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Impact of dietary fat sources and feeding level on adipose tissue fatty acids composition and lipid metabolism related gene expression in finisher pigs

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ABSTRACT

The present study investigated the effects of dietary fat sources and feeding level on performance, adipose tissue fatty acid profile and lipid metabolism related genes expression in finisher pigs. A total of 128 finisher pigs [average initial body weight (BW), 81.2 ± 0.322 kg] were allotted to 4 treatments on the basis of BW. There were 4 replicates in each treatment with 8 pigs per replicate. Pigs were fed diets containing 50.0 g/kg linseed oil or animal fat, either *ad libitum* or restricted (15.0% less) in 2 × 2 factorial arrangement for 28 d. Dietary fat source did not affect (P>0.05) average daily gain (ADG), average daily feed intake (ADFI) and gain to feed ratio (G:F). The ADG and ADFI of pigs fed *ad libitum* were greater (P<0.05) than that of restricted fed pigs. The G:F of restricted fed pigs was greater (P<0.05) than that of *ad libitum* fed pigs. Pigs fed 50.0 g/kg linseed oil diet had greater (P<0.05) concentrations of adipose tissue polyunsaturated fatty acids (PUFA) like linoleic acid and α-linolenic acid than that of pigs fed 50.0 g/kg animal fat diet. Saturated fatty acids (SFA) like palmitic acid (P<0.05), palmetoleic acid and steric acid (P<0.10) concentrations of adipose tissue were greater in pigs fed animal fat than pigs fed linseed oil. However, adipose tissue fatty acids concentrations were not affected (P>0.05) by feeding level. Adipose tissue expression of acetyl CoA carboxylase (ACC) and fatty acid synthase (FAS) were down-regulated, whereas expression of lipoprotein lipase (LPL) and hormone sensitive lipase (HSL) were up-regulated in finishing pigs fed restricted diets. However, fat sources of diet had no effects (P>0.05) on expression of ACC, FAS, LPL and HSL genes. Results obtained in the present study indicates that dietary inclusion of 50.0 g/kg linseed oil have potential to improve the adipose tissue PUFA contents, and 15.0% feed restriction resulted into down-regulation of ACC and FAS and up-regulation of LPS and HSL expression in adipose tissue.

Abbreviations: ACC, acetyl CoA carboxylase; ADFI, average daily feed intake; ADG, average daily gain; AO, animal fat; BW, body weight; CP, crude protein; DM, dry matter; FAS, fatty acid synthase; G:F, gain to feed ratio; GE, gross energy; HSL, hormone sensitive lipase; LO, linseed oil; LPL, lipoprotein lipase; ME, metabolizable energy; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids; SFA, saturated fatty acids.

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1. Introduction

With the growing concern over the relationship between diet and health, there is an increase in emphasis on modification of fat and fatty acids composition of pork and other edible animal products. Therefore, the pork industry strives for efficient production of increasingly leaner pigs with greater concentrations of polyunsaturated fatty acids (PUFA) in pork. It is well established that feeding pattern and dietary fat sources affects the performance and tissue fatty acids composition (Apple et al., 2009; Daza et al., 2003; Więcek et al., 2010). It has been reported that the fatty acids composition of pork are influenced to a greater extent by the composition of dietary fat than the quantity of feed consumed (Gatlin et al., 2002; Więcek and Skomiał, 2004; Browne et al., 2013). Also, previous studies have reported that inclusion of vegetable oils to the diets of growing–finishing pigs increase the proportion of PUFA in adipose tissue (Rey et al., 2004; Apple et al., 2009; Więcek et al., 2010). On the other hand, restricted feeding may affect the relationship between intake of fatty acids and their level in individual tissues (Więcek and Skomiał, 2004; Daza et al., 2003). Wood (1984) reported that tissue PUFA concentrations were increased in pigs when fat deposition was reduced by restricted feeding as compared to *ad libitum* intake.

Several enzymes such as acetyl-CoA carboxylase (ACC), fatty acid synthase (FAS), hormone sensitive lipase (HSL) and lipoprotein lipase (LPL) are involved in adipose tissue fat metabolism and expression of genes related to these enzymes are affected by type of diet and dietary compositions (Duran-Montge et al., 2009; Zhao et al., 2010; Tous et al., 2012). Therefore, objectives of the present study was to investigate the effects of dietary fat sources and feeding level on performance, adipose tissue fatty acids profile and lipid metabolism related genes expression in adipose tissue of finisher pigs.

2. Materials and methods

The protocols for this experiment were approved by the Institutional Animal Care and Use Committee of Kangwon National University, Chuncheon, Republic of Korea. The experiment was conducted at the facility of Kangwon National University farm and finisher pigs (Landrace × Yorkshire × Duroc) were housed in partially slatted and concrete floor pens with a pen size of 2.80 m × 5.00 m. All pens were equipped with a nipple drinker to allow *ad libitum* access to water.

2.1. Animals, diets and management

A total of 128 finisher pigs [average initial body weight (BW), 81.2 ± 0.322 kg] were randomly allotted to 4 treatments on the basis of BW. There were 4 replicate pens in each treatment with 8 pigs per pen. Pigs were fed diets containing 50.0 g/kg linseed oil or animal fat, either *ad libitum* or restricted (15.0% less than *ad libitum*) in 2 × 2 factorial arrangement. Pigs of the *ad libitum* fed group were fed twice a day (to avoid feed wastage) at 9:00 and 18:00 h, whereas pigs of restricted fed group were fed once a day at 9:00 h. Diets were formulated to contain 13.82 MJ/kg of metabolizable energy (ME) and 8.50 g/kg lysine (Table 1) and fed in meal form for 28 d. All the diets met or exceeded current nutrient requirements for grower pigs (NRC, 1998). The ingredient and chemical composition of basal diets are presented in Table 1, whereas fatty acid compositions of experimental diets are presented in Table 2.

2.2. Experimental procedures, measurements, and analyses

Pigs were weighed individually, and feed consumption was measured at the end of experiment to calculate average daily gain (ADG), average daily feed intake (ADFI) and gain to feed ratio (G:F). To study the effects of dietary fat sources and feeding level on fatty acids composition and lipid metabolism related genes expression in adipose tissue, representative pigs from each group (2 per pen) reflecting the average BW were selected and sacrificed by electrocution on d 28 of experiment. Approximately 50.0 and 5.0 g subcutaneous adipose tissue samples from the longissimus dorsi at the 10–11th rib were collected separately and stored at −80 °C until analysis of fatty acids composition and lipid metabolism related genes (ACC, FAS, LPL and HSL) expression, respectively.

2.3. Fatty acid analysis

All layers of adipose tissue from the longissimus dorsi were utilized for fatty acid determination. Total lipid was extracted from the adipose tissue samples with a chloroform and methanol (2:1, v:v) mixture and quantified gravimetrically (Folch et al., 1957). Fatty acids in each lipid were derivatized to methyl esters according to Lepage and Roy (1986). Separation of fatty acid methyl esters was achieved by gas chromatography (Shimdzu, GC-17A, Japan) equipped with 100 m fused-silica capillary column with i.d. of 0.25 mm, a 0.20 μm film coating and SP^{TM}-2560 column stationary phase (Sigma–Aldrich Co. LLC) and a flame ionization detector. Oven temperature was maintained at 175 °C for 30 min, increased at 5 °C per min to 215 °C, and then increased at 10 °C per min to 235 °C. Injector and detector temperature was maintained at 260 °C. Methyl ester standards were used to identify sample fatty acid methyl esters.