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Genetic analysis of meat quality traits in maternal lines of rabbit and their diallel cross☆

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ABSTRACT

Young rabbits, the dams of which came from a full diallel cross among four maternal lines (A, V, H and LP) and the sires from a single paternal line (R), that produce sixteen genetic groups, was carried out to evaluate the genetic groups and to estimate the crossbreeding genetic parameters of meat quality. The meat quality traits were recorded by NIRS from a sample of 285 *longissimus lumborum* muscles. Crossbreeding parameters were estimated according to Dickerson model. No differences in protein were found. The line A had significant differences with V line for intramuscular fat, and fatty acids groups. Significant differences for these traits appeared between the crossbred AH and VV (in favor of AH). As conclusion, the significant contrasts between genetic types for chemical composition of the meat are mainly consequence of direct-maternal genetic effects, having grandmaternal and maternal heterosis effects a less relevant role.

1. Introduction

Meat rabbit selection programs improves, between other traits, litter size in dam lines and growth rate in sire lines (Baselga, 2004; Rochambeau, 1988). Maximizing growth potential of sire lines is important to ensure the economic viability of rabbits producers (Cartuche, Pascual, Gómez, & Blasco, 2014); however, it can produce an undesirable effect on meat and carcass qualities because the degree of maturity at market weight is reduced (Pascual, 2007). Meat quality is a generic term used to describe properties and perceptions of meat: sensory characteristics, nutritional properties, healthiness, technological factors, microbiological and chemical safety and ethical and environment aspects. Rabbit meat has good nutritive properties because it has lower fat and higher polyunsaturated fatty acid (PUFA) content than other meats (Hernández & Gondret, 2006). The most ubiquitous fatty acids (FA) are palmitic (C16:0), oleic (C18:1 n-9) and linoleic (C18:2 n-6) acids, showing percentages higher than 20% of total FA. Rabbit meat also contains high protein content and high levels of essential amino acids (Hernández & Dalle Zotte, 2010).

Traditional methods used to determine meat chemical composition are laborious, expensive, time-consuming and destructive. New methods for meat quality evaluation were used by researchers, as e.g. ultrasound, electric nose, tastes sensing, NIRS, TOBEC and Video Image Analysis (Cross & Belk, 1992). NIRS (near infrared reflectance spectroscopy) is a fast, accurate and cheap analytical technique and rabbit is a good experimental model to measure meat quality. NIRS had been used in some studies in meat quality traits in rabbits, for example, Masoero, Xiccato, Zotte, Parigi-Bini, and Bergoglio (1994) to predicte chemical composition, Pla (2007) to discriminate between conventional and organic production, Pascual and Pla (2007) to evaluate changes in meat

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quality when selecting rabbits for growth rate or Zomeño, Blasco, and Hernández (2013) and Martínez-Álvaro, Hernández, and Blasco (2016) to predict fatty acid content in rabbit selection programs.

Some studies were made to describe the effects of genotype and crossbreeding parameters on chemical composition of meat in other species as in pigs (Larzul et al., 1997; Sellier & Monin, 1994), beef cattle (Gregory, Cundiff, & Koch, 1994), sheep (Hopkins, Fogarty, & Mortimer, 2011), chicken (Liu, Dunnington, & Siegel, 1993) or ducks (Wołoszyn et al., 2011). In rabbits, there are studies on these topics in pure lines (Hernández, Ariño, Grimal, & Blasco, 2006; Hernández, Cesari, & Blasco, 2008) but there are few studies estimating crossbreeding parameters on meat quality traits.

The objective of this work was to estimate differences and crossbreeding parameters for some meat quality traits based on NIRS measurements in rabbits, the dams of which come from a full diallel-cross among four maternal lines and the sires from a paternal line; trying to evaluate the impact of a large genetic improvement program in meat rabbit on meat quality.

2. Material and methods

2.1. Animals

The rabbit lines and the animals used for this study were the same rabbits used in Mínguez et al. (2015a) and Mínguez, Sáchez, Ragab, El Nagar, and Baselga (2015b) to measure growth and carcass traits, respectively. The genetic groups involved in the study were four pure lines (AA, VV, HH and LL) and 12 single crosses: AV, VA, AH, HA, AL, LA, VH, HV, VL, LV, HL and LH (a total of 16 genetic groups) and involved four different farms, located in Altura (Castellón, Spain), Rioseco de Tapia (León, Spain), Valencia (Spain) and Sant Carles de la Rápita (Tarragona, Spain). The genetic group VV was present on all farms allowing data connection between farms. The pure line HH was only presented in Tarragona. For this reason, pure line HH does not share the farm with A and LP lines.

