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Bovine Genome Sequencing Program: Full-length cDNA Sequencing

Status	Past
Category	International Initiatives
Sector	Agriculture
Genome Centres	Genome British Columbia & Genome Alberta
Project Leaders	Robert Holt, Steven Jones, Marco Marra & Stephen Moore

Project Description

The bovine genome is similar in size to the genomes of humans and other mammals, with an estimated 3 billion base pairs and between 25,000 to 30,000 genes. Besides its potential for improving dairy and meat products and enhancing food safety, adding the genomic sequence of the cow (*Bos taurus*) to the growing list of sequenced animal genomes will help researchers learn more about the human genome and develop new strategies in the battle against disease.

Our project was part of the larger Bovine Genome Sequencing Project, an international initiative to sequence the bovine genome led by the National Human Genome Research Institute. To discover more about individual bovine genes, we derived sequences for full-length cDNA clones, as part of a collaboration between the BC Cancer Agency Genome Sciences Centre in Vancouver and the University of Alberta.

This cataloguing of bovine transcripts is particularly timely given the tremendous cost to Canada due to bovine spongiform encephalopathy (BSE). Our sequencing effort will help in the fight against BSE, as well as create the most fundamental advances in our understanding of cattle. The results of this work will help facilitate improvements in animal health research, improve nutrition, and reduce agriculture's impact on the environment.

Determining the complete sequence for bovine cDNA clones will have long-term benefits for human health and the biotechnology industry, as well as the beef and dairy industries. The Bovine Genome Project data will underpin livestock research for the next 50 years and become the reference point to identify animals that are better suited to a particular market or environment. But the research is not limited to livestock production, as the bovine genome information is valuable to many other disciplines including evolutionary biology, population genetics, comparative genomics, and medical genetics.

Fast Facts

Highlighted outcome: High-throughput sequencing of the protein coding elements and derivation of gene structures for the cow genome, a key part of the \$53 million US Bovine Genome Sequencing Project led by the National Human Genome Research Institute

International linkages: collaboration between USDA-ARS and Cooperative State Research, Education, and Extension Service; the state of Texas; Genome Canada (Genome BC and Genome Prairie); Australia's Commonwealth Scientific and Industrial Research Organization; New Zealand's Agritech Investments, Dairy Insight, and AgResearch; the Kleberg Foundation; National Texas and South Dakota Beef Check-off Funds; Texas A&M University; and the University of Missouri at Columbia

Resources generated: all data were submitted to National Center for Biotechnology Information (NCBI), which will serve as a valuable resource for bovine genome annotation and the study of genetic variation.