Lambing Ease is Heritable but not Correlated to Litter Size in Danish Meat Sheep Breeds

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ABSTRACT: The aim of this study was to estimate genetic parameters of lambing ease (LE) and litter size (LS) in four common Danish meat sheep breeds. Data from 1990 to 2006 were analysed. A bivariate animal model was used for estimation of genetic parameters. Lambing ease showed a low heritability, both for direct (1.4% to 9.5%) and maternal (5.9% to 6.9%) genetic effects. Moderate negative direct-maternal genetic correlations (-0.18 to -0.61) was found. Total heritabilities for LE were 3.8% to 9.7%. Litter size showed also a low heritability (6.4% to 9.0%). Low and non-significant correlations between the LE and LS was found, which means that selection to improve one trait should not affect the other trait. Lambing ease should therefore be included in the selection criterion.
Keywords: lambing ease; heritability; litter size; genetic correlation; meat sheep breed

Introduction

Lambing ease is an important factor that affects profitability in all sheep enterprises. The direct losses caused by dystocia include loss of lambs, death of ewe, veterinary fees, and extra labour requirements (Dwyer (2008)). Dystocia also contributes to some long-term indirect losses, such as increased risk of subsequent health and fertility problems, increased culling, and reduced production. In spite of the importance of the traits, to our knowledge only one genetic analysis of lambing ease in sheep has been published (Brown (2007)). Selection to increase growth rates and muscling in sheep has been very effective, but the individual weight of lambs on the market has an upper limit. Hence, in order to boost income increased litter size is important. The number of lamb born per litter makes a considerable greater contribution to the total weight of lambs weaned per ewe than the growth rate of individual lambs (Bradford (1985)). If genetic variation exists for lambing ease, selection to improve this trait may help to avoid the birth losses due to difficult lambing, and increase the number of weaned lambs.

Genetic evaluations of Danish sheep is currently largely based on values from the literature. Some estimates of genetic parameters of growth traits and litter size have been published by Maxa et al. (2007). However there is a need for estimating parameters of lambing ease based on Danish data. Selection to improve lambing ease may help to avoid the birth losses and reduce labour requirements due to difficult lambing. The possibilities for simultaneous improvement of lambing ease and litter size are dependent on the genetic correlation between the traits.

The aim of this study was to estimate heritabilities of lambing ease and genetic correlations between lambing ease and litter size for the Danish populations of Oxford Down, Shropshire, Suffolk and Texel.

Materials and Methods

Data. In Denmark, about 400 of approx. 6000 flocks are participating in a national sheep recording programme, which is a tool designed to control breeding and production in sheep flocks and also the official herd book for the Danish sheep. The four most widespread meat breeds in the programme are Texel, Shropshire, Oxford Down and Suffolk, respectively. Together these breeds account for 65% of the total number of the registered flocks and 60% of the registered ewes (Stolberg (2007)). Pedigree and performance records were provided by the Knowledge Centre for Agriculture and data from 1990 to 2006 were extracted. The total number of lambings included in the analysis was 96,302 and pedigree information was traced as far back as possible.

The traits analysed were lambing ease and litter size. Lambing ease was recorded on a five point scale where 1=easy lambing without assistance, 2=easy lambing with farmer assistance, 3=difficult lambing with farmer assistance, 4=difficult lambing with veterinary assistance, and 5=caesarean section. The frequency of observations in the fifth group was less than 1%. Therefore we merged groups 4 and 5 into a group called difficult lambing with veterinary assistance. Lambing ease was scored for the lambing as a unit, hence all lambs in a litter have identical LD score. Litter size was recorded on the day of lambing as the total number of lambs born (including dead lambs). Litters with more than 4 lambs were omitted from the analyses.

Parity, sex, lambing month, birth mortality, birth weight and flock-year class were included in the analysis as fixed effects. Birth mortality was recorded at the time of delivery. Birth weight was defined as the live weight of the lamb in kg measured at the latest 24 h after birth. Within litters with more than one lamb, the mean of the lambs' sex, the mean of the lambs' birth mortality, and the mean of the lambs' birth weight was included as covariate in the model.

Model. A bivariate animal model was used for estimation of genetic parameters. The effects included in the model differed for the two traits, and they were as follows:

$$LE_{ijkop} = P_i + LM_j + FY_k + b_1 \times S_o + b_2 \times BM_o$$

$$LS_{ijkop} = P_i + LM_j + FY_k + a_{dir(o)} + a_{mat(p)} + pe_p + e_{ijkop}$$

where:

LE_{ijkopq} = the lambing ease of litter o,

LS_{ijkopq} = the size of litter o,

P_i = the fixed effect of parity i (1st to 8th parity, 8th and greater parities are pooled),

LM_j = the fixed effect of lambing month j (grouped by month, month 6-11 are pooled),

FY_k = the fixed effect of flock-year class k,

b_1 = the regression on sex,

S_o = the average sex of lambs in litter o,

b_2 = the regression on birth mortality,

BM_o = the average birth mortality of lambs in litter o,

b_3 = the regression on birth weight,

BW_o = the average birth weight of lambs in litter o,

$a_{dir(o)}$ = the random, direct, additive genetic effect of a random lamb in litter o,

$a_{mat(p)}$ = the random, maternal, additive genetic effect of ewe p,

pe_p = the random, permanent environmental effect across years of ewe p, and

e_{ijkop} = the random residual.

