

## Feasibility of a Linear Scoring Method of Udder Morphology for the Selection Scheme of Sardinian Sheep

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### ABSTRACT

Breeders are increasingly interested in improving the machine milkability of Sardinian dairy sheep by selection for udder morphology. Nine-point linear scales were developed to appraise teat placement, degree of suspension of the udder, udder depth, and degree of separation of the 2 halves. Repeatabilities within and across lactation were estimated on an experimental flock. Ewes were scored at least 3 times a year from 1999 to 2003. Within-lactation repeatabilities were greater than 0.70 for all linear traits, whereas across-lactation repeatabilities ranged from 0.59 to 0.66. The first linear combination of basic traits, obtained by principal component analysis, was highly correlated with teat placement, degree of suspension of the udder, and udder depth and showed an across-lactation repeatability of 0.76. These results indicate that an accurate evaluation of animals is possible by a single, early lifetime score. Genetic parameters of linear udder traits were estimated using a REML method applied to a sire model. Data were selected from 76,984 scores of Sardinian yearling ewes collected by 31 classifiers from 1999 to 2004. Two models were compared, one fitting the contemporary group effect as fixed and the other as random. Heritabilities of udder traits ranged from 0.19 to 0.31. The model with the random contemporary group effect produced slightly higher heritabilities and higher correlations between the sires' estimated breeding values and the daughters' average scores. As a whole, the genetic correlations between udder traits were favorable, indicating that selection for one trait will produce a positive evolution of the overall udder conformation. In particular, the degree of suspension of the udder was highly correlated with udder depth (0.82). Genetic correlations with milk yield were unfavorable but generally low, with the exception of udder depth (–0.48). Genetic trends were estimated using an animal model. Only udder depth showed a negative constant genetic

trend. Overall results indicated that genetic improvement of the udder morphology of Sardinian ewes is feasible, with major emphasis on teat placement and degree of udder suspension, traits showing the highest heritabilities and low unfavorable genetic correlations with milk yield.

**Key words:** Sardinian sheep, linear udder trait, milkability, genetic parameter

### INTRODUCTION

In western European countries (France, Spain, and Italy) breeding schemes for dairy sheep are based on a pyramidal management of the purebred population. Registered flocks are at the top of the pyramid, where artificial insemination, official milk recording (International Committee for Animal Recording, 2005), and breeding value estimations are carried out to generate genetic progress. Genetic progress is then transferred to the commercial population by means of artificial insemination or by natural-mating rams (Barillet, 1997).

The Sardinian breed is one of the most important European dairy sheep breeds. It has a commercial population of about 3,200,000 ewes and a registered population of 205,000 ewes in 1,005 flocks. The breeding goal is to increase milk yield for a standardized milking period of 162 d. The current genetic gain has been estimated as approximately 2 L/yr, corresponding to 12% of the genetic SD (Carta et al., 2004).

Recently, interest has been increasing in functional traits such as milkability. Traditionally, sheep farmers have chosen dams of sires on the basis of milk yield EBV and a subjective appraisal of udder morphology and hand-milking ease. Although the effects of this selection cannot be quantified, rapid and easy hand milking is a distinguishing feature of Sardinian ewes. Hand milking is still the most widely used technique, but machine milking has been increasingly used in recent years. Because of relevant differences between the two milking techniques, a redefinition of the concept of milking ability is required. A measure of machine-milking efficiency is the number of manual interventions needed to extract the milk retained in the udder; that is, stripping and teat cup plug-in operations. Udders

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strongly attached to the abdominal wall and with vertical teats placed on the lowest part of the cistern are less subject to teat-cup falls and need fewer manual interventions for stripping (Casu et al., 1983, 2000). By contrast, when teats are horizontal and implanted far from the udder floor, a certain amount of milk may be retained in the cistern (Sagi and Morag, 1974; Bruckmaier et al., 1997). Horizontal teats are also more susceptible to distortion during machine milking. This inhibits the ejection reflex and thus increases alveolar milk retention (Labussière, 1988). Deep udders also retain part of the milk in the cistern during the machine milking; thus, manual intervention is needed to complete the milk extraction (Casu et al., 2000). Several authors have also highlighted the strong relationship between udder depth and milk yield (Labussière, 1988; Casu et al., 2000). Finally, udder conformation may be linked to functional longevity because grazing ewes with deep udders are more exposed to injury, and consequently may be more liable to be culled.

