Genetic parameters for body weight and ultrasonic measured traits for Suffolk sheep in the Czech Republic

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Abstract

Suffolk is the most common sheep breed in the Czech Republic, and in this study, heritabilities and (co)variance components for body weight at 100 days (BW), muscle depth (MD) and fat depth (FD) were estimated. Data from 1996 to 2004 were extracted from the sheep recording database of the Czech Sheep and Goat Breeding Association. Average values for BW, MD and FD were 27.91 kg, 25.5 mm and 3.3 mm, respectively. Direct and maternal heritability for BW were 0.17 and 0.08, respectively, direct heritabilities were 0.16 for MD and 0.08 for FD. Maternal heritability estimates for ultrasonic measurements were generally low. Direct genetic correlations between BW and MD and maternal genetic correlations between BW and FD and maternal genetic correlations between BW and FD and maternal genetic correlations between BW and FD were negative, but not significantly different from zero. Favourable genetic correlations between BW and MD make ultrasound measurements a valuable tool in breeding programs focusing on growth and carcass characteristics.

Keywords: Sheep; Body weight; Muscle depth; Genetic parameters

1. Introduction

In the Czech Republic there are about 140 000 sheep of which 36% are of meat sheep breeds. A total of 29 breeds are registered in the Czech recording system and Suffolk is the most common breed, accounting for about 22% of the flocks (Holá, 2005). Knowledge on genetic parameters and heritabilities are crucial for genetic evaluation and for choosing the best selection schemes. In the Czech Republic, sheep breeding programs are based on preliminarily estimates and values from the literature. Therefore there is a need for estimating these parameters based on current Czech data.

The objective of this study was to estimate heritabilities and genetic correlations between body weight and ultrasound measured traits in Suffolk, based on data from Czech Republic.

2. Materials and methods

2.1. Data

Data were collected from 1996 to 2004 by the Czech Sheep and Goat Breeding Association. The traits studied were body weight (BW), muscle depth (MD) and fat depth (FD). Body weight was defined as the live weight of lamb adjusted to 100 days of lamb's age

(weight at 100 days was measured within \pm 20 days). At scanning, muscle depth and fat depth were recorded by using ultrasonic technology with a UST-5011U (5 MHz) probe. Ultrasonic measurements were taken over the first lumbar vertebra at the age of 100 days (\pm 20 days). MD was measured at the deepest point of the longissimus muscle. The characteristics of the data used in the analyses are presented in Table 1.

	10 291	
	272	
per sire	35	
n hyc ¹	37	
yc	2.2	
hyc	1, 18	
ire	2.1	
sire	1, 12	
no.	8 135	
mean (s.d.)	27.91 (6.04)	
no.	5 239	
mean (s.d.)	25.5 (4.2)	
no.	5 339	
mean (s.d.)	3.3 (0.9)	
	per sire n hyc ¹ yc hyc ire sire no. mean (s.d.) no. mean (s.d.) no. mean (s.d.)	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$

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

¹ Herd-year class.

2.2 Statistical methods

A multivariate animal model was used for estimation of genetic parameters. Both direct and maternal additive genetic effects, and permanent environmental effects due to repeated observations, were included in the analyses. Effects included in the model differed between the traits, and they were as follows:

 $BW_{ijklmpq} = S_i + HY_j + LS_k + AE_l + G_m + adir_p + amat_q + pe_q + e_{ijklmpq}$

 $\mathbf{MD}_{ijklmpq} = \mathbf{S}_i + \mathbf{HY}_j + \mathbf{LS}_k + \mathbf{AE}_l + \mathbf{G}_m + \mathbf{b}_1 * (\mathbf{AW}_p) + \mathbf{b}_2 * (\mathbf{LW}_p) + \mathbf{a}dir_p + \mathbf{a}mat_q + \mathbf{pe}_q + \mathbf{b}_1 * (\mathbf{AW}_p) + \mathbf{b}_2 * (\mathbf{LW}_p) + \mathbf{b}_2 * (\mathbf{$

eijklmpq

 $FD_{ijklmpq} = S_i + HY_j + LS_k + AE_l + G_m + b_3*(AW_p) + b_4*(LW_p) + adir_p + amat_q + pe_q + e_{ijklmpq}$ Where:

