

Dietary energy source largely affects tissue fatty acid composition but has minor influence on gene transcription in Iberian pigs¹

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ABSTRACT: A trial was performed to compare the effects of different dietary sources of MUFA on the fatty acid (FA) composition, lipid metabolism, and gene transcription in different tissues of Iberian pigs. Twenty-seven Iberian male pigs of 28 kg live weight (LW) were divided in 2 groups and fed with 1 of 2 isocaloric diets: a standard diet with carbohydrates as energy source (CH) and a diet enriched with high-oleic sunflower oil (HO). Ham adipose tissue was sampled by biopsy at 44 and 70 kg LW. At 110 kg LW pigs were slaughtered and backfat, loin, and liver tissues were sampled. Animals of the HO group showed higher MUFA content and lower SFA in all the analyzed tissues ($P < 0.001$). These main effects were established early during the treatment and increased only slightly along time. Small diet effects were also detected on PUFA, which showed differences according to sampling time, tissue, and lipid fraction. Effects of diet on gene expression were explored with a combined approach analyzing adipose

tissue transcriptome and quantifying the expression of a panel of key genes implicated in lipogenesis and lipid metabolism processes in backfat, muscle, and liver. Backfat transcriptome showed small effects of diet on gene expression, in number and magnitude. According to the posterior probabilities (PP) of the probe-specific expression differences between dietary groups ($PP < 0.01$), 37 genes were considered differentially expressed (DE). Gene ontology allowed relating them with several biological functions including lipid metabolic processes. Quantitative PCR confirmed several DE genes in adipose tissue (*RXRG*, *LEP*, and *ME1*; $P < 0.0001$, $P < 0.05$, and $P < 0.0001$, respectively), but no DE gene was found in loin or liver tissues. Joint results agree with a metabolic adjustment of adipose tissue FA levels by the subtle effect of the diet on the regulation of several lipid metabolism pathways, mainly FA oxidation and prostanoïd synthesis, with *LEP*, *RXRG*, and *PTGS2* genes playing mayor roles.

Key words: fatty acid profile, gene expression, Iberian pig, nutrition, oleic acid

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INTRODUCTION

Fat content and long-chain fatty acids (FA), whether in adipose or muscle tissues, are central to nutritional and sensorial values of pork (Webb and O'Neill, 2008). Dietary FA composition influences the profile of FA stored in pig tissues (Wood et al., 2004; Duran-

Montgé et al., 2009), and pig diets enriched with different sources of unsaturated FA have been essayed to improve the nutritional value of pig meat and its products (Kouba et al., 2003; Guillevic et al., 2009). The traditional fattening system of Iberian pigs is based on the intake of acorns, which provide high levels of MUFA, mainly oleic acid (López-Bote, 1998). This interaction breed–feeding system is known to be the basis of highest-quality dry-cured pig products, and it is a reference model for sustainable production of many local Mediterranean breeds (Pugliese, 2012). Monounsaturated fatty acid enriched diets, through the inclusion of high oleic acid sunflower oil, are be-

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