Identification of candidate genes for Brazilian chicken lines

ERIKA C. JORGE¹, CLÁUDIO M.R. MELO², ANA PAULA D. ANDREOTE¹, MILLOR F. DO ROSÁRIO¹, HELENA J. ALVES¹, MÔNICA C. LEDUR³ & LUIZ L. COUTINHO¹

¹Escola Superior de Agricultura ‘Luiz de Queiroz’, Piracicaba, Brazil.
²University of Santa Catarina, Florianópolis, Brazil.
³Embrapa Suínos e Aves, Concórdia, Brazil
E-mail: ecjorge@esalq.usp.br

Years of divergent selection have produced chicken lines based on phenotypic characteristics. A considerable impact in skeletal muscle quantity and quality was reached in the broiler chicken lines using traditional methods of selection. But to date, few specific genetic factors have been identified that can account for these differences between chicken lines. To search for candidate genes that may elucidate the biological mechanisms associated with these growth rates and other differences between chicken lines, a macroarray platform containing 4,534 precursor/mature skeletal muscle genes was screened using isotopically labeled cDNA from *pectoralis* muscle of layer and broiler Brazilian chicken lines. A total of 99 genes were identified as differentially expressed (P<0.05), being 62 up-regulated in the broiler line and 37 in the layer one. QRT-PCR was used to confirm this expression data. The broiler up-regulated genes have suggested changes in the expression level of genes associated with growth and cell signaling, as a result of phenotypic selection. The search for the genetic position has indicated that some of the up-regulated genes are localized inside previously mapped QTL for the chicken genome (using QTL described for the lines used in this study and for different lines). Among the 62 broiler up-regulated genes, 23 were localized inside the chromosomes 1 to 9 (few markers and QTL information is still available for the other chicken micro-chromosomes). Of these, 17 have been positioned inside previously QTL defined regions, being 7 of them mapped for yield and five for body weight. From the 37 layer up-regulated genes, 18 have been localized inside the chromosomes 1 to 8 and, of these, 9 were inside QTL, some mapped for egg number and disease resistance. Together, these results have suggested novel candidate genes, that can be useful in the comprehension of molecular consequences of selection programs and also to improve the mechanisms of animal selection for growth rates and other economic traits.