CONSTRUCTION OF GENE INTERACTION AND REGULATORY NETWORKS IN BOVINE SKELETAL MUSCLE FROM EXPRESSION DATA^{*}

A. Reverter¹, W. Barris¹, N. Moreno-Sánchez², S. McWilliam¹, Y. H. Wang¹, G. S. Harper¹, S. A. Lehnert¹ and B. P. Dalrymple¹

 ¹Cooperative Research Centre for Cattle and Beef Quality, Bioinformatics Group, CSIRO Livestock Industries, Queensland Bioscience Precinct, 306 Carmody Road, St Lucia, Qld 4067, Australia.
²Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Ctra. de la Coruña Km. 7.5; 28040 Madrid, Spain.

SUMMARY

We propose a data-driven reverse engineering approach to isolate the components of a gene interaction and regulatory network. We apply this method to the construction of a network for bovine skeletal muscle. Key nodes in the network include muscle-specific genes (MSG) and transcription factors (TF). MSG are identified from data mining the USA National Cancer Institute, Cancer Genome Anatomy Project database, while TF are predicted by accurate function annotation. A total of 5 microarray studies spanning 78 hybridisations and 23 different experimental conditions provided raw expression data. A recently-reported analytical method based on multivariate mixed-model equations is used to compute gene co-expression measures across 624 genes. The resulting network included 102 genes (of which 40 were MSG and 7 were TF) that clustered in seven distinct modules with clear biological interpretation.

^{*} From invited paper. The full text, including this abstract is published in *Australian Journal of Experimental Agriculture* **45**, (7-8) in press.