



Research Update

► Summaries of current beef cattle research

K-State examines effects of breeding for RFI in heifers

With feed costs such a significant portion of beef production, animal scientists at Kansas State University (K-State) conducted a study on heifers sired by bulls chosen for their residual feed intake (RFI) merit. What they found, said Jennifer Bormann, a researcher with K-State Research and Extension, was that although RFI has been shown to be moderately heritable, heifers that were sired by bulls with low RFI merit performed no differently than heifers sired by bulls with high RFI merit.

RFI is the difference between what an animal eats and what it is predicted to eat based on its size and growth. Animals with negative or low RFI values eat less than is expected for their level of production and are more efficient than animals with a high RFI. A low RFI is more desirable because that animal can more efficiently turn feed into beef.

“RFI has become the measurement of choice in the beef industry, but there is not a lot of research about how cows (dams) fit into the picture or if the heifers would fare differently on a more concentrated diet than the one we fed,” she said. She presented the study’s findings at K-State’s Cattlemen’s Day in March.

“Previous research has shown that RFI is moderately heritable,” she said. So she, along with colleagues Dan Moser of K-State and Twig Marston, now at the University of Nebraska–Lincoln, studied how heifers sired by bulls with high and low RFI ratings would fare when it came to their own RFI ratings.

To begin the study, bulls with low or high genetic merit for RFI were selected from the Australian Angus Association sire summary and mated to Angus-cross commercial cows at K-State’s Cow-Calf Unit in 2005 and 2006.

“There were no significant differences between heifers sired by low- or high-RFI EBV (estimated breeding values) system bulls in RFI, feed intake, feed conversion ratio or gain,” Bormann said.

Heifers in the study were developed at a relatively low rate of gain, she noted. Genetic differences in RFI calculated in growing bulls may not have been expressed on the lower plane of nutrition of the developing heifers.

Heifers sired by low-RFI bulls in the study

also had more rump fat and tended to have more ribeye area and intramuscular fat.

“Our results indicated that selection for RFI should not negatively impact carcass quality,” she said.

There is no doubt, Bormann said, that a producer would prefer to breed for animals that are as efficient as possible at converting feed to high-quality beef. But there is much still to be learned about selecting for RFI in beef breeding programs. Several other universities are also studying various aspects of the practice. K-State will continue studying the issue to try to determine the best practices when selecting for RFI.

“The bottom line,” Bormann said, “is that as selection for RFI becomes more adopted by the industry, the relationships between diet, growth rate, body composition, and RFI in heifers need to be better understood.”

More information about beef research at K-State is available on the university’s Department of Animal Science and Industry web site: <http://asi.ksu.edu>.

— by Mary Lou Peter,

K-State Research and Extension News

Research will lead to better understanding of genetic basis of disease

The U.S. Department of Agriculture (USDA) and the National Institutes of Health (NIH) announced April 23 that an international consortium of researchers has published the genome of domestic cattle, the first livestock mammal to have its genetic blueprint sequenced and analyzed. The landmark research will bolster efforts to produce better beef and dairy products and lead to a better understanding of the human genome.

The sequencing and analysis of the bovine genome was funded in part by USDA’s Cooperative State Research, Education and Extension Service (CSREES) and Agricultural Research Service (ARS), who jointly contributed approximately \$10 million. Approximately \$25 million was contributed to the project by the National Human Genome Research Institute (NHGRI), part of the NIH, which is a component of the Department of Health and Human Services (HHS).

“The cattle industry is extremely

important for U.S. agriculture, with more than 94 million cattle in the United States valued at \$49 billion,” said Agriculture Secretary Tom Vilsack. “Understanding the cattle genome and having the sequence will allow researchers to understand the genetic basis for disease in domestic cattle and could result in healthier production of meat and milk while reducing producers’ dependence on antibiotics.”

“The domestic cattle genome sequence opens another window into our own genome,” said Acting NIH Director Raynard Kington. “By comparing the human genome to the genomes of many different species, such as the domestic cattle, we can gain a clearer view of how the human genome works in health and in disease.”

In a paper published in the journal *Science*, researchers from the Bovine Genome Sequencing Project estimate that the genome of the domestic cattle (*Bos taurus*) contains approximately 22,000 genes and shares about 80% of its genes with humans. The researchers also report that the organization of human chromosomes is closer to that of domestic cattle than to those of rats or mice.

