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## Genome-Wide Association Studies Reveal Genomic Windows and Candidate Genes Related to Fat Deposition in Chickens

**Gabriel C M Moreira** , University of São Paulo/ESALQ, Piracicaba, SP, Brazil  
 Aline S.M. Cesar , University of São Paulo/ESALQ and Iowa State University, Ames, IA  
 Thaís Fernanda Godoy , University of São Paulo/ESALQ, Piracicaba, SP, Brazil  
 Clarissa Boschiero , University of São Paulo/ESALQ, Piracicaba, SP, Brazil  
 Monica Correa Ledur , Embrapa Swine and Poultry, Concordia, Brazil  
 Dorian J. Garrick , Department of Animal Science, Iowa State University, Ames, IA  
 Ana Silvia Alves M. T. Moura , São Paulo State University/FMVZ, Botucatu, Brazil  
 Luiz L. Coutinho , University of São Paulo/ESALQ, Piracicaba, SP, Brazil

Abdominal and total fat content are economically important traits in commercial chicken lines. The aims of this study were to estimate genomic heritability, and identify genomic windows and candidate genes associated with fat deposition in chickens. A total of 497 42 day-old chickens from the EMBRAPA F<sub>2</sub> Chicken Resource Population developed for QTL studies were genotyped with the 600K genotyping array (Affymetrix®). Total fat in grams (TFg) and as a percentage of dry matter (TF%), abdominal fat weight (AbFg) and its percentage (AbF%) were measured. GWAS analyses were performed with GenSel software using BayesB method ( $\pi=0.999$ ) to estimate heritability and identify 1Mb windows associated with fat deposition traits. Quality control of loci and birds was based on DishQC>0.82, sample call rate >90%, SNP call rate >98%, MAF>2% and SNPs located in autosomal chromosomes, leaving 480 samples and 441,158 SNPs. The heritability values obtained were 0.45 for AbF%, 0.42 for AbFg, 0.40 for TFg and 0.50 for TF%. The genomic windows that explained the highest proportion of genetic variance for each trait were on GGA1 at 52 Mb explaining 3.77% and 1.94% for AbF% and AbFg, respectively; on GGA1 at 168 Mb explaining 1.52% for TFg, and on GGA28 at 3 Mb explaining 1.33% for TF%. In these windows, seven candidate genes related to fatty acids biosynthesis were identified: *ITM2B*, *CTK-1*, *PGPEP1*, *USPL1*, *Slc7a1*, *USE* and *ISX*. Mutations in these genes might regulate fat deposition and, following validation, strategies for animal selection based on their genotypes could be applied to improve the quality of chicken carcass.

Back to: [Genome Mapping, Tagging & Characterization: Poultry](#)

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