**Divergent selection for intramuscular fat content in rabbits. II. Correlated responses on carcass and meat quality traits**

C. Zomeño, A. Blasco and P. Hernández

The online version of this article, along with updated information and services, is located on
the World Wide Web at:
http://www.journalofanimalscience.org/content/91/9/4532

American Society of Animal Science

www.asas.org

# Divergent selection for intramuscular fat content in rabbits.
## II. Correlated responses on carcass and meat quality traits[1]

**C. Zomeño, A. Blasco, and P. Hernández [2]**

Institute for Animal Science and Technology, Universitat Politècnica de València, PO Box 22012, 46022 Valencia, Spain

**ABSTRACT**: Correlated responses on carcass and meat quality characteristics after 3 generations of divergent selection for intramuscular fat (IMF) content were assessed by comparing the high and low lines. Selection was based on the phenotypic value of IMF content of LM, measured in 2 full sibs of the first parity. Traits measured were: BW, HCW, commercial carcass weight (CCW), reference carcass weight (RCW), scapular (SF) and perirenal fat (PF) content, meat-to-bone ratio (M:B) of the hind leg, pH of LM, color (lightness, L*; redness, a*; and yellowness, b*) of the carcass and of a LM section, protein content, and fatty acid (FA) composition of LM. A total of 174 records was used to estimate the correlated selection response. Data were analyzed using Bayesian methodology. We considered one-third of the phenotypic SD of a trait as a relevant value for the difference between lines. Then, the probability of the difference being greater than a relevant value ($P_R$) was calculated. A low $P_R$ implies that the lines compared are similar. Carcass weights ($P_R$ between 0.24 and 0.31) and M:B of the hind leg ($P_R = 0.15$) were not modified by selection for IMF content. There was a slight negative correlated response for BW, although evidence of its relevance was low ($P_R = 0.48$). Scapular fat content was similar between lines ($P_R = 0.03$). There were differences for PF content, although there was low evidence for showing its relevance ($P_R = 0.47$). Color traits of the carcass were not affected by selection ($P_R$ between 0.04 and 0.30). In muscle, L* was also similar between lines ($P_R = 0.26$). There were differences for a* and b*, although there was little evidence of their relevance ($P_R = 0.35$ and 0.40, respectively). There was a positive correlated response on muscle pH and differences could be relevant ($P_R = 0.77$). Protein content of LM was similar between lines ($P_R = 0.13$), whereas FA composition was affected by selection. There were relevant differences between lines for MUFA ($P_R = 0.99$), n-3 ($P_R = 0.95$), and n-6 ($P_R = 0.98$) percentages. For individual FA, differences were relevant for C18:1n-9 ($P_R = 0.97$) and C20:5 n-3 ($P_R = 0.98$). In conclusion, selection for IMF content may modify carcass quality by increasing PF content. Moreover, it led to some modifications in pH and FA composition of LM.

**Key words:** Bayesian inference, carcass quality, intramuscular fat, meat quality, rabbits, response to selection

## INTRODUCTION

The importance of intramuscular fat (**IMF**) content on meat quality is well established (Warriss, 2000;

Wood et al., 2008). The selection experiments developed in pigs (Suzuki et al., 2005a; Schwab et al., 2009) and cattle (Sapp et al., 2002) to increase IMF content showed that this trait responds to selection. A companion paper has reported that IMF can also be enhanced through selection in rabbits (Zomeño et al., 2013). However, there is little information about correlated responses on carcass and meat quality traits in pigs and cattle, and no information is available about rabbits.

Selection for IMF content may have consequences on other traits that should be considered. Intramuscular fat content is unfavorably genetically correlated to

4532

carcass fatness, as well as to carcass leanness (reviewed by Sellier, 1998), although these correlations showed a wide range of variation across studies. Estimates of genetic correlations between IMF and some meat quality traits have been reported (Suzuki et al., 2005b; Gjerlaug-Enger et al., 2010; Schwab et al., 2010). In rabbits, the number of publications reporting genetic parameters of meat quality traits is scarce (reviewed by Hernández and Gondret, 2006) and the genetic association between IMF and carcass and meat quality characteristics has not been investigated yet. Genetic correlations involving meat quality traits have high SE due to the difficulty of having a large amount of data to estimate them. The estimation of correlated responses is a more precise method to examine the consequences of selection for IMF on other traits.

The aim of this study was to assess the correlated responses on carcass and meat quality characteristics after 3 generations of divergent selection for IMF in rabbits.

## MATERIALS AND METHODS

All management and experimental procedures involving animals were approved by the Research Ethics Committee of the Universitat Politècnica de València.

### Animals and Experimental Design

Data from the third generation of a divergent selection experiment for IMF content of LM were used in this study. Animals were from a synthetic line, formerly selected for ovulation rate for 10 generations (Laborda et al., 2011). The base population consisted of 13 males and 83 females, obtained after selection for ovulation rate was relaxed for 2 generations. High, selected for increased IMF, and low, selected for reduced IMF, lines had ~8 males and 40 females per generation. Selection was performed on rabbits from the second parity based on the phenotypic value of IMF content measured mostly in 2 full sibs of the first parity. Some IMF measurements were made on the second or third parity. Selection pressure on females was on average 13% for the first generation and 26% for the second and third generations. Males were selected within sire families to reduce inbreeding. A total of 174 rabbits was used to estimate the correlated response on carcass and meat quality characteristics.