Correlations between all genetic effects were estimated. The residual correlation between traits and the correlation between permanent environmental effects of the dam between traits were estimated. The correlation between the permanent effect of the dam and the residual (temporary effect of lamb) was also estimated for LE and interpreted as a direct-maternal environmental correlation. Estimation of (co)variance components for both models was carried out with the AI-REML algorithm using the DMU-package (Madsen and Jensen (2010)).

The total heritability (T^2) was calculated following Eaglen and Bijma (2009):

$$T^2 = \frac{\sigma^2_{A_D} + 2\sigma_{A_{DM}} + \sigma^2_{A_M}}{\sigma^2_P}$$

Where $\sigma^2_{A_D}$ = the variance of the direct, genetic effects,

$\sigma^2_{A_M}$ = the variance of the maternal, genetic effects, $\sigma_{A_{DM}}$

= the covariance between the direct and maternal, genetic effects, σ^2_P = the total phenotypic variance.

Eaglen and Bijma (2009) argued that, with maternal effects included, T^2, is the most relevant definition of the total heritability for livestock species in which mass selection is rare, since it gives the ratio of the total heritable variance available for response to selection over the phenotypic variance.

Results and Discussion

While the results obtained from Shropshire, Suffolk and Texel partly support each other for all parameters, Oxford Down showed, in principle, completely different results for the genetic parameters. As the same model and the same procedures in preparing data were used for all four breeds, the dissimilarity is likely caused by a different data structure or less likely caused by a different genetic architecture. According to the means of the traits Oxford Down was the breed with the least lambing problems, the smallest variation in this trait, and also the breed with the highest litter size. We present the results for Oxford Down together with the other breeds (in Table 1 and 2), but because of the inconclusiveness of the estimates connected to lambing ease, the results for this breed will not be discussed further.

Table 1. Heritabilities (in bold on the diagonal), genetic correlations (below the diagonal), and environmental correlations (above the diagonal) with standard error in parenthesis, for lambing ease (LE) and litter size (LS) for Shropshire (*Sh*), Suffolk (*Su*), Texel (*T*), and Oxford Down (*O*).

Sh	LE_d[1]	LE_m[2]	LS
LE_d	**0.014 (0.01)**	0.122 (0.06)	0.004 (0.01)
LE_m	-0.606 (0.25)	**0.059 (0.01)**	0.079 (0.11)
LS	0.048 (0.26)	-0.208 (0.12)	**0.066 (0.01)**
Su	LE_d[1]	LE_m[2]	LS
LE_d	**0.095 (0.04)**	-0.005 (0.11)	0.019 (0.02)
LE_m	-0.476 (0.21)	**0.069 (0.03)**	-0.140 (0.18)
LS	0.178 (0.24)	-0.074 (0.22)	**0.066 (0.02)**
T	LE_d[1]	LE_m[2]	LS
LE_d	**0.050 (0.01)**	-0.141 (0.09)	0.013 (0.01)
LE_m	-0.176 (0.17)	**0.068 (0.01)**	-0.110 (0.15)
LS	0.053 (0.13)	-0.012 (0.09)	**0.090 (0.01)**
O	LE_d[1]	LE_m[2]	LS
LE_d	**0.003 (0.02)**	0.011 (0.11)	0.033 (0.01)
LE_m	0.894 (3.63)	**0.021 (0.01)**	-0.034 (0.18)
LS	-0.175 (1.08)	0.284 (0.27)	**0.064 (0.01)**

[1] 'd' in subscript denotes direct additive genetic effect.
[2] 'm' in subscript denotes maternal genetic effect.

Heritabilities. Heritabilities are presented in bold on the diagonal in Table 1. For lambing ease, the direct heritability ranged from 0.014 for Shropshire to 0.095 for Suffolk. The direct heritability expresses the importance of genes of the lamb for being born easily. The maternal heritabilities of lambing ease varied only slightly among the breeds, from 0.059 for Shropshire to 0.069 for Suffolk. The maternal heritability expresses the effect of the genes of the ewe for having easy lambings. Except for Suffolk, the direct heritability was larger than the maternal heritability. The only study found in the literature presenting heritabilities for lambing ease is Brown (2007), who investigated lambing ease in Australian meat sheep breeds. Brown (2007) presented a direct heritability for lambing ease of 0.06, which agrees well with our results for Texel, Shropshire and Suffolk. The maternal heritability presented by Brown (2007) was 0.04, which is also in good agreement with our study. Brown (2007) also found that the direct heritabilities were higher than the maternal heritability. The total heritability (T^2) of lambing ease ranged from 0.038 for Shropshire to 0.087 for Suffolk and indicates the heritable variance that can be used for genetic improvement as a proportion of the phenotypic variance (Table 2).

