

Genetic study investigates ways to increase productivity and tenderness of meat

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Luciana Correia de Almeida Regitano, researcher at the Brazilian Agricultural Research Corporation, Livestock Raising Division -- Southeast, during FAPESP Week Nebraska-Texas. Credit: Heitor Shimizu / Agência FAPESP

Brazil has the world's largest commercial beef herd, numbering over 225 million, yet only 20 percent of Brazil's production is intended for export.

Because of this, beef ranks 10th on the list of products exported by Brazil, after soybeans, iron ore, oil, sugarcane, automobiles, chicken, cellulose, soybean meal and coffee.

Experts suggest that exports could be much higher if Brazilian [beef](#) were of a quality similar to that produced in Australia, Argentina or Uruguay. In addition to obtaining more tender meat, another goal of research is to improve productivity. To achieve this, genetic improvement techniques are used to breed animals that gain weight more quickly or that better resist disease.

"Brazil is the world's second largest producer of beef, in an industry whose 2016 revenue exceeded US\$ 5 billion. The cost of producing Brazilian beef is one of the lowest in the world, but in order to expand market importance, beef production needs to adapt to the standards established by importers. Among quality concerns, tenderness, the amount and the type of marbling can influence the sensory characteristics and nutritional value of the beef," said Luciana Correia de Almeida Regitano, a researcher at the Brazilian Agricultural Research Corporation - EMBRAPA and faculty member of the Federal University of São Carlos (in São Paulo, Brazil).

Regitano explained that in Brazil, over 80 percent of beef cattle is Nelore. The breed, of the subspecies *Bos taurus indicus*, originated in India, but it does not produce meat that is as tender as Angus (*Bos taurus taurus*), which originated in Europe and presents more marbling. "Nelore cattle weigh less and have lower productivity and less tender meat. As a result, their price is lower," she said.

Regitano leads a follow-up to a previous study that enabled the identification of genomic areas associated with the beef's production and quality characteristics. "We initially bred approximately 800 animals for three years on five farms, from birth to slaughter, measuring the

phenotypic characteristics such as growth, production, meat quality and feed efficiency. We also collected samples of DNA and subjected them to high-density genotyping to determine specific mutations that cover the whole genome. We analyzed more than 700,000 specific mutations dispersed throughout the genome, which provided us with data on the segregation of chromosomal segments," she said.

"In 2012, we had another project approved by FAPESP that allowed us to expand the initial study and analyze tissue samples to determine the complete sequence of messenger RNAs and all microRNAs found in the tissue. MicroRNAs are small RNA molecules that modulate how messenger RNAs will be translated into proteins," Regitano explained. The proteins from the tissue samples collected were also analyzed.

"We were able to obtain a data set on 45 different phenotypes and sequenced the messenger RNA and microRNA of 200 muscle samples and 30 liver samples, in addition to analyzing proteins from 65 muscle samples. With support from the CNPq, we were also able to sequence the complete genome, each nucleotide of the genome, of 20 animals. This provided a very important set of data from which we have obtained multiple layers of genomic information on a single animal," she said.

Genomic tools

"Among the objectives of our current study are complementing the analyses of genomic association to include new phenotypes, integrating the analyses of the functional genome (RNA, microRNA and proteins), assessing the significance of the copy number variation (CNV) and training human resources in the fields of bioinformatics and genomics," Regitano explained.

Copy number variation is defined as a type of genomic structural variation that includes amplifications and losses of a specific region,

which could involve and possibly be one or more complete genes. "We are studying how these alterations could influence the expression of all the genes in muscle as well as the phenotypes assessed," the researcher asserted.

The study led to the publication of a series of articles that are expanding knowledge of the possibilities for using [genomic tools](#) that can lead to gains in quality and productivity in beef production.

In an article published in the journal *BMC Genomics*, Regitano and her group identified genes, metabolic pathways and biological processes involved in the differentiation, proliferation, protein conversion, hypertrophy and synthesis of lipids related to the area of the loin eye, a measurement that correlates with the muscularity of the animal and the thickness of its subcutaneous fat, both characteristics that have a direct impact on carcass quality and productivity.

The results of the research point to molecular processes related to the deposit of muscles and fat, which are economically important characteristics for beef production.

In another article, published in the journal *PLOS ONE* in 2016, Regitano and her colleagues described a broad genomic analysis of CNVs obtained from 723 bulls. The researchers identified 2,600 regions that represent nearly 6.5 percent of the complete genome of the animals.

The results represent the first comprehensive study of the copy number variations of Nelore cattle, with the identification of regions in which genetic alterations could have important implications in breeding animals whose meat is more tender, thus improving its potential for export and higher prices.

More information: Bárbara Silva-Vignato et al. Comparative muscle

transcriptome associated with carcass traits of Nellore cattle, *BMC Genomics* (2017). [DOI: 10.1186/s12864-017-3897-x](https://doi.org/10.1186/s12864-017-3897-x)

Vinicius Henrique da Silva et al. Genome-Wide Detection of CNVs and Their Association with Meat Tenderness in Nelore Cattle, *PLOS ONE* (2016). [DOI: 10.1371/journal.pone.0157711](https://doi.org/10.1371/journal.pone.0157711)

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