Animals were housed at the experimental farm of the Universitat Politècnica de València. Litters were homogenized by performing adoptions at birth, with 9 rabbits per litter. From weaning to 9 wk of age, rabbits were reared collectively and fed ad libitum, with a commercial diet formulated for growing rabbits with an average composition of 15.7% CP, 16.4% crude fiber, and 3.0%

fat. High and low lines were contemporarily raised. Feed intake was measured collectively during the growing period. Two rabbits (a male and a female) of the first parity of each doe were slaughtered at 9 wk of age.

### Carcass Quality Characteristics

Before slaughter, BW of rabbits were recorded. After slaughter, hot carcasses were weighed and were chilled for 24 h at 4°C. The weight of the chilled carcasses was recorded (**CCW**). These carcasses contained the head, liver, lungs, thymus, esophagus, heart, and kidneys, which were removed to obtain the reference carcass. The weight of the reference carcasses (**RCW**) was measured, containing only meat, fat, and bone. Scapular (**SF**) and perirenal fat (**PF**) were excised from the carcass and weighed. From the hind part of the carcass, the left leg was dissected to separate bone from edible meat and then the meat-to-bone ratio (**M:B**) was calculated. Carcass color (lightness, L*; redness, a*; and yellowness, b*) was measured on the surface of the fourth lumbar vertebra of the right side, using a CR300 Minolta Chroma Meter (Minolta Camera, Osaka, Japan).

### Meat Quality Characteristics

The muscle pH was measured at 24 h postmortem in the LM muscle at the level of the fifth lumbar vertebra of the left side and recorded with a Crison pH-meter Basic 20+ (Crison Instruments, Barcelona, Spain). The LM were excised from the carcass. Meat color was measured at the seventh lumbar vertebra transversal section of the right LM muscle. The variables L*, a*, and b* were recorded, as previously indicated. Meat obtained from LM was ground, freeze dried, and scanned with near infrared reflectance spectroscopy (**NIRS**; model 5000, FOSS NIRSystems Inc., Hillerod, Denmark). Protein content and fatty acid (**FA**) composition of LM was determined applying calibration equations previously developed (Zomeño et al., 2012). Protein content was expressed as g/100 g of muscle on a fresh basis and FA composition as a percentage of total FA.

### Statistical Analyses

Correlated responses on carcass and meat quality traits were estimated by comparing the high and low lines at the third generation of selection. Differences between lines for each trait were estimated by fitting the following univariate model:

$$y_{ijkl} = LG_i + S_j + PO_k + p_{ikl} + e_{ijkl}$$

where $y_{ijkl}$ is a phenotypic measure for a trait, $LG_i$ is the effect of line generation (7 levels: base population, H line-first generation, L line-first generation, H line-second generation, L line-second generation, H line-third generation, and L line-third generation), $S_j$ is the effect of gender (2 levels), $PO_k$ is the effect of parity order (3 levels), $p_{ikl}$ is the effect of common litter (334 levels), and $e_{ijkl}$ is the residual of the model.

Bayesian inference was used. Each trait was assumed to be conditionally distributed as follows:

$$\mathbf{y} \mid \mathbf{b}, \mathbf{p}, \sigma^2_e \sim N\,(\mathbf{Xb} + \mathbf{Wp}, \mathbf{I}\sigma^2_e),$$

where $\mathbf{b}$ is the vector including LG, S, and PO effects; $\mathbf{p}$ is the vector of common litter effects, including genetic and environmental effects of the litter; $\mathbf{X}$ and $\mathbf{W}$ are the known incidence matrices; $\sigma^2_e$ is the residual variance, and $\mathbf{I}$ is an identity matrix of appropriate order. Bounded uniform priors were used to represent vague previous knowledge of $\mathbf{b}$. Prior knowledge concerning common litter effects was represented by assuming that they were normally distributed, conditionally on the associated variance component, as follows:

$$\mathbf{p} \mid \sigma^2_p \sim N\,(\mathbf{0}, \mathbf{I}\sigma^2_p),$$

where $\sigma^2_p$ is the common litter variance and $\mathbf{I}$ is an identity matrix of the same order as the number of levels of common litter effects. Bounded uniform priors were used for residual and common litter variances.

Marginal posterior distributions for all unknowns were estimated using Gibbs sampling. The program Rabbit developed by Institute for Animal Science and Technology (Valencia, Spain) was used for all procedures. Chains of 60,000 samples with a burn-in period of 10,000 were used. One sample of each 10 was saved to avoid high correlations between consecutive samples. Convergence was tested using the Z-criterion of Geweke. Details of the procedure can be found in Blasco (2001). These parameters were obtained from the marginal posterior distributions of the differences between lines: median of the marginal posterior distribution of the difference ($\mathbf{D_{H-L}}$); probability of lines being different (probability of the difference between high and low lines being >0 when this difference is >0, or probability of the difference being <0 when this difference is <0; $\boldsymbol{P}$); greatest posterior density region at 95% ($\mathbf{HPD_{95\%}}$); guaranteed value of a difference ($\mathbf{k}$) with a probability of 80% (limit of interval [k, +∞) when the difference is >0 or limit of interval (−∞, k] when the difference is <0) and probability of relevance (probability of the difference being greater than a relevant value; $\boldsymbol{P_R}$). The use of Bayesian inference in meat quality analyses was proposed by Blasco (2005). A relevant value ($\mathbf{R}$) is a minimum amount having biological or economic significance, and it is the difference to be detected in experimental designs. For most productive traits, the economic importance of a difference is relevant when it ranges between one-half and one-third of SD of the trait. Thus, we considered one-third of the phenotypic SD of each trait as a relevant value for the differences between lines. The SD was calculated using all data of the selection experiment (668 rabbits). The k values are displayed in tables only when $D_{H-L}$ and k value have the same sign.

