likely will have the tools necessary to genetically improve cattle and cattle performance and to develop ways to safeguard beef supplies and battle bioterrorism.

"Our work is a mirror image of that being done with crops, except that animals require longer generation times," explains Harris Lewin, a professor of animal sciences and director of the W.M. Keck Center for Comparative and Functional Genomics at the University of Illinois at Urbana-Champaign. Lewin is coordinating the project with Steve Kappes, USDA-ARS in Clay Center, Neb.

"Once the project is complete, scientists will have the tools to ... activate specific genes for specific functions at specific times," Lewin says. "This project makes order of the disorder. When we are done, and we are nearly done, we will have an ordered physical map from one end to the other of each of the cattle chromosomes. We can create from that a detailed

genome map that is an assembly of cattle chromosomes.

Sequencing will begin in the spring."

Once sequencing is complete, Lewin says, scientists will be able to use genome-based technologies to perform a number of tasks, including speeding the diagnosis of exposure to animal pathogens or chemical agents, for example, in the case of bioterrorism. In addition, researchers will be able to analyze any gene suspected of controlling traits of economic importance to the cattle industry.

"We will be able to understand the genes that control higher reproduction and higher marbling, if that is what the industry desires," Lewin says. "We will also get better tools to understand breeds and genotypes. All of the information will be publicly available so any scientist can work on whatever gene or trait they want."

Lewin anticipates priorities might include university work with marker-assisted

breeding and genome-based pharmaceutical and feed improvements for cattle producers.

"Genomics in the next 10 to 15 years will interest feed and animal health companies and allow them to recommend feeding precise ingredients at very precise times by adding molecules to the feed," he says. "There is pressure for growth promotants and feed additives to become more 'environmentally friendly,' and antibiotics in feed will need suitable replacements. We may be able to add cultures or proteins or other materials to feed to perform these functions without leaving residues in the meat."

Lewin is confident Angus breeders will be some of the first to find success with genome-based technology.

"Angus breeders are traditionally early adopters of new genetic technology, and this is a logical progression of technology," he says. "Selection will become more accurate as standards are defined by the

industry. And as market demands change, Angus producers will be able to rapidly shift to what consumers want within the breed. Angus producers will not only sustain their business, they should find expanded domestic and international opportunities."

In addition to aiding the cattle industry, the cattle genome sequence will provide an invaluable resource for deciphering the human genetic code, Lewin says.

"We have found that 25% of our BAC (bacterial artificial chromosome)-end sequences have a match to the human genome," he says. "The National Institutes of Health will likely contribute \$50 million toward cattle genome sequencing because of its value in developing the human genome map."

Lewin cautions, as with any new product, scientists will need to monitor how the genome knowledge is combined with technology and to be sure uses are thoroughly tested.

"We have to be cognizant of potential misuse of gene manipulation, and to be sure new products and new efficiencies are used correctly," he says. "When transgenics is coupled with cloning, and big pieces of genetic material are moved, we need to be very careful. We must never lose sight of the need to preserve our genetic diversity."

AY

Technically speaking

The genome project involves creating a sequence-ready bacterial artificial chromosome (BAC) map that will be anchored to the human genome map by reference points called comparatively-anchored sequence tagged sites (CASTS). All 280,000 clones of the BAC library will be fingerprinted. Then, sequencing will be done of the ends of at least 100,000 of the fingerprinted BAC-clones.

The BAC fingerprints will be merged with the BAC-end sequence data to create a sequence-ready map. The entire ordered array of cattle BAC clones, called contigs, will then be "scaffolded" to specific cattle chromosomes. A thorough sequence-ready map will be computer-generated so a draft sequence of the entire cattle genome can be done.