00-09 Co-expression network analysis identifies genes associated with iron content in bovine muscle

Wellison Jarles da Silva Diniz[1*], Aline Silva Mello Cesar[2], Ludwig Geistlinger[3], Polyana Cristine Tizioto[2], Priscila Silva Neubern de Oliveira[3], Juliana Afonso[1], Marina Ibelli Pereira Rocha[1], Andressa Oliveira de Lima[1], Carlos Eduardo Buss[1], Luiz Lehmann Coutinho[2], Luciana Correia de Almeida Regitano[3]

*Department of Genetic and Evolution, Federal University of São Carlos, São Carlos, São Paulo, Brazil. *wjarles09@gmail.com*
Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, São Paulo, Brazil
Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil

Iron is an essential cofactor required for several biological functions. The iron content in the body is known to be influenced by several factors including genetic composition. However, there is limited knowledge about potentially functional genes and metabolic pathways related to the iron content in cattle. To identify candidate gene networks associated with muscle iron content, we performed weighted gene co-expression network analysis (WGCNA) in a Nelore population of 60 steers. Gene expression was measured with RNA-Seq in *Longissimus dorsi* muscle samples and genomic estimated breeding values for iron content (GEBV-IC) were used as a quantitative trait. After quality control of raw reads and normalization, blockwise modules function was carried out using the 800 highest connected genes, and the signed network was constructed using a $\beta = 14$ ($R^2 = 0.89$). From the co-expression modules detected by WGCNA, we found six modules to be significantly correlated with GEBV-IC. Response to the hormone, mRNA metabolic process, and mitochondrial organization were biological process found significantly enriched for the genes presented in the associated modules. We identified as hub *Pin1* and *MRPL* genes which are iron responsive and play a major role in metabolism, cell division, and growth. Genes involved with muscle structure development such as *ACTA1*, *SRF,* and *GSK3A* were identified. The transcription factor *SRF* stimulates both cell proliferation and differentiation, and it is a master regulator of the actin cytoskeleton. The detected co-expression modules in this study provide evidence for substantial interplay between genes in processes influencing iron content. Further studies will be required to understand the underlying regulatory mechanisms of the observed co-expression networks.

Keywords: Gene expression, network analysis, systems biology.

This project was supported by FAPESP (12/23638-8, 15/09158-1).