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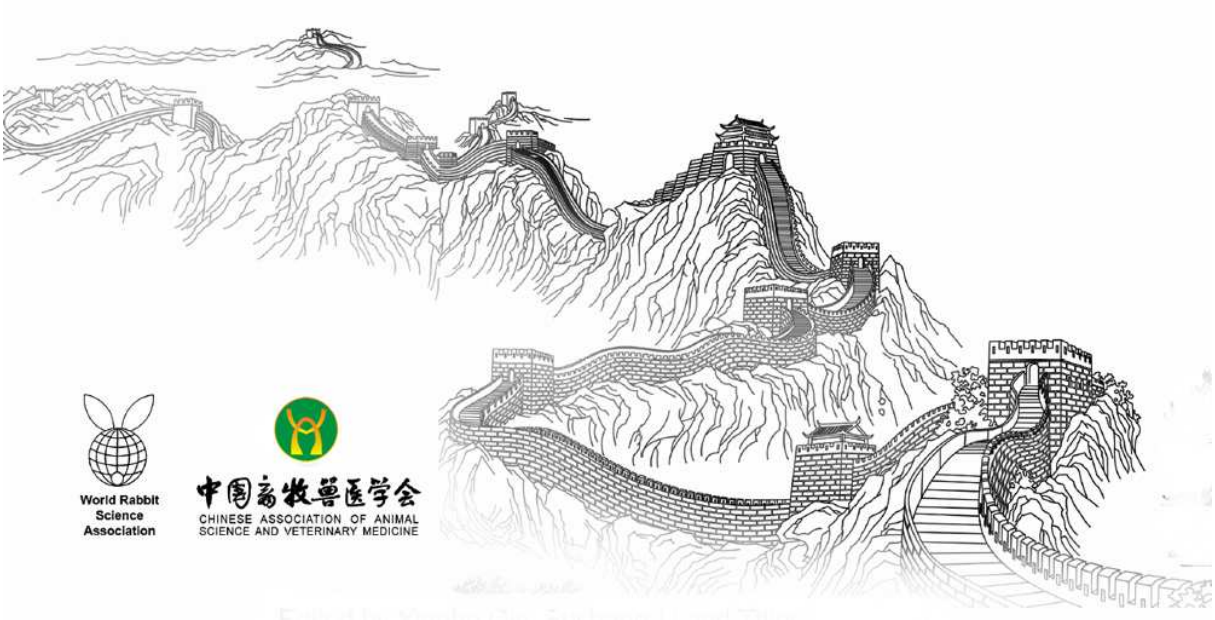

GENETIC ANALYSIS OF MEAT QUALITY TRAITS IN THE PROGENY OF RABBIT DOES COMING FROM A DIALLEL CROSS

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ABSTRACT

The aim of the study was to evaluate several genetic groups for meat quality traits (Intramuscular fat, protein and fatty acid groups) measured in the *Longissimus* muscle (LM) in young rabbits from dams generated in a full diallel cross among four maternal lines - sixteen genetic groups - and sires from a single paternal line. The maternal lines (A, V, H and LP) are selected for litter size at weaning and the paternal line (R) is selected for postweaning average daily gain. The meat quality traits were recorded by NIRS from a sample of 285 LM. The sixteen genetic groups were distributed in four Spanish farms but only one genetic group (V) was present in all farms in order to connect records among these farms and to be used as reference group. The average values for all traits were within the values found in published research. No differences in protein were found between lines, crossbreds or reciprocal crosses. The line A showed significant differences with respect to the V line for intramuscular fat (0.23 g/100 g of muscle), and fatty acid groups SFA, MUFA and PUFA; 67, 66 and 34 (mg/100 g of muscle), respectively. No significant differences appeared for the rest of lines but it seem that the line A had the high values for these traits. Significant differences appeared between the crossbred AH and VV (with higher values for AH) for IMF (0.15 g/100 g of muscle), and fatty acid groups (SFA, MUFA and PUFA) of 47, 40 and 20 (mg/100 g of muscle) respectively. No significant differences were found in the rest of contrasts. For the contrast AV-VA the significant difference in SFA was favourable to A line as sire (70 mg/100g muscle) because this crossbred (AV) had the smaller value. As an overall conclusion of the study it can be indicated that the fattiest meat could be obtained from any genetic type involving the A line while the leanest meat would be obtained from types involving the V line.

Key words: Rabbit, Genetic Effect, Diallel Cross, Meat traits, Maternal Lines

INTRODUCTION

Rabbit meat has good nutritive properties because it has lower fat and higher polyunsaturated fatty acids (PUFA) content than other meats (Hernández and Gondret, 2006). Nowadays, meat quality characteristics are not a key point in meat rabbit production industry. However, it is highly desirable to know the putative effect that selection for other traits might have on the quality of the meat. Thus, in case of a negative effect, the selection process could be modified (Hernández et al., 2004). On the other hand, the reproductive characteristics of the rabbit make this specie an excellent research animal model (Hernández et al., 2004) to generate, after selection experiments, animal material that could be used to deeply explore the biological process behind the different meat quality traits.