Table 2. Total heritability of LE (T^2) and proportion of permanent environmental variance of the phenotypic variance (r^2) with standard errors in parenthesis for lambing ease (LE) and litter size (LS) for Shropshire (*Sh*), Suffolk (*Su*), Texel (*T*), and Oxford Down (*O*).

	T^2	$r2$	
	LE	LE	LS
Sh	0.038 (0.01)	0.053 (0.01)	0.058 (0.01)
Su	0.087 (0.03)	0.065 (0.02)	0.059 (0.02)
T	0.097 (0.02)	0.027 (0.01)	0.045 (0.01)
O	0.037 (0.02)	0.051 (0.01)	0.042 (0.01)

The heritabilities for litter size in this study were generally low (Table 1). Heritabilities were estimated for the total number of lambs born, including dead lambs. Three of the breeds (Oxford Down, Shropshire and Suffolk) showed nearly the same heritability, ranging from 0.064 in Oxford Down to 0.066 in Shropshire and Suffolk. For Texel, a somewhat higher heritability (0.090) was estimated. The heritabilities obtained in the present study are slightly higher than those presented by Maxa et al. (2007), who estimated the heritability for number of lambs alive in the litter after 24h after birth on a subset of the data set used in the present study. Norberg et al. (2005) presented heritabilities for litter size that ranged from 0.08 to 0.13 in populations of Nordic sheep breeds in Denmark. Van Haandel and Visscher (1995) estimated the heritability for litter size at birth for crosses between Isle de France and Finnish Landrase to be 0.16. In the same study, litter size at 24 h after birth was estimated to be 0.08. Janssens et al. (2004) presented heritabilities for litter size for Suffolk and Texel sheep using different models, ranging from 0.06 to 0.07 and from 0.09 to 0.13, respectively. In general, our results for the heritability of litter size are in agreement with those found in the literature.

Genetic correlations. Genetic correlations between the traits are presented below the diagonal in Table 1. For Texel, Suffolk and Shropshire there was a moderate, negative genetic correlation between the direct and maternal genetic effect for lambing ease of -0.176, -0.476 and -0.606, respectively. This unfavourable genetic correlation shows that a lamb, which has genes for being born easily, tends to have genes for having more difficult lambing, when it becomes a dam. Robinson (1972) proposed that environmental circumstances can induce negative correlations between direct and maternal effects, especially when field data are analysed, where some changes in measuring the trait or husbandry practices might alter these relationships.

In all breeds, all genetic correlations between lambing ease and litter size were low and not significantly different from zero, and we can generally say that no evidence of correlations between these traits has been found. This means that selection to improve one trait can not be expected to affect the other trait. No estimates between these traits were found in the literature. However, Brown (2007) estimated the genetic correlation between lambing ease and the number of lambs weaned to be negative (-0.26), meaning that genetically more fecund ewes tend to have easier lambings.

Permanent environmental effects. Proportions of phenotypic variance explained by permanent environmental effects were generally small for both traits (Table 2). Residual correlations between lambing ease and litter size were generally low and not significantly different from zero. Brown (2007) estimated the maternal permanent environmental effect for lambing ease to account for 24%, which is somewhat higher than in our study.

Conclusion

Lambing ease is a heritable trait and should be included in the selection criterion even though the heritable variance that can be used for genetic improvement as a proportion of the phenotypic variance is low. Direct and maternal genetic effects are unfavourably correlated and the maternal genetic effects appear to make up the largest part of the total genetic variation. Low genetic correlations between lambing ease and litter size were found, which means that selection to improve one trait should not affect the other trait.

Literature Cited

Bradford, G. E. (1985) *Genetics of reproduction in sheep* (Eds R. B. Land, D. W. Robinson), Butterworths, London. pp. 3-18.
Brown, D.J. (2007) *Proc. 17th AAABG*. pp.268-271.
Dwyer, C. M. (2008) *Small Rum. Res*. 76:31-41.
Eaglen, S.A.E., and Bijma, P. (2009) *J. Dairy Sci.* 92:2229–2237.

Janssens S., Vandepitte W., and Bodin, L. (2004) *Genet. Sel. Evol.* 36:543–562.

Madsen, P., and Jensen, J. A. (2010). DMU. Version 6, release 4.6.

Maxa, J., Norberg, E., Berg, P., et al. (2007) *Small Rumin. Res.* 68:312-317.

Norberg, E., Berg, P., and Pedersen, J. (2005) *Acta Agri. Scand Sec. A.* 55:123-127.

Robison, O. W. (1972) *J. Anim. Sci.* 35:1303-1315.

Stolberk, L. M. (2007) Tal om får og geder 2006. Dansk Landbrugsrådgivning, Landscenteret, Dansk Kvæg, Århus, pp. 5-11 (in Danish with English summary).

Van Haandel E. B. P. G., and Visscher, A. H. (1995) *Livest. Prod. Sci.* 43:129–136.