In the 1980s, classification of overall udder shape based on 4 classes was proposed in Italy (Casu et al., 1989). The method was easy to apply, but it had the disadvantage that the evaluation of basic traits was combined into a single score. It also prevented an accurate ranking of animals, because it was based on only 4 classes and the categorical nature of data was not suitable for genetic evaluation with BLUP animal models. In dairy cattle, direct scoring for basic type traits with linear extended scales has solved these problems (Schaeffer et al., 1985; Meyer et al., 1987; Visscher and Goddard, 1995). A linear scoring method to evaluate the udder traits of sheep was proposed by De la Fuente et al. (1996) and applied to Spanish breeds (Fernandez et al., 1997; Serrano et al., 2002; Legarra and Ugarte, 2005).

The overall objective of this study was to investigate the feasibility of a linear scoring method to evaluate udder morphology for the selection scheme of Sardinian dairy sheep to improve their machine milkability by selection for udder morphology. Specific objectives were to estimate within- and across-lactation repeatabilities of linear udder traits in an experimental flock, as well as heritabilities and genetic correlations between udder traits and milk yields from first-lactation records collected in registered flocks.

## MATERIALS AND METHODS

### *Description of the Appraisal Method*

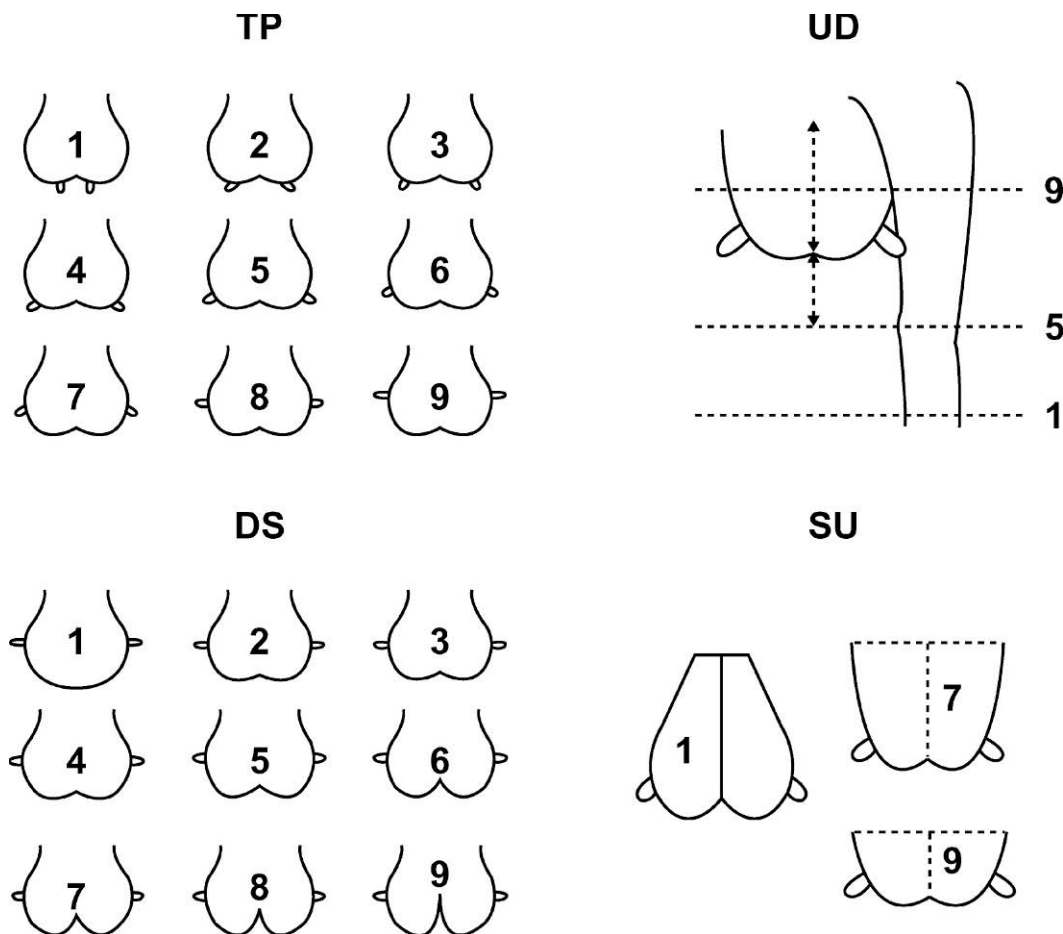
The method considers 4 udder traits (Figure 1), each scored with a 9-point linear scale: teat placement (TP), udder depth (UD), degree of separation of the 2 halves (DS), and degree of suspension of the udder (SU). Teat

