

RESEARCH ARTICLE

Open Access

Longissimus dorsi transcriptome analysis of purebred and crossbred Iberian pigs differing in muscle characteristics

Cristina Óvilo^{1*}, Rita Benítez¹, Almudena Fernández¹, Yolanda Núñez¹, Miriam Ayuso², Ana Isabel Fernández¹, Carmen Rodríguez¹, Beatriz Isabel², Ana Isabel Rey², Clemente López-Bote² and Luis Silió¹

Abstract

Background: The two main genetic types in Iberian pig production show important phenotypic differences in growth, fattening and tissue composition since early developmental stages. The objective of this work was the evaluation of muscle transcriptome profile in piglets of both genetic types, in order to identify genes, pathways and regulatory factors responsible for their phenotypic differences. Contemporary families coming from pure Iberian pigs (IB) or from crossing with Duroc boars (DU×IB) were generated. Piglets (14 from each genetic type) were slaughtered at weaning (28 days) and *longissimus dorsi* was sampled for composition and gene expression studies. RNA was obtained and hybridized to Affymetrix *Porcine Genechip* expression arrays.

Results: Loin muscle chemical composition showed significant differences between genetic types in intramuscular fat content (6.1% vs. 4.3% in IB and DU×IB animals, respectively, $P = 0.009$) and in saturated ($P = 0.019$) and monounsaturated fatty acid proportions ($P = 0.044$). The statistical analysis of gene expression data allowed the identification of 256 differentially expressed (DE) genes between genetic types (FDR < 0.10), 102 upregulated in IB and 154 upregulated in DU×IB. Transcript differences were validated for a subset of DE genes by qPCR. We observed alteration in biological functions related to extracellular matrix function and organization, cellular adhesion, muscle growth, lipid metabolism and proteolysis. Candidate genes with known effects on muscle growth were found among the DE genes upregulated in DU×IB. Genes related to lipid metabolism and proteolysis were found among those upregulated in IB. Regulatory factors (RF) potentially involved in the expression differences were identified by calculating the *regulatory impact factors*. Twenty-nine RF were found, some of them with known relationship with tissue development (*MSTN*, *SIX4*, *IRX3*), adipogenesis (*CEBPD*, *PPARGC1B*), or extracellular matrix processes (*MAX*, *MXI1*). Correlation among the expression of these RF and DE genes show relevant differences between genetic types.

Conclusion: These results provide valuable information about genetic mechanisms determining the phenotypic differences on growth and meat quality between the genetic types studied, mainly related to the development and function of the extracellular matrix and also to some metabolic processes as proteolysis and lipid metabolism. Transcription factors and regulatory mechanisms are proposed for these altered biological functions.

Keywords: Iberian pig, Transcriptome, Genetic type, Transcription factors, Growth, Meat quality, Metabolism

* Correspondence: ovilo@inia.es

¹Dpto Mejora Genética Animal, INIA, Ctra Coruña km 7.5, Madrid 28040, Spain

Full list of author information is available at the end of the article