



PROCEEDINGS OF THE 11th WORLD RABBIT CONGRESS

Qingdao (China) - June 15-18, 2016

ISSN 2308-1910

Session Breeding and Genetics

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Full text of the communication

How to cite this paper :

Lenoir G., Morien F., 2016 - Estimation of genetic parameters for carcass traits evaluated by in vivo real-time ultrasonography in meat rabbit breeding. Proceedings 11th World Rabbit Congress - June 15-18, 2016 - Qingdao - China, 71-75.



ESTIMATION OF GENETIC PARAMETERS FOR CARCASS TRAITS EVALUATED BY *IN VIVO* REAL-TIME ULTRASONOGRAPHY IN MEAT RABBIT BREEDING

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ABSTRACT

This study aims to determine the possibility to improve the dressing out percentage (DoP) using one or more criteria measured in-vivo by ultrasonography. There were 647 animals from the X Hycole line tested between March and September 2014. The ultrasound measurements performed at 71 or 72 days of age on the *Longissimus dorsi* muscle between the 2nd and the 3rd lumbar vertebrae were the width (W2-3), the depth (D2-3) and the surface (S2-3) of the muscle. The next day, the DoP and the live weight were measured at the slaughterhouse. The trait S2-3 had the highest heritability (0.20) and the most favourable phenotypic and genetic correlations with the trait DoP (0.53 and 0.74 respectively). These results suggest the possibility to improve the dressing out percentage by selection of the S2-3 trait.

Key words: Rabbit, Real-time ultrasound, Carcass traits, Genetic parameters

INTRODUCTION

In Europe, the dressing out percentage has become in the recent years an important economic criterion for the meat rabbit industry. For this study, this criterion is defined as the ratio between the weight of the carcass, measured just after slaughter (with head, thoracic viscera, liver and kidneys and without sleeves, skin, and abdominal viscera) and the live weight measured before slaughter (Baumier and Retailleau, 1986). This trait is influenced by three components: hot carcass weight, skin weight and the weight of the digestive tracts (Rouvier, 1970). For rabbits, the dressing out percentage has an heritability between 0.24 and 0.55 depending on the breed and the measurement conditions (Garreau *et al.*, 2008; Larzul *et al.*, 2005 and Nagy *et al.*, 2006). In the case of the Hycole X line, the heritability of this trait is 0.24 (\pm 0.05). In this line, the dressing out percentage improved by the selection is measured on collaterals. This type of selection results in a lower selection intensity, due to the use of part of the selection candidates to measure dressing out percentage. Moreover, such measures are difficult to implement in industrial slaughterhouses.

An *in-vivo* imaging method, computerised tomography (CT-scan) is used in Hungary in the selection of Pannon line to evaluate the surface of *Longissimus dorsi* muscle (L-value) and the thigh volume (Matics *et al.*, 2014). Several tests realized, by Hycole, on 327 bucks from the X line in 2012 and 2013 highlighted that this method is accurate but difficult to use routinely and has a high cost. Silva *et al.* (2012) demonstrated the feasibility of using real-time ultrasonography to assess muscularity and carcass composition of rabbits, especially on the *Longissimus dorsi* and thigh, and the ability of these traits to predict carcass composition.

We decided to make measurements only on the *Longissimus dorsi* according to the data available in literature and results of an initial study performed in March 2014. Objectives of this preliminary study were to define an appropriate method of restraint to realize repeatable measures and determine the most suitable site for RTU measurements (saddle, shoulder and thigh). The objectives of this work are to define one or more heritable traits, measurable by real-time ultrasonography (RTU) on candidates for selection, improving the dressing out percentage (DoP) and evaluate the possibility to use the RTU method routinely.

MATERIALS AND METHODS

Data

The measurements have been carried out between March and October 2014 on 647 male and female animals from the X paternal line from 7 different groups and born in the Hycote breeding farm. These rabbits are collaterals of the candidates for selection. This line is indexed on the average daily gain between 28 and 68 days (ADG), the fattening viability (taking into account mortality and morbidity) and the dressing out percentage (DoP), using the BLUP method. These animals were weaned at 28 days of age and then fattened on 2 different farms (A and B) in cage by 2 with a restricted feeding. At 71 or 72 days of age, the day before slaughtering, the animals were evaluated by *in vivo* RTU. The measurements were performed using a Hitachi EUB-555 ultrasound system connected to a 7.5 MHz linear array probe. Animals were previously clipped. All the measurements were carried out by a single operator, to avoid operator effect. A method of restrain has been developed in order to standardize the animal's position during RTU measures. The muscle measurements were performed on the *Longissimus dorsi* between the 2nd and 3rd lumbar vertebra (site 2-3) on right and left sides. The site 2-3 was chosen due to a better measurements repeatability. Traits measured are the surface (S2-3), the depth (D2-3) and the width (W2-3) of the muscle on the right and left sides. Analysed values are the average between the records measured on the right and left sides. At 72 or 73 days of age, animals were individually weighed (LW) after a fasting of 12h. Three hours later, they were slaughtered. The individual weight of the hot carcass (CW) was measured immediately after slaughter. In this study, the DoP is the ratio between CW and LW. The pedigree file used for estimations includes all bucks and does from X line born between 2000 and 2014, whether 60 207 animals.