## RESULTS

Descriptive statistics of BW and carcass composition are presented in Table 1. Table 2 shows descriptive statistics for carcass and meat quality measurements, and Tables 3 and 4 for protein content and FA composition.

For all the traits analyzed, Monte Carlo SE were very small. Therefore, they are not displayed in the tables. The Geweke test did not detect lack of convergence in any case.

### Correlated Response on Body Weight and Carcass Measurements

Features of the marginal posterior distributions of the differences between high and low lines for BW and carcass composition in the third generation of selection are shown in Table 5. Body weights and carcass weights were greater in the low line than in the high line ($P$ between 0.83 and 0.96). However, the estimated differences represent a low percentage of the mean (2.95% for BW, 2.14% for HCW, 1.85% for CCW, and 2.06% for RCW) and guaranteed values of differences with a probability of 80% were very small. In some cases, we are also interested in knowing which will be the minimum difference between lines with a determined probability. When using estimates of the difference in this discussion, we only guarantee a minimum value with a probability of 50%. Thus, a minimum value with a probability of 80% improves the discussion. Notice that although 0

**Table 1**. Descriptive statistics of BW (g) and carcass composition (g) of rabbits

| Trait[1] | Mean | SD | CV × 100 | No. animals |
|---|---|---|---|---|
| BW | 1,651 | 138 | 8.4 | 174 |
| HCW | 983 | 83 | 8.4 | 174 |
| CCW | 943 | 82 | 8.7 | 174 |
| RCW | 748 | 68 | 9.1 | 174 |
| SF | 3.33 | 0.83 | 25.0 | 173 |
| PF | 6.66 | 2.18 | 32.7 | 174 |

[1]CCW = chilled carcass weight; RCW = reference carcass weight; SF = scapular fat content; PF = perirenal fat content.

**Table 2.** Descriptive statistics of carcass and meat quality measurements of rabbits

| Trait[1] | Mean | SD | CV × 100 | No. animals |
|---|---|---|---|---|
| M:B | 4.30 | 0.55 | 12.8 | 114 |
| C L* | 55.2 | 2.4 | 4.3 | 173 |
| C a* | 3.43 | 0.92 | 26.7 | 174 |
| C b* | −0.66 | 1.88 | −285 | 167 |
| LM pH | 5.59 | 0.10 | 1.7 | 174 |
| LM L* | 53.4 | 2.6 | 4.8 | 173 |
| LM a* | 3.96 | 1.11 | 28.0 | 174 |
| LM b* | 0.91 | 0.83 | 91.4 | 173 |

[1]M:B = meat-to-bone ratio of the hind leg; C L* = lightness of the carcass surface; C a* = redness of the carcass surface; C b* = yellowness of the carcass surface; LM pH = pH of LM; LM L* = lightness of LM; LM a* = redness of LM.; LM b* = yellowness of LM.

was included in some $HPD_{95\%}$, $P$ was >0.95. This is because the right tail of the distribution is considered in $P$ but not in $HPD_{95\%}$; see Blasco (2005). In this study, we have considered one-third of the phenotypic SD of a trait as a relevant difference between lines. The probability of the difference being greater than R was intermediate for BW ($P_R = 0.48$), indicating little evidence for showing whether differences were relevant or not. For carcass weights, differences were not relevant, as indicated by the low $P_R$ (between 0.24 and 0.31). For SF content, differences between lines were irrelevant ($P_R = 0.03$; Table 5). However, for PF content, the high line had a greater value than the low line ($P = 0.95$), with the difference being 1.06 g. This represents a correlated response of 15.9% of its mean. This difference was at least 0.53 g, with a probability of 80%. Considering 1.10 g as a relevant value, there was low evidence for showing whether differences were relevant or not ($P_R = 0.47$).

**Table 3.** Descriptive statistics of protein content (g/100g muscle) and fatty acid composition (percentage of total fatty acids) of LM

| Trait[1] | Mean | SD | CV × 100 | No. animals |
|---|---|---|---|---|
| Protein | 21.7 | 0.4 | 2.0 | 174 |
| SFA | 35.7 | 2.1 | 6.0 | 174 |
| MUFA | 23.7 | 2.2 | 9.1 | 174 |
| PUFA | 39.8 | 3.6 | 9.1 | 174 |
| n-3 | 7.07 | 0.86 | 12.2 | 174 |
| n-6 | 33.4 | 2.4 | 7.1 | 174 |
| n-6/n-3 | 4.64 | 0.39 | 8.4 | 170 |
| PUFA/SFA | 1.16 | 0.06 | 5.6 | 174 |

[1]SFA = C14:0 + C15:0 + C16:0 + C17:0 + C18:0; MUFA = C16:1 + C18:1n-9 + C18:1n-7; PUFA = C18:2n-6 + C18:3n-3 + C20:2n-6 + C20:3n-6 + C20:4n-6 + C20:5n-3 + C22:4n-6 + C22:5n-3 + C22:6n-3; n-3 = C18:3n-3 + C20:5n-3 + C22:5n-3 + C22:6n-3; n-6 = C18:2n-6 + C20:2n-6 + C20:3n-6 + C20:4n-6 + C22:4n-6.