The analyses, which involved comparing the domestic cattle genome sequence to those of the human, dog, mouse, rat, opossum and platypus, provide critical insights into the structure and function of the human genome. The findings will also assist researchers working to improve the quality and safety of beef and dairy products. In addition, genomic information can be used to develop better strategies for treating and preventing diseases that affect cattle.

Like humans and other mammals, the chromosomes of domestic cattle contain segmental duplications, which are large, almost identical copies of DNA present in at least two locations in a genome. Segmental duplications in the human genome are associated with a variety of human disorders, including a form of mental retardation and other neurological and birth defects.

In the domestic cattle genome, researchers found that some of these chromosomal rearrangements affect genes related to immunity, metabolism, digestion, reproduction and lactation. For instance, researchers think some of these changes may

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explain the unique ability of cattle to convert grass and other low-energy food sources into high-energy muscle, fat and milk.

Segmental duplications in the domestic cattle genome have also resulted in specialized roles for genes involved in immune response, such as those that make antimicrobial proteins in milk and their intestines. Researchers think these genes developed over time in response to the diversity of microbes that domestic cattle encounter and the vulnerability of animals that live in large herds to the spread of infectious diseases.

The breed of cattle selected for genome sequencing was Hereford, which is used in beef production. The effort to sequence and analyze the domestic cattle genome took six years and involved more than 300 scientists from 25 countries.

A related paper also appears in the April 22 issue of *Science*. In that paper, the Bovine HapMap Consortium unveils a map that charts key DNA differences, called haplotypes, among the diverse branches of the bovine tree. The scientists compared the Hereford genome sequence with those of six other breeds: the Holstein, Angus, Jersey, Limousin, Norwegian Red and Brahman. Follow-up studies were then done on 497 cattle from 19 geographic and biologically distinct breeds. The species represent the humpless *taurine* cattle most commonly found in Europe, Africa and East and West Asia and the *indicine* cattle found in India, South and West Asia and East Africa.

Generally, the bovine HapMap indicates that present-day cattle came from a diverse ancestral population from Africa, Asia and Europe that has undergone a recent rapid decrease in population size, probably due to domestication. Researchers can use the bovine HapMap to track DNA differences between cattle breeds to assist discovery of traits for better meat and milk production.

“The bovine HapMap will be a valuable resource and will transform how dairy and beef cattle are bred,” said Richard Gibbs, Baylor College of Medicine’s Human Genome Sequencing Center in Houston. “Genetic tools are already being developed and proving useful to the dairy industry, and we predict they will be applied to improve the beef industry. We hope the information will also be used to come up with innovative ways to reduce the environmental impact of cattle, such as greenhouse gases released by herds.”

Along with the *Science* papers, researchers published 20 companion reports describing

more detailed analyses of the domestic cattle genome sequence in journals from the open access publisher BioMed Central. All of the articles can be freely accessed at www.biomedcentral.com/series/bovine.

The Bovine Genome Sequencing Project was led by researchers at Baylor College of Medicine, part of NHGRI’s Large-Scale Sequencing Research Network, ARS, Georgetown University and CSIRO Australia. The HapMap project was led by Baylor College of Medicine, ARS and the University of Missouri.

Sequencing the bovine genome is part of USDA’s “Blueprint for USDA Efforts in Agricultural Animal Genomics,” a 10-year plan developed in 2007 for research, education and Extension in animal genomics in an effort to improve animal production practices.

Funding for the \$53 million cattle genome-sequencing project was provided by an international group consisting of CSREES; ARS; NHGRI; the state of Texas; Genome Canada through Genome British Columbia; the Alberta Science and Research Authority; CSIRO; Agritech Investments Ltd., Dairy Insight Inc. and AgResearch Ltd., all of New Zealand; the Research Council of Norway; the Kleberg Foundation; and National, Texas and South Dakota Beef checkoff funds.

— *USDA News*

Researchers address antibiotic resistance in food chain

More than 80 scientists gathered outside Washington, D.C., April 2-3 for a conference addressing the occurrence of antibiotic resistance in the food chain. The event, “Food Safety and Public Health Frontier: Minimizing Antibiotic Resistance Transmission through the Food Chain,” was co-hosted by Ohio State University (OSU) and the CSREES.