Where:

$$\begin{split} BW_{ijklmpq} &= body \ weight \ of \ animal \ p; \\ MD_{ijklmpq} &= muscle \ depth \ of \ animal \ p; \\ FD_{ijklmpq} &= fat \ depth \ of \ animal \ p; \\ S_i &= fixed \ effect \ of \ animal \ p; \\ HY_j &= fixed \ effect \ of \ herd-year \ class; \\ LS_k &= fixed \ effect \ of \ herd-year \ class; \\ LS_k &= fixed \ effect \ of \ litter \ size; \\ AE_l &= fixed \ effect \ of \ age \ of \ ewe \ (years); \\ G_m &= fixed \ effect \ of \ genotype \ group \ (three \ groups: 1 = purebred; 2 = max. \ 6.5\% \ of \ other \ breed \ genes; 3 = max. \ 12\% \ of \ other \ breed \ genes); \\ AW_p &= age \ at \ weighting \ (days) \ of \ animal \ p; \\ LW_p &= live \ weight \ at \ the \ day \ of \ weighting \ (kg) \ of \ animal \ p; \\ b_1 &= regression \ coefficient \ of \ MD \ on \ AW \ of \ animal \ p; \end{split}$$

 b_2 = regression coefficient of MD on LW of animal p;

 b_3 = regression coefficient of FD on AW of animal p;

 b_4 = regression coefficient of FD on LW of animal p; $adir_p$ = random direct additive genetic effect of animal p; $amat_q$ = random maternal additive genetic effect of animal q; pe_q = random permanent environmental effect of ewe on lambs BW, MD and FD; $e_{ijklmnopq}$ = random residual.

Homogenous residual variance was assumed for all models. Estimation of (co)variance components for all models was carried out with the AI-REML algorithm using the DMU package (Madsen & Jensen, 2004), and heritabilities were calculated based on these estimates. Genetic correlations were estimated with a bivariate model, however, estimate genetic correlations between MD and FD did not succeed.

3. Results and discussion

3.1. Means of traits

Means and standard deviations of the traits are given in Table 1. Overall means of BW, MD and FD were 27.91 kg, 25.5 mm and 3.3 mm, respectively. These results agree well with estimates found for Suffolk in the literature (Stanford et al., 2001; Jones et al., 2004).

3.2. Heritabilities

Heritabilities (in bold on the diagonal) and genetic correlations (below the diagonal), with standard error in parenthesis are presented in Table 2.

					I dole II
FD_a^{1} FD_m^{2}	MD_m^2 FD _a	MD_a^{-1}	$\mathrm{BW_m}^2$	BW_a^{-1}	
				0.17 (0.04)	BW _a
			0.08 (0.03)	-0.60(0.14)	BW_m
		0.16 (0.04)	-0.37(0.20)	0.47(0.14)	MD _a
	0.04 (0.02)	-0.63(0.18)	0.59(0.23)	-0.38(0.26)	MD _m
.08 (0.03)	nc 0.08	nc	-0.04(0.26)	-0.22(0.20)	FD _a
0.69(0.21) 0.03 (0.02)	nc -0.6	nc	-0.13(0.32)	0.22(0.30)	FD _m
.08 (0.03) 0.69(0.21) 0.03 (0.02)	0.04 (0.02) nc 0.08 nc -0.6	0.16 (0.04) -0.63(0.18) nc nc	-0.37(0.20) 0.59(0.23) -0.04(0.26) -0.13(0.32)	$\begin{array}{c} -0.00(0.14) \\ 0.47(0.14) \\ -0.38(0.26) \\ -0.22(0.20) \\ 0.22(0.30) \end{array}$	MD _a MD _m FD _a FD _m

Table 2.

