Mapping the
Bovine Genome

by Kindra Gordon

Sequencing the bovine genetic code is the result of a $53-million international project that was launched in December 2003. The research is being carried out by a team at the Baylor College of Medicine's Human Genome Sequencing Center (HGSC) in Houston, Texas, and is being led by Richard Gibbs, who also participated in the first mapping of the human genetic code in 2001.

The first draft of the sequence was done with DNA from a Line 1 Hereford cow from the U.S. Department of Agriculture (USDA) research station in Miles City, Mont. She was used because of extensive inbreeding within the herd, providing more homozygous genetics to map. USDA's Ronnie Green, Agricultural Research Service (ARS) national program leader for food animal production, says this initial draft is the first step in the sequencing process, and it represents only about half of what the final genome assembly will be, which should be completed and released by fall 2005.

Green explains that scientists plan to do some sequencing of the genome of the Angus, Limousin, Holstein, Jersey, Norwegian Red and Brahman breeds to better understand individual gene variation among breeds. But, he adds that this will be lighter sequencing among those breeds and the final genome sequence will be from the Line 1 Hereford female.

The bulk of the bovine genome project has been funded by the National Institutes of Health (NIH) with about $600,000 for research provided through the beef checkoff. Additional work to develop more detailed information about individual cattle genes is being conducted at the British Columbia Cancer Research Center in Vancouver, B.C., Canada.

Genomics 101

Genomics research really got underway in 1986 when the term was coined for the new scientific discipline of mapping, sequencing and analyzing genomes. The first step of genomic research is to develop road maps of each chromosome — genetic linkage maps. In 1994 the first cattle linkage map was published in both Australia and the United States. After the development of a linkage map, chromosomal regions that are important to economically relevant traits (ERTs) can then be identified through a process known as "fine mapping." These regions are known as quantitative trait loci (QTL).

A simplified example of this genome sequencing would be to compare it to trying to find an old high school buddy (i.e., find a gene for tenderness). We know that he lives somewhere in Colorado (in the bovine genome). We use DNA markers and gene mapping to find out that he is in the Denver metro area. If we can sequence the Denver metro area, we can identify every person there and pinpoint individual addresses, including that of our lost friend whom we can now visit.

Some of the current DNA tests available in the livestock industry today through fine mapping research include:

- ► Thyroglobulin — marbling (GeneStar® Marbling);
- ► Calpastatin — tenderness (GeneStar® Tenderness);
- ► Calpain — tenderness;
- ► Leptin — fat deposition; and
- ► Diacylglycerol acetyltransferase (DGAT) — fat deposition in milk.

In the future, researchers expect the QTL identified to be for numerous other traits — particularly in the areas of disease resistance and reproduction. That process should be sped up since the bovine genome has been completely sequenced and is now available to scientists around the world in a free public database.

Human implications

It's expected that bovine genome sequencing developments will move forward fairly quickly because animals are viewed as an important tool in human disease research.

Green explains that the bovine genome is similar in size to the genomes of humans and other mammals, containing approximately three billion DNA base pairs and an estimated 25,000 genes, with the locations of the human genome correlating about 85%-90% to the bovine genome.

Because of these similarities, Green says scientists can use comparative mapping between species to learn about traits.

He says the NIH are paying for most of the research into sequencing the bovine genome — as they've done for the chicken genome as well — because they want to use that information for comparative mapping in humans.

Green adds, "The phenotypes that we've mapped and collected in the livestock industry provide a significant amount of information on livestock genetics compared to the information the human medical community has. Scientists will be able to leverage that data and work backwards in the human."