**Table 4.** Descriptive statistics of individual fatty acid composition (percentage of total fatty acids) of LM of rabbits

| Trait | Mean | SD | CV × 100 | No. animals |
|---|---|---|---|---|
| C14:0 | 1.36 | 0.32 | 23.8 | 174 |
| C15:0 | 0.48 | 0.02 | 4.2 | 174 |
| C16:0 | 21.7 | 1.5 | 7.1 | 174 |
| C16:1 | 0.89 | 0.55 | 62.1 | 150 |
| C17:0 | 0.70 | 0.04 | 5.7 | 174 |
| C18:0 | 8.79 | 0.63 | 7.2 | 174 |
| C18:1 n-7 | 1.67 | 0.12 | 7.0 | 173 |
| C18:1 n-9 | 20.0 | 1.7 | 8.6 | 174 |
| C18:2 n-6 | 21.5 | 1.8 | 8.6 | 174 |
| C18:3 n-3 | 1.25 | 0.30 | 24.0 | 172 |
| C20:2 n-6 | 0.32 | 0.04 | 11.1 | 169 |
| C20:3 n-6 | 0.62 | 0.08 | 13.7 | 168 |
| C20:4 n-6 | 6.48 | 1.00 | 15.5 | 169 |
| C20:5 n-3 | 1.89 | 0.36 | 18.9 | 171 |
| C22:4 n-6 | 2.37 | 0.37 | 15.8 | 174 |
| C22:5 n-3 | 0.98 | 0.19 | 19.3 | 169 |
| C22:6 n-3 | 3.34 | 0.70 | 21.0 | 167 |

***Correlated Response on Carcass and Meat Quality Characteristics***

Table 6 shows features of estimated marginal posterior distributions of the differences between high and low lines for carcass and meat quality characteristics. The M:B ratio of the hind leg was not affected by the selection process ($P_R = 0.15$). Line low showed greater values for L* ($P = 0.87$) and b* ($P = 0.96$) of the carcass. However, differences were not relevant ($P_R = 0.28$

**Table 5.** Features of estimated marginal posterior distributions of differences between high and low lines for BW (g) and carcass composition (g)

| Trait | $D_{H-L}$[1] | $P$[2] | $HPD_{95\%}$[3] | | $k_{80\%}$[4] | R[5] | $P_R$[6] |
|---|---|---|---|---|---|---|---|
| BW | −48.8 | 0.96 | −109 | 4.45 | −25.8 | −50 | 0.48 |
| HCW | −21.0 | 0.88 | −56.1 | 14.8 | −6.06 | −30 | 0.31 |
| CCW[7] | −17.4 | 0.83 | −54.9 | 16.2 | −2.17 | −30 | 0.24 |
| RCW[7] | −15.4 | 0.85 | −44.0 | 14.9 | −3.20 | −25 | 0.27 |
| SF[7] | −0.05 | 0.60 | −0.39 | 0.36 | – | −0.40 | 0.03 |
| PF[7] | 1.06 | 0.95 | −0.11 | 2.34 | 0.53 | 1.10 | 0.47 |

[1]$D_{H-L}$ = median of the marginal posterior distribution of difference.

[2]$P$ = probability of the difference being >0 when $D_{H-L}$ >0 and probability of the difference being <0 when $D_{H-L}$ <0.

[3]$HPD_{95\%}$ = greatest posterior density region at 95% of probability.

[4]$k_{80\%}$ = limit of the interval [k, +∞) when $D_{H-L}$ >0 and (-∞, k] when $D_{H-L}$ <0 at 80% of probability. It is displayed in the table only when $D_{H-L}$ and $k_{80\%}$ have the same sign.

[5]R = relevant value defined as one-third of SD of the trait.

[6]$P_R$ = probability of relevance (probability of the difference being greater than R).

[7]CCW = chilled carcass weight; RCW = reference carcass weight; SF = scapular fat content; PF = perirenal fat content.

**Table 6.** Features of the estimated marginal posterior distributions of the differences between high and low lines for carcass and meat quality measurements

| Trait | $D_{H-L}$[1] | $P$[2] | HPD$_{95\%}$[3] | | $k_{80\%}$[4] | R[5] | $P_R$[6] |
|---|---|---|---|---|---|---|---|
| M:B[7] | 0.07 | 0.72 | –0.18 | 0.31 | – | 0.20 | 0.15 |
| C L*[7] | –0.53 | 0.87 | –1.48 | 0.35 | –0.14 | –0.80 | 0.28 |
| C a*[7] | –0.04 | 0.60 | –0.33 | 0.27 | – | –0.30 | 0.04 |
| C b*[7] | –0.47 | 0.96 | –1.03 | 0.05 | –0.24 | –0.60 | 0.30 |
| LM pH | 0.04 | 0.99 | 0.01 | 0.08 | 0.03 | 0.03 | 0.77 |
| LM L*[7] | –0.51 | 0.88 | –1.41 | 0.32 | –0.15 | –0.80 | 0.26 |
| LM a*[7] | –0.28 | 0.95 | –0.63 | 0.05 | –0.14 | –0.35 | 0.35 |
| LM b*[7] | –0.26 | 0.97 | –0.54 | 0.01 | –0.14 | –0.30 | 0.40 |

[1]$D_{H-L}$ = median of the marginal posterior distribution of difference.

[2]$P$ = probability of the difference being >0 when $D_{H-L}$ >0 and probability of the difference being <0 when $D_{H-L}$ <0.

[3]HPD$_{95\%}$ = greatest posterior density region at 95% of probability.

[4]$k_{80\%}$ = limit of the interval [k, +Y) when $D_{H-L}$ >0 and (-Y, k] when $D_{H-L}$ <0 at 80% of probability. It is displayed in the table only when $D_{H-L}$ and $k_{80\%}$ have the same sign.

[5]$R$ = relevant value defined as one-third of SD of the trait.

[6]$P_R$ = probability of relevance (probability of the difference being greater than R).

[7]M:B = meat-to-bone ratio of the hind leg; C L* = lightness of the carcass surface; C a* = redness of the carcass surface; C b* = yellowness of the carcass surface; LM L* = lightness of LM; LM a* = redness of LM; LM b* = yellowness of LM.

