58th Annual Meeting of the European Association for Animal Production in Dublin, Ireland
Session 25.5, Abstract 444

Genetic parameters for M. longissimus depth, fat depth and carcass fleshiness and fatness in Danish Texel and Shropshire

J. Maxa[a,b,*], E. Norberg[a], P. Berg[a], J. Pedersen[c]
[a]*Department of Genetics and Biotechnology, University of Aarhus, Research Centre Foulum, P.O. Box 50, 8830 Tjele, Denmark*
[b]*Institute of Animal Breeding and Genetics, University of Göttingen, Albrecht-Thaer-Weg 3, 37075 Göttingen, Germany*
[c]*Danish Agricultural Advisory Service, Udkærsvej 15, Skejby, 8820 Aarhus N, Denmark*
[*]*e-mail address: jmaxa@gwdg.de*

Abstract

Genetic parameters for muscle depth (MD) and fat depth (FD) and carcass conformation score (FORM) and carcass fatness (FAT) were estimated for Danish Texel and Shropshire, the most common sheep breeds in Denmark. Data used in this study were collected from 1990 to 2005 by the Danish Agricultural Advisory Service. A multivariate animal model was used for estimation of (co)variance components for muscle depth (MD), fat depth (FD), carcass conformation score (FORM) and carcass fatness (FAT). Heritabilities for MD were similar 0.28 and 0.29 for both breeds. Different heritabilities were found for FD; 0.39 for Texel and 0.12 for Shropshire. Carcass conformation was highly heritable, 0.45 for Texel and 0.36 for Shropshire. The heritability for FAT was 0.11 for Texel and 0.19 for Shropshire. Genetic correlations between MD and FORM, and FD and FAT were positive and favourable which support the use of ultrasound measurements on live animals as good predictors for final carcass classification.

Keywords: *Carcass classification, genetic parameters, fat depth, muscle depth, sheep*

Introduction

From the total amount of 10,000 sheep flocks in Denmark approximately 475 of these are participating in an intensive registration programme. Texel and Shropshire are the most common breeds. Until now, the breeding programme in Denmark has mainly been based on genetic parameters obtained from the literature. Therefore there is a need for estimating heritabilities and genetic correlations based on Danish data. Today, the major income from the sheep industry is meat production, and an economically sustainable production is conditional on the farmer's ability to produce high quality carcasses. Ultrasound measures on live animals are a relatively low cost method, which can give us information on carcass traits for further inclusion in genetic evaluation programs. Several studies have evaluated genetic parameters for traits measured by ultrasound in sheep (Fogarty, 1995; Larsgard and Olesen, 1998; Näsholm, 2004; Maxa et al., 2007) and some studies presented genetic parameters for carcass grades (Olesen and Husabo, 1994; Moreno et al., 2001). But there are very few studies presenting genetic correlations between ultrasound measures and carcass grades, based on EUROP carcass classification system.

The aim of this study was to estimate heritabilities and genetic correlations between ultrasound measurements on live animals and carcass measurements obtained from slaughterhouses based on EUROP carcass classification in Texel and Shropshire populations in Denmark.

Materials and methods

Data

Data were collected from 1990 to 2005 by the Danish Agricultural Advisory Service. Pedigrees were traced back to 1980. The traits analyzed were muscle depth (MD), fat depth (FD), carcass conformation score (FORM) and carcass fatness (FAT). The measurements of MD and FD were recorded by ultrasound technology and taken on the right side of the lamb over the first *lumbar vertebra* at an age of approximately 138 days. The carcass classification at Danish commercial slaughter houses followed the EU system. Since 1995, carcass conformation has been determined by visual assessment of shape described by the letters E-U-R-O-P, where each of the classes are subdivided into three sub-classes (15 grades in total). The fatness class is determined by a visual appraisal of external fat deposits and graded into five classes. The characteristics of the data used in the analyses are presented in the Table 1.

