

Chicken skeletal muscle-associated macroarray for gene discovery

E.C. Jorge¹, C.M.R. Melo², M.F. Rosário¹, J.R.S. Rossi¹, M.C. Ledur³, A.S.A.M.T. Moura⁴ and L.L. Coutinho¹

¹Departamento de Zootecnia, Escola Superior de Agricultura

"Luiz de Queiroz", Universidade de São Paulo, Piracicaba, SP, Brasil

²Departamento de Aquicultura, Universidade Federal de Santa Catarina, Florianópolis, SC, Brasil

³Embrapa Suínos e Aves, Genética e Melhoramento Animal, Vila Tamanduá, Concórdia, SC, Brasil

⁴Departamento de Produção Animal,

Faculdade de Medicina Veterinária e Zootecnia de Botucatu,

Universidade Estadual Paulista Júlio de Mesquita Filho, Botucatu, SP, Brasil

Corresponding author: L.L. Coutinho E-mail: llcoutin@esalq.usp.br

Genet. Mol. Res. 9 (1): 188-207 (2010) Received November 4, 2009 Accepted December 2, 2009 Published February 2, 2010

ABSTRACT. Macro- and microarrays are well-established technologies to determine gene functions through repeated measurements of transcript abundance. We constructed a chicken skeletal muscle-associated array based on a muscle-specific EST database, which was used to generate a tissue expression dataset of ~4500 chicken genes across 5 adult tissues (skeletal muscle, heart, liver, brain, and skin). Only a small number of ESTs were sufficiently well characterized by BLAST searches to determine their probable cellular functions. Evidence of a particular tissue-characteristic expression can be considered an indication that the transcript is likely to be functionally significant. The skeletal muscle macroarray platform was first used to search for evidence of tissue-specific expression, focusing on the biological function of genes/transcripts, since gene expression profiles generated across tissues were found to be reliable and consistent. Hierarchical clustering analysis revealed consistent clustering among genes assigned to 'developmental

growth', such as the ontology genes and germ layers. Accuracy of the expression data was supported by comparing information from known transcripts and tissue from which the transcript was derived with macroarray data. Hybridization assays resulted in consistent tissue expression profile, which will be useful to dissect tissue-regulatory networks and to predict functions of novel genes identified after extensive sequencing of the genomes of model organisms. Screening our skeletal-muscle platform using 5 chicken adult tissues allowed us identifying 43 'tissue-specific' transcripts, and 112 co-expressed uncharacterized transcripts with 62 putative motifs. This platform also represents an important tool for functional investigation of novel genes; to determine expression pattern according to developmental stages; to evaluate differences in muscular growth potential between chicken lines, and to identify tissue-specific genes.

Key words: *Gallus*; Gene expression; Skeletal muscle; Tissue-specific expression