**Table 7.** Features of the estimated marginal posterior distributions of the differences between high and low lines for protein content (g/100g muscle) and fatty acid composition (percentage of total fatty acids) of LM

| Trait | $D_{H-L}$[1] | $P$[2] | HPD$_{95\%}$[3] | | $k_{80\%}$[4] | R[5] | $P_R$[6] |
|---|---|---|---|---|---|---|---|
| Protein | –0.05 | 0.72 | –0.23 | 0.12 | – | –0.15 | 0.13 |
| SFA[7] | 0.86 | 0.98 | 0.00 | 1.65 | 0.50 | 0.70 | 0.64 |
| MUFA[7] | 1.58 | 1 | 0.85 | 2.33 | 1.27 | 0.70 | 0.99 |
| PUFA[7] | –1.57 | 0.99 | –2.85 | –0.32 | –1.02 | –1.10 | 0.79 |
| n-3[7] | –0.47 | 1 | –0.75 | –0.22 | –0.36 | –0.25 | 0.95 |
| n-6[7] | –1.87 | 1 | –2.79 | –0.91 | –1.47 | –0.90 | 0.98 |
| n-6/n-3 | 0.19 | 0.99 | 0.02 | 0.34 | 0.12 | 0.15 | 0.67 |
| PUFA/SFA | –0.04 | 1 | –0.07 | –0.01 | –0.03 | –0.03 | 0.80 |

[1]$D_{H-L}$ = median of the marginal posterior distribution of difference.

[2]$P$ = probability of the difference being >0 when $D_{H-L}$ >0 and probability of the difference being <0 when $D_{H-L}$ <0.

[3]HPD$_{95\%}$ = greatest posterior density region at 95% of probability.

[4]$k_{80\%}$ = limit of the interval [k, +∞) when $D_{H-L}$ >0 and (-∞, k] when $D_{H-L}$ <0 at 80% of probability. It is displayed in the table only when $D_{H-L}$ and $k_{80\%}$ have the same sign.

[5]$R$ = relevant value defined as one-third of SD of the trait.

[6]$P_R$ = probability of relevance (probability of the difference being greater than R).

[7]SFA = C14:0 + C15:0 + C16:0 + C17:0 + C18:0; MUFA = C16:1 + C18:1n-9 + C18:1n-7; PUFA = C18:2n-6 + C18:3n-3 + C20:2n-6 + C20:3n-6 + C20:4n-6 + C20:5n-3 + C22:4n-6 + C22:5n-3 + C22:6n-3; n-3 = C18:3n-3 + C20:5n-3 + C22:5n-3 + C22:6n-3; n-6 = C18:2n-6 + C20:2n-6 + C20:3n-6 + C20:4n-6 + C22:4n-6.

and 0.30, respectively). Differences for a* of the carcass were also irrelevant ($P_R$ = 0.04). Muscle pH was higher in the high line than in the low line ($P$ = 0.99), with a difference between lines of 0.04. This difference was at least 0.03, with a probability of 80%. The $P_R$ was moderately high for this trait (0.77), indicating that the difference could have some consequences on meat quality. Color parameters of the muscle (L*, a*, and b*) were greater in line low ($P$ between 0.88 and 0.97), but differences were not relevant for L* ($P_R$ = 0.26). For a* and b*, the intermediate $P_R$ (0.35 and 0.40, respectively) showed low precision for inferring on the relevance of differences.

Features of estimated marginal posterior distributions of the differences between the high and low lines for protein content and FA composition of LM are presented in Tables 7 and 8. Differences for protein content were irrelevant ($P_R$ = 0.13). However, there were differences for FA composition. Saturated FA and MUFA percentages were greater in the high line than in the low line ($P$ = 0.98 and 1, respectively). Conversely, PUFA ($P$ = 0.99), n-3, and n-6 ($P$ = 1) percentages were greater in the low line. Favorable values for FA ratios were found for the low line, exhibiting decreased n-6/n-3 values and greater PUFA/SFA values than the high line ($P$ = 0.99 and 1, respectively). Differences for MUFA, n-3, and n-6 percentages were relevant ($P_R$ between 0.95 and 0.99). For SFA and PUFA percentages, as well as n-6:n-3

and PUFA:SFA ratios, there was a moderate to high $P_R$ ($P_R$ between 0.64 and 0.80), indicating that differences might be relevant.

The high line showed greater values for C14:0, C15:0, C16:0, C16:1, and C18:1 n-9 and C18:3 n-3 percentages ($P$ between 0.87 and 1; Table 8). The low line had greater percentages of C17:0, C18:0, C18:1 n-7, C18:2 n-6, and long-chain PUFA ($P$ between 0.82 and 1; Table 8). Differences for C18:1 n-9, C20:5 n-3, and C22:4 n-6 were relevant ($P_R$ between 0.92 and 0.98). The $P_R$ ranged from moderate to high for C14:0, C18:0, C20:3n-6, and C20:4 n-6 ($P_R$ between 0.80 and 0.88), showing that differences can be relevant. For C16:0, C16:1, and C22:6 n-3, $P_R$ was intermediate (between 0.56 and 0.65), indicating that there was low evidence of its relevance. The differences for C15:0, C17:0, C18:1 n-7, and C20:2 n-6 percentages were very small. They represent a small percentage of the mean (between 1.79 and 3.13%) and were not relevant ($P_R$ between 0.19 and 0.33). Similarly, differences for C18:2 n-6, C18:3 n-3, and C22:5 n-3 were not relevant ($P_R$ between 0.07 and 0.25).