Table 1. Number of records and means (with S.D. in parenthesis) for each trait for Danish Texel and Shropshire.

		Texel	**Shropshire**
Animals in pedigree		68989	49582
Average scanning weight (kg)		41.1 (5.9)	38.5 (6.9)
Mean age at scanning (days)		137.8 (21.4)	137.9 (35.1)
Average carcass weight (kg)		22.4 (3.3)	21.0 (3.6)
Mean age at slaughter (days)		220.6 (61.7)	198.6 (63.8)
Muscle depth (mm)	no.	1335	1147
	means	28.7 (3.3)	25.9 (3.8)
Fat depth (mm)	no.	1335	1146
	means	4.5 (1.5)	4.8 (1.6)
Carcass conformation (1-15)	no.	4916	3886
	means	10.1 (1.8)	9.3 (1.8)
Carcass fatness (1-5)	no.	4913	3885
	means	2.7 (0.5)	3.3 (0.7)

Statistical methods

Genetic parameters were estimated using a multivariate animal model, including direct additive genetic effects for all traits and common litter effects for MD and FD. Common litter effects for FORM and FAT were not significant and therefore excluded from the analyses. Effects included in the model differed between the traits, and were as follows:

$$MD_{ijklmnpq} \text{ and } FD_{ijklmnpq} = S_i + FY_j + LM_k + NB_l + NA30_m + P_n + b_{1,}*(SCW_p) + a\mathit{dir}_p + c_q + e_{ijklmnpq}$$

$$FORM_{ijklmnop} \text{ and } FAT_{ijklmnop} = S_i + FY_j + LM_k + NB_l + NA30_m + P_n + SLM_o + b_2*(SLW_p) + a\mathit{dir}_p + e_{ijklmnop}$$

where:

$MD_{ijklmnpq}$ = muscle depth of animal *p*;
$FD_{ijklmnpq}$ = fat depth of animal *p*;
$FAT_{ijklmnop}$ = carcass fatness of animal *p*;
$FORM_{ijklmnop}$ = carcass conformation of animal *p*;
S_i = fixed effect of sex;
FY_j = fixed effect of flock-year class;
LM_k = fixed effect of lambing month of ewe (grouped by month, with months 7-11 pooled);
NB_l = number of offspring born in litter;
$NA30_m$ = number of offspring in litter 30 days post partum;
P_n = fixed effect of parity of ewe;
SLM_o = fixed effect of slaughter month of animal *p*;
SCW_p = live weight at the day of scanning (kg) of animal *p*;
SLW_p = slaughter weight (kg) of animal *p*;
b_1 = regression coefficient of MD or FD on SCW of animal *p*;
b_2 = regression coefficient of FORM or FAT on SLW of animal *p*;
$a\mathit{dir}_p$ = random direct additive genetic effect of animal *p*;
c_q = random effect of common litter;
$e_{ijklmnpq}$ and $e_{ijklmnop}$ = random residual.

Homogenous residual variance was assumed for all models. Estimation of (co)variance components for all models was carried using the DMU package (Madsen & Jensen, 2000), and heritabilities and genetic correlations were calculated based on these estimates.

Results and discussion

Means and standard deviations for each trait are shown in Table 1. Shropshire had on average lower MD and larger FD compared to Texel. The carcass conformation score were somewhat higher for Texel then for Shropshire, while carcass fat score was higher for Shropshire compared to Texel. The *in vivo* measurements of MD and FD correspond to FORM and FAT, which were recorded on the carcass after slaughter.