2.2. Crossbreeding design and management

The crossbreeding design and the procedure of slaughter were described in Mínguez et al. (2015a, 2015b)). After slaughtering, the carcasses were stored at 4 °C during 24 h and then, in the meat laboratory of the Department of Animal Science of the Universidad Politécnica de Valencia (UPV), the *longissimus lumborum* muscles (LL) were excised from the carcasses.

2.2.1. Meat quality traits

Muscle pH at 24 h. post mortem was obtained in the LL 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). Meat colour (lightness, L*; redness, a*; and yellowness, b*) was measured at the seventh lumbar vertebra in a transversal section of the right LL. Meat obtained from the LL was ground, freeze-dried and stored at − 80 °C until analyses. Meat was scanned with near infrared reflectance spectroscopy (NIRS) (model 5000, FOSS NIRSystems INC., Hilleroed, Denmark). Protein content and fatty acid (FA) composition of the LL were determined applying calibration equations previously developed (Zomeño, Juste, & Hernández, 2012).

2.3. Data recording and statistical model

The pH was measured in a total of 950 LL which came from carcasses that were used by Mínguez et al. (2015b) and the other meat quality traits were recorded in a sample of 285 LL of these animals.

The model used in the analysis was:

$$Y_{jkl} = GG_j + F_k + S_l + e_{jkl}$$

where: Y_{jkl} is a record of the trait; GG_j is the effect of genetic group (16 levels); F_k is the effect of the farm (4 levels, one level for each farm); S_l is the effect of the sex and e_{jkl} is the residual effect.

Estimates of the differences between all the genetics groups and VV animals, crossbreeding parameters (proposed by Dickerson (1969)) and the estimable functions of the crossbreeding parameters were calculate according to Mínguez et al. (2015a).

Table 1
Descriptive statistics of pH, colour, intramuscular fat (IMF), protein, fatty acid groups and fatty acid ratios of the *Longissimus lumborum* muscle (LL).

Trait	N[a]	Mean	SD[b]	Minimum	Maximum
pH	950	5.66	0.17	5.05	6.20
L*	285	51.52	3.37	39.07	59.89
a*	285	4.69	1.44	1.97	9.72
b*	285	1.61	1.44	− 1.80	6.97
Groups (g/100 g muscle)					
IMF	285	1.21	0.22	0.80	2.09
Protein	285	22	0.40	20	23
Groups (mg/100 g muscle)					
SFA	285	308	66	173	546
MUFA	285	232	70	99	491
PUFA	285	331	36	243	449
n-3 PUFA	285	54	3	47	66
n-6 PUFA	285	277	35	208	409
Ratios					
n-6/n-3	285	5.10	0.47	3.94	7.95
PUFA/SFA	285	1.09	0.08	0.84	1.29

[a] N = number of LL.
[b] SD = standard deviation.

3. Results and discussion

3.1. Descriptive statistics

Tables 1 and 2 show descriptive for the traits measured. The value for pH was similar to those obtained in previous studies (Hernández, Aliaga, Pla, & Blasco, 2004; Hernández & Gondret, 2006; Zomeño, 2013) and is in the optimum range to avoid potentials problems related with meat pH. In rabbit, pH ranges between 5.4 and 6.4 depending on muscle location (Hulot & Ouhayoun, 1999) and it does not look like a potential problem for meat quality. Our results, jointly with previous

Table 2
Descriptive statistics of individual fatty acid composition (mg/100 g muscle) of the *Longissimus lumborum* muscle (LL).

Trait	N[a]	Mean	SD[b]	Min[c]	Max[d]
C14:0	285	14.2	5.2	1.0	32.0
C15:0	285	4.3	0.9	2.6	7.8
C16:0	285	200	45	119	387
C16:1	285	15.8	9.7	3.3	56.7
C17:0	285	6.0	1.1	3.6	10.5
C18:0	285	70	9	52	108
C18:1 n-7	285	14.1	2.3	9.4	23.4
C18:1 n-9	285	192	54	90	402
C18:2 n-6	285	196	36	124	326
C18:3 n-3	285	14.0	4.4	4.6	30.1
C20:2 n-6	285	2.6	0.6	1.9	4.2
C20:3 n-6	285	4.2	0.4	3.3	7.7
C20:4 n-6	285	45.9	2.5	29.3	51.7
C20:5 n-3	285	12.4	1.5	7.4	16.2
C22:4 n-6	285	16.5	0.4	15.4	19.3
C22:5 n-3	285	6.4	0.8	1.8	10.0
C22:6 n-3	285	21.0	2.5	4.6	27.5

[a] N = number of LL.
[b] SD = standard deviation.
[c] Min = minimum.
[d] Max = maximum.