placement is the external height of the cistern, that is, the distance between the teats and the lowest part of the udder. The best score is 1, for teats placed on the lowest part of the udder, and the worst is 9, for teats located above the area with the maximum radius of curvature. Udder depth is the distance between the udder cleft and the abdominal wall, taking as a reference point the line joining the hocks; UD is scored 1 (the worst) for deep udders close to the ground, 5 for clefts at the hocks level, and 9 (the best) for shallow udders close to the abdominal wall. The SU is the ratio between the udder attachment width and udder height. The best score is 9, for udders with an attachment width much larger than the UD, and the worst is 1, for udders with an attachment width much smaller than the UD. The score of 7 is given to apparently square udders, which are the easiest to evaluate. Finally, DS scores the strength of the median ligament. The worst score for DS is 1, with no separation between the left and right glands, whereas 9 is the best, for udders clearly divided into 2 halves.

The strength of the median ligament and SU are scored in the same way in France (Marie-Etancelin et al., 2003). In the Spanish scoring method (De la Fuente et al., 1996), the SU is not scored directly but may be deduced by combining the udder attachment score (i.e., the perimeter of udder insertion on the abdominal wall) and the UD score. Udder depth and TP are traits included in the scoring systems used in France (Marie et al., 1999) and, with scales in the opposite direction, in Spain (De la Fuente et al., 1996).

### *Repeatability of Udder Traits on an Experimental Farm*

This trial was conducted at an experimental farm because of the difficulties involved in performing repeated scoring on young and adult ewes in the registered flocks. A flock of 933 ewes was evaluated for the 4 udder traits from 2000 to 2003. The ewes were born between November and December 1998, with lambings occurring between January and March 2000 for first parities and between November and December for later parities. Udders were scored monthly in 2000, when all ewes were in first lactation. In the following years, animals were evaluated 3 times during lactation (beginning, middle, and late lactation). Scoring was performed in the milking parlor just prior to milking by 4 operators working in alternate pairs. Each ewe was thus evaluated by at least 2 classifiers at every round of scoring. During the 4 yr of the experiment, 23,296 double individual scores were recorded in 15 rounds of scoring. Previous analyses showed high repeatability between classifiers, ranging from 0.76 for DS to 0.83 for SU



**Figure 1.** Nine-point linear scales for udder traits: TP = teat placement; UD = udder depth; DS = degree of separation of the 2 halves; SU = degree of suspension of the udder.

(Marie-Etancelin et al., 2003), These results indicated that a single randomly selected score per ewe and date of scoring could be used to simplify the models, limit calculations, and simulate field conditions in which a single operator would score each ewe. The final data set included 10,966 records from 894 ewes.

A single-trait analysis was performed to estimate the repeatability of udder morphology traits within and across lactations. The categorical nature of the traits was ignored (i.e., all traits were treated as continuous), as has been suggested in previous works (Carta et al., 1999; Serrano et al., 2002). These previous studies did not find substantial differences in the results obtained by statistical analysis of raw data or Snell-transformed data (Snell, 1964). To test whether the appraisal method could rank animals for the overall morphology of the udder, repeatabilities were also estimated for two linear combinations of the basic traits. These were obtained by principal component analysis on the basis of the eigenvectors of the correlation matrix of udder

traits. Principal component analysis was performed using the Princomp SAS procedure (SAS Institute, 2000).

The mixed linear model used for estimating repeatabilities was

$$y_{ijklm} = \text{PLS}_i + \text{CD}_j + a_k + ap_{kl} + e_{ijklm} \quad [1]$$

where  $y_{ijklm}$  was the score for udder traits TP, UD, DS, and SU, or for their linear combination (principal component 1 or 2) for ewe  $k$  at the considered round of scoring;  $\text{PLS}_i$  was the combination of lactation stage  $\times$  parity number (10 classes of 20 DIM and 4 parities);  $\text{CD}_j$  was the fixed effect of the classifier within the date of scoring (75 levels);  $a_k$  was the random effect of ewe  $k$  (894 levels);  $ap_{kl}$  was the random effect of ewe  $k$  within parity  $l$  (3,144 levels); and  $e_{ijklm}$  was the random residual. All random effects were considered normal and were independently distributed. Variance components were estimated using the REML method provided by the ASREML software (Gilmour et al., 2002).

