60º CONGRESSO BRASILEIRO DE GENÉTICA
26 a 29 de agosto de 2014 Casa Grande Hotel Resort • Guarujá • SP • Brasil
www.sbg.org.br - ISBN 978-85-89109-06-2

Discovery of candidate genes for fatness in chickens based on genotyping with 600K SNP chip in a QTL region

Moreira, GCM[1]; Pértille, F[1]; Godoy, TF[1]; Brassaloti, R[1]; Boschiero, C[1]; Ledur, MC[2]; Coutinho, LL[1].

[1]Escola Superior de Agricultura Luiz de Queiroz, USP, Piracicaba, SP; [2]EMBRAPA Suínos e Aves, Concórdia, Santa Catarina, SC

gcmmoreira@usp.br

Keywords: chicken, fat deposition, HD chip 600 K, SNP.

Identification of SNPs and regions associated with production traits is possible based on genotyping with high-density (HD) SNP panels. Data analysis of HD genotyping in a target region previously associated with an economic trait allows the more precisely identification of candidate genes. The objective of this study was to perform high-density SNP genotyping in 96 chickens from the EMBRAPA F_2 Chicken Resource Population to identify SNPs in a QTL region of the chicken chromosome 3: 33,595,706-42,632,651 bp previously associated with fat deposition (Campos et al., 2009). Ten chickens from one parental layer line (CC) and 86 from the F_2 experimental population were genotyped with 600K SNP chip. DNA from blood samples was extracted with DNAzol® protocol. Genotyping was performed using the HD *Chicken 600K Affymetrix® Axiom®* by GeneTitan® (Affymetrix). Data analyses were conducted using *Affymetrix Genotyping Console* software and the R statistical environment. Functional annotation of SNPs identified in the target region was performed with ANNOVAR software (v.2013aug23, Wang et al. (2010)). DAVID Gene Functional Classification tool (v. 6.7, Huang et al. (2009)) was employed to identify genes involved in metabolic pathways with default parameters, and genes related to lipid metabolism were selected. From 96 individuals genotyped, 93 were maintained according the quality controls (Dish QC >0.82), corresponding to 42 males and 51 females. SNPs call rate (>96%) and minor alleles frequency (MAF >5%) were used as SNP filter. SNPs located on sex chromosomes were removed from the analysis. After call rate and MAF filtering, 572,531 SNPs were maintained; however, 4.61% of these SNPs were located on sex chromosomes and were subsequently removed. From a total of 546,124 SNPs, 65.6% were located in macrochromosomes, 34.3% located in microchromosomes and 0.1% located in LGE22C19W28_ES0C23 and LGE64. Approximately 89% of the SNPs from the HD SNP chip were identified in the Brazilian experimental population. In the QTL region, ~22,000 SNPs were identified representing an average density of 2.43 SNPs/kb. After SNPs annotation, we obtained 79 genes containing genetic variants. Following gene ontology and gene metabolic pathways analysis, 10 candidate genes potentially involved in lipid metabolism were selected: *THBS2*, *RYR2 and SMOC2* related to cell adhesion and calcium binding; *PSMB1*, *PIGM* and *LGALS8* related to proteolysis, carbohydrate and glycerophospholipids metabolism, and *DLL1*, *TBP*, *TAF5L* and *SPRTN* related to cell differentiation, DNA repair and transcriptional regulation. All genotyped SNPs will be used in a genome-wide association study to accurately identify SNPs, regions and genes associated with fatness in chickens.

Financial support: CAPES.