Considering all these factors our objective was to estimate differences with regard to traits related with the chemical composition of the meat, for animals whose dams came from a full diallel-cross among four maternal lines and the sires from a paternal line. Our final purpose was to detect genetic differences across the different maternal lines that might be involved in a large program for the genetic improvement of meat rabbit production.

MATERIALS AND METHODS

Animals, Experimental design and Traits.

The present study involved animals which were the progeny of a crossbred dam and a purebred sire coming from a line selected for body weight gain at fattening (R line). Dams came from a full diallel cross among four maternal lines (A, V, H and LP) all of them selected for litter size at weaning but having a different genetic origin. Thus, the maternal genetic groups involved in the experiment were 4 pure lines (A, V, H and LP) and 12 single crosses (AV, VA, AH, HA, AL, LA, VH, HV, VL, LV, HL and LH). The first letter of the genetic group name corresponds to the sire line and the second one to the dam line name. L is used to identify the LP line.

The animals of A, V and LP lines were kept as closed populations since the beginning of the selection process for prolificacy (number of weaning) until the present and were housed on the farm of the Animal Science Department, Universidad Politécnica de Valencia (**U.P.V.**). The current generations of these lines are 46th, 42nd and 11st, respectively. The H line was housed on the same farm until its 10th generation of selection (May, 2004) when it was moved to another farm 180 km north of Valencia (San Carlos de la Rápita, Tarragona); this line is now in its 25th generation of selection. The process of foundation and selection can be consulted in Estany et al., (1989) for the A and V lines, Cifre et al. (1998) for the H line, Sanchez et al. (2008) for LP line and Estany et al. (1992) for R line.

The study was carried out in four different farms in Spain, located in Altura (Castellón, Rioseco de Tapia (León,), Valencia and Sant Carles de la Rápita (Tarragona). In each farm, the same experimental design was performed. The genetic group VV was present in all farms allowing data connection between farms. Twenty five females of each genetic group from the different farms were inseminated by bucks of the R line. At weaning (at 28 d of age), 120 young rabbits of each genetic group were randomly sampled, avoiding whole litters. The young rabbits were individually identified by a number tattooed on the ear and placed in collective cages of eight individuals, all of them belonged to the same genetic group, until marketing at 63 d of age. During post-weaning period, rabbits were fed *ad libitum*, with a standard commercial pellet diet and fresh water.

The transport of the rabbits to the slaughterhouse was less than 12 hours, including load and unload of the animals. In the load of the rabbits, the genetic groups were randomized (each box contained one animal from each genetic group) to avoid differences due to waiting times at the slaughterhouse. After slaughtering, the carcasses were stored at 4º C during 24 hours and then, in the meat laboratory of the Department of Animal Science of the UPV, the *Longissimus muscles* (LM) were excised from the carcasses. Meat obtained from the LM was ground, freeze-dried and stored at -80º C until analyses. Meat was scanned with near infrared reflectance spectroscopy (NIRS) (model 5000, FOSS NIRSystems INC., Hilleroed, Denmark) and intramuscular fat (IMF), protein content (Protein) and fatty acid groups (SFA, MUFA, PUFA) composition of the LM were determined applying calibration equations previously developed (Zomeño et al., 2012). These equations directly yield protein and IMF content expressed as g/100 g of muscle in a fresh basis, and fatty acid composition expressed as mg /100 g of muscle in a fresh basis.

Statistical Analysis

The model used for the analysis of all the meat quality traits was:

$$Y_{ijkl} = GG_j + F_k + S_l + e_{ijkl},$$

where Y_{ijkl} 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); S_l is the effect of the sex and e_{ijkl} is the residual effect.

Estimates of the differences between all the genetics groups and VV animals were obtained by least squares, using the program blupf90 (Misztal et al., 2002). In addition to the estimates of the group effects,

the error (co)variance matrix between them was retained in order to get the errors of the reported contrasts. The residual variance required to solve the models were estimated in a previous REML step.

RESULTS AND DISCUSSION

The means (standard error) for meat quality traits were 1.21(0.22), 22(0.40), 208(66), 232(70) and 331(36) for IMF, Protein (in g/100g of muscle), SFA, MUFA and PUFA (in mg/100g muscle) respectively. These values were within the range of other studies (Hernández et al., 2004; Zomeño et al., 2012). The contrasts between the dam effects of the lines for the studied traits can be observed in Table 1. Regarding IMF, the line A had the higher content, being significant the difference with respect to line V. Non-significant differences were found for the content of protein between the lines. Significant differences in the contrast A-V were found for all fatty acid groups (in favour of the A line), and despite non-significant differences with the other lines, it seems that the line A had the highest content for fatty acid groups (SFA, MUFA and PUFA) in agreement with its highest value for IMF

Table 1: Contrasts (standard error) between the lines for intramuscular fat ([1]**IMF,** g/100g muscle), protein (g/100g muscle) and fatty acid groups ([2]**SFA,** [3]**MUFA,** [4]**PUFA,** mg/100g muscle) of the *Longissimus muscle.*