Heritabilities of all the traits are presented in bold on the diagonal in Table 2. The direct heritability for MD was 0.29 for Texel and 0.28 Shropshire. Our estimates agree well with those presented by Jones et al. (2004) for Texel, Charollais and Suffolk, who found heritabilities of 0.29, 0.30 and 0.32, respectively. Using weight and age as covariates in two separate analyses, Fernandes et al. (2004) reported heritabilities of 0.29 and 0.38, respectively. The direct heritabilities for FD differed significantly between Texel and Shropshire in our study, with heritabilities of 0.39 and 0.12, respectively. The assumption of homogenous residual variance was checked by plotting residuals from the models used against predicted observations. There was no evidence of this assumption being violated. The low heritability for FD for Shrophire compared to Texel is explained by a higher environmental variation and a lower genetic variation. Additive genetic variance in FD for Texel (0.208) was twice as large as to Shropshire (0.103). Common litter and residual variances for FD were larger for Shropshire compare to Texel. The estimated heritability for Texel is in agreement with the values reported by Bishop et al. (1996), who found the heritability of FD for intensively reared Scottish Blackface lambs to be 0.39, and Jones et al. (2004), who found the heritability of FD for Texel to be 0.38. The estimates for Shropshire obtained in this study are similar to those reported by Maxa et al. (2007) for

Suffolk, who estimated the direct heritability of FD to be 0.08. Larsgard & Olesen (1998) reported the direct heritability for FD at weaning to be 0.05.

The estimated heritabilities for FORM were 0.45 for Texel and 0.36 for Shropshire. The estimates for Shropshire agree well with those presented by Moreno et al. (2001), who found a heritability of 0.37 for conformation score in an experimental herd of INRA401 sheep. Moreno et al. (2001) pointed out that high heritabilities mainly were a result of the standardized environment and the high genetic variability available in the INRA401 breed. Analyzing conformation score, using a similar scale as used in the present study, Pollott et al. (1994) and Näsholm (2004) reported somewhat lower heritability for different breeds in Britain (0.29) and in Sweden (0.21-0.27). The heritabilities estimated for FAT were larger for Shropshire than for Texel. For subcutaneous fat score and carcass fatness grade, Wolf et al. (1981) found the heritability to be 0.27 and Näsholm (2004) estimated heritabilities between 0.25 and 0.29.

Table 2. Direct heritabilities (in bold on the diagonal) and genetic correlations (below the diagonal), with standard error in parenthesis, for muscle depth (MD), fat depth (FD), carcass conformation (FORM) and carcass fatness (FAT) for Danish Texel and Shropshire.

	MD	FD	FORM	FAT
Texel				
MD	**0.29** (0.07)			
FD	0.20 (0.17)	**0.39** (0.07)		
FORM	0.80 (0.15)	0.12 (0.18)	**0.45** (0.05)	
FAT	0.34 (0.32)	0.21 (0.32)	0.16 (0.16)	**0.11** (0.04)
Shropshire				
MD	**0.28** (0.09)			
FD	-0.36 (0.33)	**0.12** (0.07)		
FORM	0.49 (0.21)	-0.01 (0.31)	**0.36** (0.05)	
FAT	0.27 (0.25)	0.66 (0.31)	-0.03 (0.15)	**0.19** (0.05)

Genetic correlations are presented below the diagonal in Table 2. Muscle depth and FORM were highly correlated for both breeds, with a correlation of 0.80 for Texel and 0.49 for Shropshire. Similar estimates for Texel were presented by Olesen & Husabø (1994) for the genetic correlations between MD and muscling score (0.88) for Norwegian Dala and Spælsau. These results show that animals with a high MD tend to have leaner carcasses and vice versa. Genetic correlations between FD and FAT were high for Shropshire (0.66) but not significantly different from zero for Texel (0.21). Olesen & Husabø (1994) estimated genetic correlations between FD and fat score to be 0.39, but the estimate was subject to large standard errors. The positive genetic correlations between FD and FAT indicate that animals with a large FD measured in vivo will result in a carcass with a high fatness score. Favourable genetic correlations between MD and FORM and FD and FAT, show that ultrasound measures on live animals are good predictors also for final carcass classification.