## DISCUSSION

Rabbit carcasses have a small percentage of dissectible fat (Pla et al., 1996). Scapular and perirenal fat tissues are 2 of the main carcass fat depots and, on

**Table 8.** Features of the estimated marginal posterior distributions of the differences between high and low lines for individual fatty acid composition (percentage of total fatty acids) of LM

| Trait | $D_{H-L}$[1] | $P$[2] | HPD$_{95\%}$[3] | | $k_{80\%}$[4] | $R$[5] | $P_R$[6] |
|---|---|---|---|---|---|---|---|
| C14:0 | 0.16 | 1 | 0.04 | 0.28 | 0.11 | 0.10 | 0.85 |
| C15:0 | 0.01 | 0.96 | 0.00 | 0.01 | 0.01 | 0.01 | 0.19 |
| C16:0 | 0.65 | 0.98 | 0.05 | 1.23 | 0.39 | 0.60 | 0.56 |
| C16:1 | 0.29 | 1 | 0.07 | 0.51 | 0.19 | 0.20 | 0.65 |
| C17:0 | −0.02 | 0.97 | −0.03 | 0.00 | −0.01 | −0.02 | 0.33 |
| C18:0 | −0.33 | 1 | −0.53 | −0.12 | −0.24 | −0.20 | 0.88 |
| C18:1 n-7 | −0.03 | 0.86 | −0.07 | 0.02 | −0.01 | −0.04 | 0.27 |
| C18:1 n-9 | 1.16 | 1 | 0.59 | 1.73 | 0.92 | 0.50 | 0.97 |
| C18:2 n-6 | −0.34 | 0.82 | −1.12 | 0.34 | −0.04 | −0.60 | 0.25 |
| C18:3 n-3 | 0.06 | 0.87 | −0.04 | 0.15 | 0.02 | 0.10 | 0.10 |
| C20:2 n-6 | −0.01 | 0.94 | −0.03 | 0.00 | −0.01 | −0.02 | 0.28 |
| C20:3 n-6 | −0.06 | 1 | −0.10 | −0.02 | −0.05 | −0.04 | 0.88 |
| C20:4 n-6 | −0.45 | 0.99 | −0.81 | −0.13 | −0.31 | −0.30 | 0.80 |
| C20:5 n-3 | −0.24 | 1 | −0.36 | −0.10 | −0.18 | −0.10 | 0.98 |
| C22:4 n-6 | −0.19 | 1 | −0.31 | −0.06 | −0.14 | −0.10 | 0.92 |
| C22:5 n-3 | −0.03 | 0.84 | −0.10 | 0.03 | 0.00 | −0.06 | 0.07 |
| C22:6 n-3 | −0.23 | 0.97 | −0.48 | 0.01 | −0.12 | −0.20 | 0.60 |

[1]$D_{H-L}$ = median of the marginal posterior distribution of difference.

[2]$P$ = probability of the difference being >0 when $D_{H-L}$ >0 and probability of the difference being <0 when $D_{H-L}$ <0.

[3]HPD$_{95\%}$ = greatest posterior density region at 95% of probability.

[4]$k_{80\%}$ = limit of the interval [k, +∞) when $D_{H-L}$ >0 and (-∞, k] when $D_{H-L}$ <0 at 80% of probability. It is displayed in the table only when $D_{H-L}$ and $k_{80\%}$ have the same sign.

[5]$R$ = relevant value defined as one-third of SD of the trait.

[6]$P_R$ = probability of relevance (probability of the difference being greater than R).

average, account for 65% of carcass dissectible fat in the rabbit (Hernández et al., 2006). In this study, SF and PF represented a very small percentage of the chilled carcass (1.06%), which is in line with previous studies (Hernández et al., 2006; Zomeño et al., 2010).

Values for carcass and meat color variables, and muscle pH were similar to those obtained in previous studies (Hernández et al., 2004, 2006). The M:B ratio of the hind leg, used as an indicator of the M:B ratio of carcass (Hernández et al., 1996), was less than in other studies. Results for protein content and FA profile obtained in this study were close to values reported for LM of rabbits (reviewed by Hernández and Dalle Zotte, 2010).

### Correlated Response on Body Weight and Carcass Measurements

After 3 generations of divergent selection for IMF, the difference between high and low lines for IMF content was 0.09 g/100 g of muscle (Zomeño et al., 2013). This difference represents a direct selection response of 9% of its mean. Selection for IMF content resulted in a

slightly negative correlated response on BW. However, carcass weight and M:B ratio, which determine carcass yield, were not affected by selection for IMF. Regarding adipose tissues of the carcass, SF content was not modified, but there was a positive correlated response on PF content. These findings are in agreement with Schwab et al. (2009), who obtained no correlated responses in growth performance traits and greater values of backfat measurements (mm) in a pig line selected for increased IMF. Genetic correlations between IMF content and backfat have been studied in pigs, showing a wide range—from 0.04 (reviewed by Sellier, 1998) to 0.64 (Solanes et al., 2009). These estimates suggest that part of the genetic variation of IMF is independent of the genetic variation in overall lipid content of the carcass. In fact, Sapp et al. (2002) obtained no correlated response on fat thickness in bulls selected for IMF content, indicating that selection for increased IMF can be achieved without increasing carcass fat.

### Correlated Response on Carcass and Meat Quality Characteristics

Meat color is related to the appearance of the product and consequently it is crucial for the consumer. Rabbit carcasses are usually commercialized as whole, but retail cuts are increasing in importance. Hence, carcass and muscle color are essential quality traits. Carcass color traits were not affected by selection for IMF. In muscle, L* was also similar between lines. However, there was a response on a* and b*, with low evidence of its relevance. Schwab et al. (2009) observed an increased muscle light reflectance and Hunter L* in a pig line selected for increased IMF. Different values of genetic correlations between lightness and IMF have been published. In pigs, Sellier (1998) reported a null genetic correlation, whereas Suzuki et al. (2005b) and Schwab et al. (2010) estimated moderate positive genetic correlations (0.42 and 0.52, respectively) and Gjerlaug-Enger et al. (2010) reported a moderately low negative genetic correlation (–0.20).