“Instead of focusing on antibiotic usage, either for human health or in agriculture, this conference focused on understanding the overall picture of the emergence, circulation and persistence of antibiotic resistance in microbial ecosystems,” said Hua Wang, an OSU microbiologist and associate professor of food science and technology, and the conference’s primary organizer. “Our goal was to provide a balanced picture on factors contributing to the problem for targeted intervention.”

The conference featured 30 scientific presentations. Participants discussed risk assessment and antibiotic resistance

reduction strategies, proposed future research directions, and education and outreach approaches for industry, regulators, public health authorities and consumers. Organizers of the conference plan to summarize findings reported at the conference and report them to USDA to use as inputs in planning for future actions.

The conference keynote address was given by Abigail Salyers of the University of Illinois. She noted that antibiotics are used at very low concentrations in agriculture, but bacteria can still grow resistant to the antibiotics, and the food produced by that livestock could then enter the food supply, potentially putting human health at risk. However, there’s insufficient data to measure the risks in such a scenario, she said. Commensal bacteria — microorganisms that are harmless or are thought to provide health benefits — represent an emerging risk due to their active involvement in horizontal gene transmission of antibiotic resistance genes, including to pathogens.

— *Adapted from release by Martha Filipic, OSU, & USDA’s CSREES*

Technologies Improve FMD Detection and Control

Improving the detection and control of foot-and-mouth disease (FMD) in cattle could result from technology being developed and tested by ARS scientists. The United States hasn’t had an outbreak of FMD since 1929, but being prepared for an outbreak is a priority for the U.S. government.

One study used infrared cameras to detect elevated hoof temperatures, a symptom of FMD in cattle. Infrared technology could detect elevated temperatures up to two days before cattle develop clinical signs. Cheaper and faster than existing screening methods, this technology could allow scientists and veterinarians to identify potentially infected cattle in large groups, without examining animals individually.

ARS scientists have also collaborated with the biotechnology company Tetracore to develop a test that can detect RNA from the FMD virus in less than two hours. In the event of an FMD emergency, laboratories throughout the United States could use this technology to diagnose samples rapidly.

In related work, ARS chemist Marvin Grubman and his colleagues are making improvements to the FMD vaccine they developed. The vaccine can be produced without using infectious FMD materials, which means it can be produced on the U.S.

mainland without the need for expensive, high-containment production facilities.

Tests have shown that the vaccine becomes effective a mere seven days after it's been administered. Although this is one of the fastest vaccines available, Grubman and his colleagues wanted faster protection. In a recent study, Grubman found that proteins called interferons can offer protection while animals are developing an antibody response to the vaccine, increasing their resistance.

ARS, the U.S. Department of Homeland Security and biopharmaceutical company GenVec Inc. of Gaithersburg, Md., are now collaborating to develop the new FMD vaccine for inclusion in the U.S. Veterinary Vaccine Stockpile. They are also working to combine the interferons and the FMD vaccine so they can be administered concurrently.

Read more about this research in the April 2009 issue of *Agricultural Research* magazine, available online at www.ars.usda.gov/is/AR/archive/apr09/disease0409.htm.

— by Laura McGinnis, ARS News Service

Study seeks to show how organic farming is changing the face of U.S. agriculture

This spring, USDA will conduct the first-ever wide-scale survey of organic farming in the United States, Agriculture Secretary Tom Vilsack announced late April, to find out how the growth of organic farming is changing the face of U.S. agriculture.

“The Organic Production Survey is a direct response to the growing interest in organics among consumers, farmers and businesses,” Vilsack said. “This is an opportunity for organic producers to share their voices and help ensure the continued growth and sustainability of organic farming in the United States.”

The 2007 Census of Agriculture counted more than 20,000 U.S. farms engaged in organic production.

The survey will look at many aspects of organic farming during the 2008 calendar year — from production and marketing practices, to income and expenses. It will focus not only on operations that are

currently engaged in organic production, but also on those making the transition to organic agriculture.

The results will help shape future decisions regarding farm policy, funding allocations, availability of goods and services, community development and other key issues. In addition, the information can help producers make informed decisions about the future of their own farming operations.

USDA's National Agricultural Statistics Service (NASS) will mail the survey in early May to all known organic producers in the United States. NASS will publish results in winter 2009.

For more information about the survey, visit www.agcensus.usda.gov or call 1-800-727-9540.

— USDA News