Genetic correlations between MD and FD for Texel were positive and moderate. From these positive genetic correlations we can conclude that animals with larger amount of muscle will tend to have more fat as well. The genetic correlation estimated in our study between MD and FD was negative for Shropshire, but for both breeds, the correlations were not significantly different from zero. Muscle depth and FAT were moderately correlated for both Texel (0.34) and Shropshire (0.27). For Texel, the positive genetic correlations between MD and FAT coincided with the positive genetic correlations between MD and FD for Texel, mentioned above. We expect that animals with larger MD measured *in vivo* will obtain higher conformation scores as well as higher fatness scores in the EUROP scoring system. Genetic correlations between FD and FORM were 0.12 for Texel and -0.01 for Shropshire, but they were not significantly different from zero. The genetic correlations between FORM and FAT in this study were 0.16 for Texel and -0.03 for Shropshire. Because of the positive genetic correlations between these two traits, selecting animals for high carcass conformation will also result in somehow higher carcass fatness.

Conclusions

Heritabilities for muscle depth, fat depth, carcass conformation and carcass fatness were comparable with those found in the literature. Favourable genetic correlations between muscle depth and carcass conformation, and fat depth and carcass fatness highlight the possibility of using in vivo measurements as a selection tool to improve carcass quality in sheep.

References

Bishop, S. C., Conington, J., Waterhouse, A., & Simm, D. (1996). Genotype x environment interactions for early growth and ultrasonic measurements in hill sheep. *Animal Science, 62*, 271-277.

Fernandes, T. L., Wilton, J. W., & Tosh, J. J. (2004). Estimates of genetic parameters for ultrasound-measured carcass traits in sheep. *Canadian Journal of Animal Science, 84*, 361-365.

Fogarty, N. M. (1995). Genetic parameters for live weight, fat and muscle measurements, wool production and reproduction in sheep: a review. *Animal Breeding Abstracts, 3*, 101-143.

Jones, H. E., Lewis, R. M., Young, M. J., & Simm, G. (2004). Genetic parameters for carcass composition and muscularity in sheep measured by X-ray computer tomography, ultrasound and dissection. *Livestock Production Science, 90*, 167-179.

Larsgard, A. G., & Olesen, I. (1998). Genetic parameters for direct and maternal effects on weights and ultrasonic muscle and fat depth of lambs. *Livestock Production Science, 55*, 273-278.

Madsen, P., & Jensen, J. (2000). A user's guide to DMU. A package for analyzing multivariate mixed models. Version 6, release 4.4, Tjele, Denmark.

Maxa, J., Norberg, E., Berg, P., & Milerski, M. (2007). Genetic parameters for body weight, longissimus muscle depth and fat depth for Suffolk sheep in the Czech Republic. *Small Ruminant Research,* 72, 87-91.

Moreno, C., Bouix, J., Brunel, J. C., Weisbecker, J. L., Francois, D., Lantier, F., & Elsen, J.M. (2001). Genetic parameter estimates for carcass traits in the inra401 composite sheep strain. *Livestock Production Science, 69*, 227-232.

Näsholm, A. (2004). Direct and maternal genetic relationships of lamb live weight and carcass traits in Swedish sheep breeds. *Journal of Animal Breeding and Genetics, 121*, 66-75.

Olesen, I., & Husabø, J.O. (1994). Effect of using ultrasonic muscle depth and fat depth on the accuracy of predicted phenotypic and genetic values of carcass traits on live ram lambs. *Acta Agriculturæ Scandinavica, Section A, Animal Science, 44*, 65-72.

Pollott, G. E., Guy, D. R., & Croston, D. (1994). Genetic parameters of lamb carcass characteristics at three end-points: fat level, age and weight. *Animal Production, 58*, 65-75.

Wolf, B. T., Smith, C., King, J. W. B., & Nicholson, D. (1981). Genetic parameters of growth and carcass composition in crossbred lambs. *Animal Production, 32*, 1-7.