Methods

The descriptive analysis of the data and the estimation of linear correlation coefficients (Pearson method) were performed using the R software version 3.1.0 (R Core Team, 2014). Traits were analysed individually to test the significance of the fixed effects by analysis of variance with several factors using the ASReml software (Gilmour *et al.*, 2009). Fixed effects retained after analyses were ($p < 0.001$): the birth week (7 levels), the fattening farm (2 levels) and age at slaughter (2 levels). Live weight (LW) before slaughtering has also been added as a covariate for all traits except for LW. Litter size at birth and gender were not significant ($p > 0.1$) for all traits. Similarly, slaughter age was not retained for W2-3 and DoP variables ($p > 0.1$). Genetic parameters (variance and covariance components) were estimated with the restricted maximum likelihood method (REML) applied to an animal model using ASReml. In addition, a random effect was included into the model: genetic additive effect of the animal. The common-litter effect (p) wasn't included because 20% of the animals were the only representatives of their litter. Estimations of the genetic parameters for S2-3 and DoP traits with or without this effect have been performed with a data set including the animals from litters with at least two representatives, whether 517 animals. These estimations give identical heritabilities and variance (p) / variance (total) ratio close to 0. Traits were analysed individually as at first and then bivariate model were used in order to estimate genetic correlations.

RESULTS AND DISCUSSION

Averages and phenotypic correlations

The LW measured (Table 1) is lower than the values usually observed (- 250 g) in this line. In order to standardize the fattening conditions between the two farms, animals were restricted to 70% of their *ad libitum* consumption. This important rationing level has an adverse effect on the DoP criterion (Gidenne *et al.*, 2009). Dressing out percentage is the trait with the lowest phenotypic variability (3.90%). The coefficients of variation criteria measured by ultrasound are greater (9-15%). Phenotypic correlations (r) between traits measured *in-vivo* and dressing out percentage are all favourable. The LW criterion is low correlated with DoP ($r = 0.17$). The weight of the hot carcass (CW) has a correlation with the DoP higher than the live weight ($r = 0.49$). Criteria measured by RTU are moderately correlated with DoP ($0.40 < r < 0.53$). The S2-3 criterion has the highest correlation with

DoP ($r = 0.53$). These phenotypic correlations are of the same order as those published by Szendro *et al.* (1996) between the L-value obtained by CT-scan and the DoP (from 0.53 to 0.65).

Table 1: Basic statistics of measured parameters

Traits	Average	Standard deviation	Coefficient of variation
LW (g)	2692	260	9.66%
Age (d)	72.5	0.5	0.69%
CW (g)	1516	160	10.55%
DoP (%)	56.3	2.2	3.90%
W2-3 (mm)	18.37	2.10	11.43%
D2-3 (mm)	26.04	2.40	9.22%
S2-3 (cm ²)	3.87	0.59	15.24%

Genetic parameters

Heritability values are between 0.06 and 0.25 (Table 2). Precisions of heritabilities estimates are quite low, given the sample size. For the live weight (LW), heritability (0.25) is of the same order as that obtained in the literature (0.22 Larzul *et al.*, 2005; 0.20 to 0.26 Matics *et al.*, 2014), although it is probably overestimated due to the non-inclusion of the common-litter effect. Heritability of the dressing out percentage (0.17) is lower than the values observed in the literature, 0.24 (Garreau *et al.*, 2008) to 0.55 (Larzul *et al.*, 2005). Heritability of the DoP criterion (measured under the same conditions) on a sample of 2890 animals from the X line is 0.24. The lower heritability in this case is probably explained in part by the sample size. The criteria D2-3 and S2-3 have higher heritability (0.16 and 0.20) than the W2-3 criterion (0.06), but with low accuracy. The W2-3 measurement is more difficult to achieve than D2-3 and S2-3, because it has more variations due to the probe position and muscle movement of the animals. These values seem a bit low compared to the heritability estimation for L-value (0.33 Nagy *et al.*, 2006). This difference is probably explained in part by the greater precision of CT-scan method compared to the *in vivo* RTU method and by the higher number of animals controlled. In addition, L-value is estimated from two points of measures between the 2nd/3rd and the 4th/5th lumbar vertebrae, improving certainly measurement accuracy. In Pietrain pig breed, the heritability of the loin depth at 100 kg measured by *in vivo* RTU is between 0.25 and 0.34 (Sourdioux *et al.*, 2009). The S2-3 criterion is one that offers the highest heritability among the traits measured by RTU and the most favourable phenotypic correlation with the dressing out percentage. Due to its heritability and its phenotypic variability (15.24%), the criterion S2-3 can be improved by selection, although these trends must be analysed with caution due to the low precision of some estimate.

