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Decoding the Cattle Genome

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As a treasure map may lead to buried treasure, scientists are following genetic markers to predict the genetic make-up of agriculturally important animals. The next generation “map” of genotyping and genome sequencing technologies may identify the traits that underlie the expression of growth, development, reproduction, and the onset of complex disease. This knowledge will revolutionize the live-stock industries. >>

With funding from USDA Cooperative State Research, Education, and Extension Service (CSREES), a team of scientists in Missouri are using the bovine genome sequence to create a new series of diagnostic tools to improve animal products and production efficiency.

All living organisms contain DNA, which is the blueprint of life. Within the DNA are chromosomes that house neatly packaged genes. Each gene is a segment of DNA that accounts for an inheritable trait.

The genome of an organism is the complete assemblage of all of the chromosomes found in that organism.

Variations in a gene can reduce or intensify the importance of an agriculturally important trait, such as growth or disease tolerance. These variations are caused by single nucleotide polymorphism (SNP, or “snip”). Genes are complex structures; a snip is a variation of a single link in that structure. The type of link can differ between members of the same species as well as within the chromosome of the same animal.

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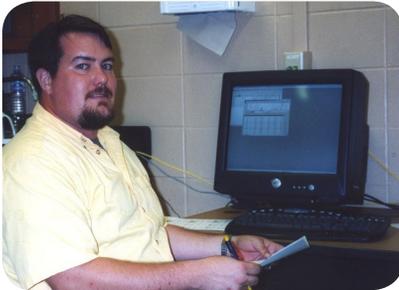
Right: High-density SNP genotyping reagents arrive at the Taylor lab.

Credit: R.D. Schnabel



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Above: Matt McClure scoring microsatellite genotypes.

Credit: R.D. Schnabel

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Scientists are closing in on a final draft of the whole genome sequence for many agriculturally important animals, including cattle, swine, chicken, and horses. These draft sequences, however, represent only a single individual from each species. Variations within the genome, some of which are responsible for economically important traits, are mostly unknown. To compensate for this, scientists use well-known genetic markers to identify variation within a trait.

Tracing the inheritance of these markers through generations allows scientists to develop inheritance patterns that can detect the presence of genes associated with economically important traits.

At the University of Missouri, Jerry Taylor and his colleagues have constructed a snip test to identify variations in Angus cattle. Results from this test helped create a genetic map within the genome of the Angus. Researchers are now using this map to test for the presence of genes that cause variation in economically important traits, such as the efficiency of growth and carcass composition.

"The importance of this [test] is not only that it makes genotyping so much simpler and it combines the mapping and fine-mapping phases of a gene discovery project," Taylor said, "but that it may also be used to develop diagnostics to predict the genetic merit of animals."

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Scientists are also using this tool to develop genetic tests that will predict the total genetic merit of important production and product quality traits in beef and dairy cattle

The Missouri group joined a consortium involving scientists from the USDA's Agriculture Research Service facilities at Beltsville, MD, the Roman L. Hruska U.S. Meat Animal Research Center at Clay Center, NE, and the University of Alberta to develop the high-density SNP assay for cattle.

CSREES funded this research project through the National Research Initiative Animal Genome program. Through federal funding and leadership for research, education, and extension programs, CSREES focuses on investing in science and solving critical issues impacting people's daily lives and the nation's future. For more information, visit www.csrees.usda.gov. ■