Traits	A-H	A-LP	A-V	H-V	LP-H	LP-V
[1]IMF	0.15(0.11)	0.14(0.08)	0.23(0.08)*	0.08(0.08)	0.01(0.11)	0.09(0.08)
Protein	-0.10(0.20)	0.05(0.14)	0.17(0.15)	0.27(0.14)	-0.15(0.20)	0.13(0.15)
[2]SFA	49(33)	38(23)	67(24)*	19(23)	10(33)	29(24)
[3]MUFA	58(33)	41(23)	66(24)*	8(23)	17(33)	25(24)
[4]PUFA	26(18)	24(13)	34(13)*	7(13)	3(18)	10(13)

[1]. IMF intramuscular fat; [2]. SFA saturated fatty acids; [3]. MUFA monounsaturated fatty acids; [4]. PUFA polyunsaturated fatty acids; *$P < 0.05$ (significant difference at $\alpha = 0.05$).

In commercial farms crossbred does are the most common type of females, thus a characterization of their meat quality traits could be relevant. For this purpose all the crossbred types were compared to the VV type (Table 2). In the comparison between the different crossbred groups and one particular purebred group we will assess not only differences with respect to heterotic effects but also differences generated by direct-maternal and grand-maternal effects (Mínguez et al., 2015). Table 2 shows significant differences between AH and VV. This agrees with the result commented before in the Table 1. No significant differences were found for the protein content.

Table 2: Contrasts (standard error) between crossbred genetic groups[1] and V line for intramuscular fat (**IMF,** g/100g muscle), protein (g/100g muscle) and fatty acid groups ([2]**SFA,** [3]**MUFA,** [4]**PUFA,** mg/100g muscle) of the *Longissimus muscle*.

Traits	[1]AH-VV	AL-VV	AV-VV	HV-VV	LH-VV	LV-VV	All-VV
[2]IMF	0.15(0.05)*	0.05(0.05)	0.02(0.05)	0.06(0.05)	0.07(0.05)	-0.06(0.05)	0.05(0.04)
Protein	0.10(0.1)	0.01(0.1)	0.02(0.1)	0.01(0.1)	0.01(0.1)	0.10(0.1)	0.03(0.1)
[3]SFA	47(16)*	17(16)	8(16)	19(16)	24(16)	-18(16)	16(12)
[4]MUFA	40(16)*	13(16)	2(16)	16(16)	16(16)	-18(16)	11(12)
[5]PUFA	20(9)*	4(9)	0(9)	7(9)	6(9)	-10(9)	4(6)

[1.] One cross and its reciprocal are considered together; [2] SFA saturated fatty acids; [3]. MUFA monounsaturated fatty acids; [4] PUFA polyunsaturated fatty acids; L:LP line; *$P < 0.05$ (significant difference at $\alpha = 0.05$).

The importance of using a particular line either as sire or dam in a cross was assessed by testing the differences between a particular cross and its reciprocal (Table 3), these contrasts are reflecting the existence of grand-maternal genetic effects. For the contrast AV-VA the significant difference in SFA was lower for the group in which the A line is acting as sire; in this sense we indicate the favourable cross to

be AV because a desirable feature in a breeding program would be to reduce the level of SFA. Nevertheless, it can be indicated that the magnitude of both heterotic and grand-maternal effects is low because of the scarce presence of significant figures in tables 2 and 3.

Table 3: Contrasts (standard error) between reciprocal crosses for intramuscular fat (**IMF,** g/100 g muscle), protein (g / 100 g muscle) and fatty acid groups ([1]**SFA,** [2]**MUFA,** [3]**PUFA,** mg/100 g muscle) of the *Longissimus muscle*.

Traits	AH-HA	AL-LA	AV-VA	HV-VH	LH-HL	LV-VL
IMF	0.10(0.1)	-0.09(0.1)	-0.02(0.1)	0.11(0.1)	0.08(0.1)	0.01(0.1)
Protein	0.10(0.2)	0.11(0.2)	0.02(0.2)	-0.19(0.2)	0.21(0.2)	0.09(0.2)
[1]SFA	46(32)	-18(32)	-70(32)*	41(32)	25(32)	-8(32)
[2]MUFA	40(33)	-17(33)	-58(33)	32(33)	22(33)	-3(33)
[3]PUFA	17(18)	-8(18)	-29(18)	15(18)	10(18)	-3(18)

[1]. SFA saturated fatty acids; [2]. MUFA monounsaturated fatty acids; [3]. PUFA polyunsaturated fatty acids; *$P < 0.05$ (significant difference at $\alpha = 0.05$).

CONCLUSIONS

Some significant differences were observed between the different genetic types involved in the diallel cross conducted. These differences were detected between A and V lines for SFA, MUFA and PUFA; meat from A line is the fattiest; no significant differences were found for contrasts involving other lines and the A line but there were indications that the A line had the highest contents of the different types of fatty acids. Regarding the comparisons between the crosses and V line, the crossbred AH was superior for IMF, SFA, MUFA and PUFA. In general, the reciprocal cross effects were not significant but the cross AV was preferable over VA with regard to SFA content. In spite of all this it can be concluded that the observed significant contrasts are mainly consequence of direct-maternal genetic effects, playing grand-maternal and heterotic effects a much lower role in the control of the studied traits.

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