Table 2: Genetic parameters of the different traits measured. Heritabilities in diagonal and genetic correlations above diagonal (\pm standard error). ND: not determined value (convergence problem).

	LW	CW	DoP	W2-3	D2-3	S2-3
LW	0.25 ± 0.11	0.99 ± 0.02	0.32 ± 0.49	0.60 ± 0.33	0.45 ± 0.30	0.57 ± 0.24
CW		0.18 ± 0.09	0.46 ± 0.41	0.59 ± 0.37	0.68 ± 0.22	0.65 ± 0.20
DoP			0.17 ± 0.09	ND	ND	0.74 ± 0.32
W2-3				0.06 ± 0.06	ND	ND
D2-3					0.16 ± 0.08	0.92 ± 0.10
S2-3						0.20 ± 0.08

Genetic correlations between the different criteria are given in Table 2. The criteria are as a whole positively correlated. The accuracy of estimates for some correlations is low, illustrated by standard error estimatia are strongly correlated ($r = 0.99$). The correlation between the DoP and LW is moderate, close to those published by Larzul *et al.* (2005), even though the accuracy of the estimate is low. All the traits measureion higher than 0.20, and requires certain precautions regarding the

interpretation of trends. LW and CW criterd by RTU (S2-3, D2-3 and W2-3) are moderately correlated with LW and CW criteria ($0.45 < r < 0.68$). The S2-3 criterion is highly correlated with the dressing out percentage (0.74) and with the criterion D2-3. On the other hand, for the criteria D2-3 and W2-3 correlations with the criterion DoP could not be determined. The genetic improvement of the muscle surface at the point 2-3 would tend to improve the dressing out percentage measured after slaughter of the animals. Nagy *et al.* (2006) highlighted a lower positive genetic correlation (0.46) between the L-value estimated by CT-scan and the DoP. This criterion was the subject of a divergent selection experiment, realised by Szendro *et al.* (1996) on the Pannon line, and have shown a difference of 1.8 points of DoP between the two lines (+ and -) after the second generation of selection. This result confirms the interest to use a measure obtained by *in vivo* imaging on the *Longissimus dorsi* muscle in order to improve the dressing out percentage.

Between October 2014 and December 2015 additional measures of S2-3 and LW criteria were performed. On the data set of 2662 animals, heritability of LW and S2-3 criteria are respectively 0.21 ± 0.01 and 0.26 ± 0.05 . The genetic correlation between the two criteria amounted to 0.50 ± 0.16 . The previously trends observed tend to be confirmed by those additional measures. These data were used to estimate genetic correlations between S23 and the indexed traits: ADG and fattening survival. Correlation between S23 and fattening viability criteria tends to be null to slightly positive (0.19 ± 0.20) but with a low accuracy. At the opposite, genetic correlation between S23 and ADG traits tends to be negative (-0.36 ± 0.20). A selection on S23 trait tends to have a negative effect on ADG and neutral to slightly positive effect on fattening viability. These correlations must take into account in the choice of weighting applied on each trait of the global index.

CONCLUSIONS

This study has highlighted the possibility of a direct selection with the S2-3 criterion measured by RTU in order to improve the size of the saddle and indirectly the dressing out percentage (measured hot). The measurements realised by RTU offer a lower accuracy than those done by CT-scan, however, this method offers the advantage to used directly on farm and do not emit harmful radiation. This approach can replace the selection of the dressing out percentage measured on collaterals. The S2-3 criterion has been included into the genetic selection objective of the X line since December 2014. The continuation of this study involves the validation of the genetic correlation between DoP and S2-3 by performing additional measurements. In addition, it is necessary to assess the impact of this selection on the evolution of the weight of the saddle and on carcass shrink.

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