Selection for IMF resulted in a positive correlated response on muscle pH. This finding is consistent with the relationship between ultimate pH and postmortem metabolism of muscle. Greater IMF can lead to an increase in oxidative metabolism and, consequently, to an increased postmortem pH (Gjerlaug-Enger et al., 2010). To our knowledge, only 1 study investigated the correlated response on muscle pH [Schwab et al. (2009) in pigs], but no effect of selection for IMF was detected on this trait. A wide range of estimates of genetic correlations between IMF and muscle pH in pigs have been published. Suzuki et al. (2005b) reported a moderate negative relationship (–0.51); Schwab et al. (2010) found no

relevant association (0.01); and Gjerlaug-Enger et al. (2010) estimated small (0.11) or moderate (0.42) positive genetic correlations.

Rabbit meat is characterized by reduced fat and greater protein content, and favorable FA composition, compared with meat of other species (Hernández and Gondret, 2006). Results of this experiment showed no correlated response on protein content. Previous selection experiments for IMF content did not focus on correlated response on protein content. To our knowledge, there is only 1 study reporting genetic correlations between protein and IMF content [Gjerlaug-Enger et al. (2010), in pig], in which moderate negative genetic correlations were estimated.

The positive correlated responses on SFA and MUFA percentages, and negative correlated responses on PUFA percentage and PUFA:SFA ratio are related to the direct selection response on IMF content. Lines were contemporarily raised and fed with the same diet. The feed intake during the growing period was also similar for both lines (1.68 and 1.66 kg of feed/kg of BW in high and low lines, respectively). Thus, correlated response on FA composition should be attributed to the selection process for IMF. De Smet et al. (2004) highlighted an increase in SFA and MUFA content, and a decrease in PUFA with increasing fat content, resulting in a decrease of the relative proportion of PUFA and reduction in the PUFA:SFA ratio. According to these authors, the relationship between fat content and FA composition is explained by the different FA composition of the 2 major lipid fractions, phospholipids and triacylglycerols, and by the relative contribution of these fractions to total lipids. Similarly, Sellier et al. (2010) reported a negative genetic correlation between IMF and PUFA:SFA ratio (–0.39), as well as between PUFA and SFA (–0.83), and MUFA (–0.73) percentages of LM in pigs. A positive relationship was also found by Nogi et al. (2011) between IMF and MUFA (0.23) in beef cattle.

The PUFA:SFA and n-6:n-3 ratios are used to evaluate the nutritional quality of the meat. Our results showed values close to the recommendations (>0.45 for PUFA/SFA and <4 for n-6/n-3; Hernández and Dalle Zotte, 2010), and were more favorable for low line, with greater PUFA/SFA and lower n-6/n-3 values, than for high line.

The correlated response on the individual FA percentages showed a similar pattern as for the FA groups, with an increase in SFA (C14:0 and C16:0) and MUFA (C16:1 and C18:1 n-9), and a decrease in PUFA (C20:3 n-6, C20:4 n-6, C20:5 n-3, C22:4 n-6, and C22:6 n-3) in the line selected for increased IMF, although there was low evidence for showing the relevance of the response on C16:0, C16:1, and C22:6 n-3. When measuring C20:3 n-6, C22:4 n-6, and C22:6 n-3 with NIRS, we obtained

a very poor accuracy (Zomeño et al., 2012). Thus, estimated differences between lines for these FA should be treated with caution. Suzuki et al. (2006) reported positive genetic correlations between IMF and C14:0 (0.21) and C16:0 (0.49) in pigs. Pitchford et al. (2002) also obtained a positive genetic association between IMF and C16:0 (0.43) in beef cattle. A moderately high genetic correlation between IMF and C18:1 n-9 (0.47) in pigs was reported by Ros-Freixedes et al. (2012). In beef cattle, small but also positive genetic correlations were reported by Nogi et al. (2011) between IMF and C18:1n-9 (0.19). These authors also obtained a negative genetic correlation between IMF and C18:0 (–0.27), which is in line with the negative correlated response on this FA found in our study.

Several thousands of data are needed to estimate genetic correlations accurately. Due to the difficulty of having a large amount of data in meat quality experiments, genetic correlations of the studies mentioned above have large SE. Results of the present experiment, based on a comparison between lines, confirm reported correlations and display a greater precision.

In conclusion, carcass quality may be affected by selection for IMF content, producing an increase in PF content. However, there was low evidence of the relevance of the response on this trait. Selection for IMF content also led to some modifications in muscle pH and FA composition.

## LITERATURE CITED

Blasco, A. 2001. The Bayesian controversy in animal breeding. J. Anim. Sci. 79:2023–2046.

Blasco, A. 2005. The use of Bayesian statistics in meat quality analyses: A review. Meat Sci. 69:115–122.

De Smet, S., K. Raes, and D. Demeyer. 2004. Meat fatty acid composition as affected by fatness and genetic factors: A review. Anim. Res. 53:81–98.

Gjerlaug-Enger, E., L. Aass, J. Odegard, and O. Vangen. 2010. Genetic parameters of meat quality traits in two pig breeds measured by rapid methods. Animal 4:1832–1843.

Hernández, P., S. Aliaga, M. Pla, and A. Blasco. 2004. The effect of selection for growth rate and slaughter age on carcass composition and meat quality traits in rabbits. J. Anim. Sci. 82:3138–3143.

