

## UC Davis-led Research Consortium Explores Milk Genome

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In tandem with the publication of the entire cattle genome, a consortium of researchers led by scientists at the University of California, Davis, are unveiling the first comprehensive overview of the portion of the genome, or entire collection of genes, responsible for milk and milk production in cattle and six other species of mammals.

Findings from the study by the Bovine Lactation Genome Consortium paint a vivid picture of the molecular evolution of milk and lactation, and will be published in the April 24 issue of the online journal *Genome Biology*.

The paper appears as a companion piece to the landmark sequencing of the entire cattle genome, which will be published in two reports in the April 24 issue of the journal *Science*. That announcement marks the climax of a six-year effort to complete, analyze and interpret the cattle genome. The massive project was carried out by a collaborative of more than 300 scientists from 25 countries, including the UC Davis researchers. It was coordinated by the Baylor College of Medicine Human Genome Sequencing Center.

Data produced by the overall genome sequencing will enable researchers to identify genetic variations in cattle that are important not only for milk production and milk composition but also for reproduction, feed efficiency, meat quality and disease resistance. It will have direct application in helping to guide the selection of high-performing individuals in cattle breeding programs.

“The sequencing of the cattle genome represents a breakthrough for the study of milk and lactation,” said Danielle Lemay, the lead author on the milk genome study and a bioinformatician and nutrition scientist in UC Davis’ Department of Food Science and Technology.

“When paired with existing data, the bovine genome sequence is something of a modern Rosetta stone, making it possible to identify and interpret the significance of genes related to milk and lactation,” she said.

Researchers note that the genome sequence and the identification of sequence variation will improve the accuracy and efficiency of genetic selection in cattle by allowing the evaluation of an animal’s whole genome. The genome sequence also opens the door to the identification and description of all cattle genes and to the understanding of their function in relation to production traits. This information will be valuable in improving the sustainability of the dairy and beef cattle breeding systems.

## The milk genome

The milk-genome researchers focused on cattle genes involved with milk and the lactation process because of the unique role that milk plays in the lives of cattle, humans and all other mammals.

“Milk uniquely informs us about nutrition because it is the only food that has evolved specifically to nourish mammals,” said UC Davis professor and food scientist Bruce German.

“Because milk is produced for offspring at great physiological expense to the mother, we can theorize that there are few superfluous components in milk,” he said.

“Generation after generation, those animals that are able to produce more nourishing milk perpetuate their genes through the survival and reproductive success of their offspring.”

### **Study findings**

In the companion paper on the milk genome, the researchers identified 197 milk-protein genes and more than 6,000 milk-production genes within the overall cattle genome. They dramatically narrowed the search for genes that affect milk traits by overlaying this data on existing information regarding 238 DNA segments that are known to be associated with particular traits.

“Overall, the findings of our study support the hypothesis that the biological roots of milk production in mammals are quite ancient and that the evolution of milk has been constrained in order to maximize the survival of both mother and offspring,” said Juan Medrano, a professor of animal genetics in UC Davis’ Department of Animal Science.

In the study, the researchers examined the genomes of cattle, humans, dogs, mice and rats -- all mammals that carry their young for long periods in the mother’s body, where they are nourished by a placenta. This genome comparison also included the opossum, as representative of marsupials, which carry their young in a pouch after birth, and the platypus, which is one of only two species of mammals that lay eggs rather than giving birth to live young.

By comparing the genes of these seven species of mammals, they discovered that, compared to other cattle genes, the individual milk and milk-production genes are:

- more likely to be found in all mammals, despite the wide diversity of lactation strategies;
- less likely to have changed as new species evolved; and
- evolving more slowly in cattle than in other species.

The researchers also found that the milk proteins that remained the same across species were those proteins related to secreting milk in mammals. Conversely, those

milk proteins that had diverged the most from species to species were those associated with the nutritional and immunological components of milk.

This suggests that the immunological component of milk is tailored to the particular needs of each species and highlights the need for future nutrition research to examine how foods might be tailored to meet individual immunological needs, the researchers noted.

### **The research consortium and funding**

The Bovine Lactation Genome Consortium is a team of 19 scientists with specialties spanning molecular biology, immunology, food science, evolutionary biology, bioinformatics, statistics, mammary biology, animal genetics and bovine biology. The team was born out of the International Milk Genomics Consortium, which was initiated in 2004 by UC Davis scientists and housed at the **California Dairy Research Foundation** to study the biological processes underlying mammalian milk genomics. More information about the consortium and its members is available at: <http://lactoknow.ucdavis.edu/>.

Funding for researchers participating in the bovine lactation genome study was provided by the International Milk Genomics Consortium, the National Institute of Environmental Health Sciences, the U.S. Department of Agriculture Agricultural Research Service, New Zealand's Foundation for Research Science and Technology, the **California Dairy Research Foundation**, the National Human Genome Research Institute, Genome Canada and Genome BC, the Swiss National Science Foundation, Australia's Cooperative Research Centre for Innovative Dairy Products, and the Gardiner Foundation.

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