



# Systems genetics and genome-wide association approaches for analysis of feed intake, feed efficiency, and performance in beef cattle

M.H.A. Santana<sup>1</sup>, M.C. Freua<sup>1</sup>, D.N. Do<sup>2</sup>, R.V. Ventura<sup>1,3</sup>,  
H.N. Kadarmideen<sup>4</sup> and J.B.S. Ferraz<sup>1</sup>

<sup>1</sup>Departamento de Medicina Veterinária,  
Faculdade de Zootecnia e Engenharia de Alimentos,  
Universidade do Estado de São Paulo, Pirassununga, SP, Brasil

<sup>2</sup>Department of Animal Science, McGill University,  
Sainte-Anne-de-Bellevue, Quebec, Canada

<sup>3</sup>Centre for Genetic Improvement for Livestock,  
University of Guelph, Guelph, Ontario, Canada

<sup>4</sup>Section for Animal Welfare and Disease Control,  
Faculty of Health and Medical Sciences,  
University of Copenhagen, Frederiksberg, Denmark

Corresponding author: M.H.A. Santana  
E-mail: miguel-has@hotmail.com

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**ABSTRACT.** Feed intake, feed efficiency, and weight gain are important economic traits of beef cattle in feedlots. In the present study, we investigated the physiological processes underlying such traits from the point of view of systems genetics. Firstly, using data from 1334 Nellore (*Bos indicus*) cattle and 943,577 single nucleotide polymorphisms (SNPs), a genome-wide association analysis was performed for dry

matter intake, average daily weight gain, feed conversion ratio, and residual feed intake with a Bayesian Lasso procedure. Genes within 50-kb SNPs, most relevant for explaining the genomic variance, were annotated and the biological processes underlying the traits were inferred from Database for Annotation, Visualization and Integrated Discovery (DAVID) and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases. Our results indicated several putative genomic regions associated with the target phenotypes and showed that almost all genomic variances were in the SNPs located in the intergenic and intronic regions. We further identified five main metabolic pathways related to ion transport, body composition, and feed intake control, which influenced the four phenotypes simultaneously. The systems genetics approach used in this study revealed novel pathways related to feed efficiency traits in beef cattle.

**Key words:** Dry matter intake; Feed intake; Performance traits; Residual feed intake; Variance partitioning