¹= 'a' in subscript denotes direct additive genetic effect ² 'u' in subscript denotes metamol additive genetic effect

 2 = 'm' in subscript denotes maternal additive genetic effect

nc= models did not converge

The direct heritability for BW was 0.17 and similar to those presented for meat sheep breeds in a comprehensive review by Safari et al. (2005). Notter (1998) found a heritability for BW of 0.21 for Suffolk, however, Tosh and Kemp (1994) have earlier reported higher estimates (0.39) for Hampshire sheep. Direct genetic parameters for body weights are of increased importance with increasing age (Matika et al., 2003), because of growth traits measured on animals close to their birth are under strong influence of the dam. This influence decreases with increasing age of the animal. The estimated maternal heritability for BW was 0.08 and agreed well with results for meat sheep breeds (0.10) presented in a review of Safari et al. (2005).

The direct heritability for MD was 0.16. This estimate is lower compare to those presented by Larsgard and Olesen (1998) for Norweigan Dala crosses (0.32). Furthermore, Larsgard and Olesen (1998) reported a large difference in direct heritability for MD at preweaning (0.05) compared to weaning (0.32). Most studies analysing ultrasound measures have ignored the maternal genetic effects. The maternal heritability for MD in our study was 0.04 and agrees with results for Suffolk (0.03) reported by Maniatis and Pollott (2002) and Larsgard and Olesen (1998) for Norweigan Dala crosses (0.05). The direct heritability for FD in our study was 0.08. Somewhat lower estimates for FD at weaning weight (0.05) were reported by Larsgard and Olesen (1998). Our results differ from those obtained by Maniatis and Pollott (2002) for Suffolk, which range from 0.17 to 0.19. The maternal heritability for FD in our study was 0.03, and this agreed well with results obtained by Larsgard and Olesen (1998) and Maniatis and Pollott (2002) which found a maternal heritability of 0.04 and 0.05, respectively.

3.3. Genetic correlations

The correlation between direct and maternal genetic effects (r_{am}) on BW in this study was -0.60. This is similar to that reported by Neser et al. (2001) for Dorper sheep (-0.58). For Suffolk, even higher negative r_{am} (-0.95) was reported by Maniatis and Pollot (2002), while lower, but also negative r_{am} (-0.20) was found by Notter (1998). In the literature, estimates of r_{am} for body weight at different ages are mainly negative, but vary considerably between studies. Negative correlations between direct and maternal effects, especially when field data is analyzed, can be due to environmental circumstances (Robison, 1972).

Genetic correlations between direct and maternal genetic effects for MD and FD were -0.63 and -0.69, respectively. In contrast to our results, Maniatis and Pollott (2002) obtained positive direct-maternal correlations for MD, ranging from 0.08 to 0.17, and direct-maternal correlations for FD ranging from -0.07 to 0.05. Larsgard and Olesen (1998) estimated r_{am} between MD and FD to be close to zero.

Genetic correlation between the direct effects on BW and MD was as expected positive (0.47) and agree well with results for Suffolk (0.41) reported by Jones et al. (2004). Maternal genetic correlation between BW and MD was large and positive (0.59). The genetic correlation between the direct genetic effect on BW and maternal genetic effect on MD was negative (-0.38) and almost the same size as the genetic correlation between the maternal genetic effect on BW and direct genetic effect on MD (-0.37).

The direct genetic correlation between BW and FD was negative (-0.22). However, the estimate was not significantly different from zero. If the FD was measured in older animals then we could expect positive genetic correlations between weight and FD. Conington et al. (1995) reported a correlation of -0.21 between weight at weaning and average fat depths. Maternal genetic correlation between BW and FD was negative (-0.13), but not significantly different from zero. The correlation between the direct genetic effect on BW and maternal genetic effect on FD was positive (0.22), but not significantly different from zero, and the correlation between the maternal genetic effect on FD was close to zero.

4. Conclusions

The heritabilities obtained for body weight in this study were within the range reported in the literature. The direct heritabilities for muscle and fat depth were somewhat lower compared to the literature, probably because most studies analysing ultrasound measurements have ignored the maternal genetic effects. Favourable genetic correlations between body weight and muscle depth support the value of using ultrasound measurements in breeding programs.

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