Hernández, P., B. Ariño, A. Grimal, and A. Blasco. 2006. Comparison of carcass and meat characteristics of three rabbit lines selected for litter size or growth rate. Meat Sci. 73:645–650.

Hernández, P., and A. Dalle Zotte. 2010. Influence of diet on rabbit meat quality. In: C. de Blas, and J. Wiseman, editors, Nutrition of the rabbit. CAB Int., Wallinford, Oxon, UK. p. 163–178.

Hernández, P., and F. Gondret. 2006. Rabbit meat quality and safety. In: L. Maertens and P. Coudert, editors, Recent advances in rabbit sciences. ILVO, Melle, Belgium. p. 267–290.

Hernández, P., M. Pla, and A. Blasco. 1996. Prediction of carcass composition in the rabbit. Meat Sci. 44:75–83.

Laborda, P., M. L. Mocé, M. A. Santacreu, and A. Blasco. 2011. Selection for ovulation rate in rabbits: Genetic parameters, direct response, and correlated response on litter size. J. Anim. Sci. 89:2981–2987.

Nogi, T., T. Honda, F. Mukai, T. Okagaki, and K. Oyama. 2011. Heritabilities and genetic correlations of fatty acid compositions in longissimus muscle lipid with carcass traits in Japanese Black cattle. J. Anim. Sci. 89:615–621.

Pitchford, W. S., M. P. B. Deland, B. D. Siebert, A. E. O. Malau-Aduli, and C. D. K. Bottema. 2002. Genetic variation in fatness and fatty acid composition of crossbred cattle. J. Anim. Sci. 80:2825–2832.

Pla, M., P. Hernández, and A. Blasco. 1996. Carcass composition and meat characteristics of two rabbit breeds of different degrees of maturity. Meat Sci. 44:85–92.

Ros-Freixedes, R., J. Reixach, M. Tor, and J. Estany. 2012. Expected genetic response for oleic acid content in pork. J. Anim. Sci. 90:4230–4238.

Sapp, R. L., J. K. Bertrand, T. D. Pringle, and D. E. Wilson. 2002. Effect of selection for ultrasound intramuscular fat percentage in Angus bulls on carcass traits of progeny. J. Anim. Sci. 80:2017–2022.

Schwab, C. R., T. J. Baas, and K. J. Stalder. 2010. Results from six generations of selection for intramuscular fat in Duroc swine using real-time ultrasound. II. Genetic parameters and trends. J. Anim. Sci. 88:69–79.

Schwab, C. R., T. J. Baas, K. J. Stalder, and D. Nettleton. 2009. Results from six generations of selection for intramuscular fat in Duroc swine using real-time ultrasound. I. Direct and correlated phenotypic responses to selection. J. Anim. Sci. 87:2774–2780.

Sellier, P. 1998. Genetics of meat and carcass traits. In: M. F. Rothschild and A. Ruvinsky, editors, The genetics of the pig. CAB Int., New York. p. 463–510.

Sellier, P., L. Maignel, and P. Bidanel. 2010. Genetic parameters for tissue and fatty acid composition of backfat, perirenal fat and longissimus muscle in Large White and Landrace pigs. Animal 4:497–504.

Solanes, F. X., J. Reixach, M. Tor, J. Tibau, and J. Estany. 2009. Genetic correlations and expected response for intramuscular fat content in a Duroc pig line. Livest. Sci. 123:63–69.

Suzuki, K., M. Irie, H. Kadowaki, T. Shibata, M. Kumagai, and A. Nishida. 2005b. Genetic parameter estimates of meat quality traits in Duroc pigs selected for average daily gain, longissimus muscle area, backfat thickness, and intramuscular fat content. J. Anim. Sci. 83:2058–2065.

Suzuki, K., M. Ishida, H. Kadowaki, T. Shibata, H. Uchida, and A. Nishida. 2006. Genetic correlations among fatty acid compositions in different sites of fat tissues, meat production, and meat quality traits in Duroc pigs. J. Anim. Sci. 84:2026–2034.

Suzuki, K., H. Kadowaki, T. Shibata, H. Uchida, and A. Nishida. 2005a. Selection for daily gain, loin-eye area, backfat thickness and intramuscular fat based on desired gains over seven generations of Duroc pigs. Livest. Prod. Sci. 97:193–202.

Warriss, P. D. 2000. Meat science. An introductory text. CABI Publishing, Wallinford, Oxon, UK.

Wood, J. D., M. Enser, A. V. Fisher, G. R. Nute, P. R. Sheard, R. I. Richardson, S. I. Hughes, and F. M. Whittington. 2008. Fat deposition, fatty acid composition and meat quality: A review. Meat Sci. 78:343–358.

Zomeño, C., A. Blasco, and P. Hernández. 2010. Influence of genetic line on lipid metabolism traits of rabbit muscle. J. Anim. Sci. 88:3419–3427.

Zomeño, C., P. Hernández, and A. Blasco. 2013. Divergent selection for intramuscular fat content in rabbits. I. Direct response to selection. J. Anim. Sci. 90:4526–4561.

Zomeño, C., V. Juste, and P. Hernández. 2012. Application of NIRS for predicting fatty acids in intramuscular fat of rabbit. Meat Sci. 91:155–159.

| References | This article cites 24 articles, 12 of which you can access for free at: |
|---|---|
| | http://www.journalofanimalscience.org/content/91/9/4532#BIBL |
| **Citations** | This article has been cited by 1 HighWire-hosted articles: |
| | http://www.journalofanimalscience.org/content/91/9/4532#otherarticles |