Repeatability within lactation ( $r_w$ ) and across lactations ( $r_b$ ) was calculated as follows:

$$r_w = (\sigma_a^2 + \sigma_{ap}^2) / (\sigma_a^2 + \sigma_{ap}^2 + \sigma_e^2) \quad [2]$$

$$r_b = (\sigma_a^2) / (\sigma_a^2 + \sigma_{ap}^2 + \sigma_e^2) \quad [3]$$

where  $\sigma_a^2$ ,  $\sigma_{ap}^2$ , and  $\sigma_e^2$  were the estimated variances for the ewe, the ewe within parity, and residual effects, respectively.

### Genetic Analysis in Registered Flocks

The proposed appraisal method for udder morphology has been applied in the registered Sardinian flocks since 1999 for TP and UD; SU and DS were introduced in 2000. Farms were visited once a year by 1, or occasionally 2, classifiers and only yearling ewes were scored. Because of the seasonality of lambings, which typically occur in late winter for yearlings, farm visits occurred between April and June so that the maximum number of lactating primiparous ewes in each flock was scored. The ewes were evaluated prior to the morning or afternoon milking. Thirty-one trained classifiers scored a total of 76,984 ewes in 2,104 flock-years, from 1999 to 2004. Milk yield was available for all scored ewes. Genetic parameters for udder traits and their genetic correlations with milk yield, expressed as mature ewe equivalents (MEE; Carta et al., 1998b), were estimated on a subset of data that included ewes with known sires from connected flocks. In the Sardinian breeding scheme, controlled natural mating is managed by keeping ewes in separate groups, each with a single sire. Natural-mating rams usually serve one or a few flocks, but AI, which currently produces about 20% of female replacement, generates genetic ties between flocks. Therefore, only records from flock-years with daughters of at least one sire who had offspring in at least one other flock-year including daughters of other sires were retained. This selection resulted in 61,976 records for TP and UD and 50,675 records for SU and DS. Heritabilities and genetic correlations between udder traits and MEE were estimated using a REML method applied to a sire model. A sire model was used instead of an animal model to reduce calculation time. Genetic parameter estimates were not expected to be less accurate than with the animal model, because the appraisal was applied only for 6 yr and the number of scored dams was low; thus, the contribution of dam-daughter pairs to the estimate of additive genetic variance was small. Male relationships were considered using the sire-maternal grand sire model. The final pedigree file for TP and UD included 2,874 males, of which 2,150 were sires of scored ewes. The pedigree file

for SU and DS included 2,479 rams, of which 1,816 were sires of scored ewes.

Two models were compared to choose the best one for estimating genetic parameters and genetic trends. For the model with the random contemporary group effect (**RAN**),

$$Y_{ijklm} = LS_i + YC_j + FYC_{lj} + s_k + e_{ijklm} \quad [4]$$

where  $Y_{ijklm}$  was the score of ewe  $m$  for udder trait TP, UD, SU, or DS;  $LS_i$  was the fixed effect of lactation stage  $i$  (17 levels of 10 DIM);  $YC_j$  was the fixed effect of year-classifier  $j$  (123 levels for TP and UD and 105 levels for SU and DS);  $FYC_{lj}$  was the random effect of flock  $l$  within year-classifier  $j$  (1,768 levels for TP and UD and 1,434 levels for SU and DS);  $s_k$  was the additive genetic random effect of sire  $k$  (2,150 levels for TP and UD and 1,816 for SU and DS); and  $e_{ijklm}$  was the random residual.

The model of analysis with the fixed contemporary group effect (**FIX**) included the same effects as the RAN model with the exception of flock-year classifier, which was fitted as a fixed effect instead of a random effect, as in the RAN model. The FIX model assumed that all differences between contemporary groups were due to management, whereas the RAN model assumed that part of the difference between contemporary groups was due to random additive genetic or environmental effects. In genetic models, contemporary groups are more frequently included as fixed. The main reason for treating them as random in the current analysis was that, as suggested by Schaeffer et al. (2001), differences in management should have little effect on conformation traits. This was even more likely in the current study, where animals were scored only once, at the beginning of their productive lives. Thus, comparing an animal's score to the overall mean rather than to the mean of the contemporary group seemed more correct, and this was achieved by fitting this effect as random. This can lead to more accurate breeding-value predictions, especially in situations in which the contemporary group size is small (Frey et al., 1997; Van Bebber et al., 1997). However, it can also lead to a bias in breeding-value estimates because of a nonrandom association between animals and environmental effects, such as elite sires being used in the better-managed flocks (Van Vleck, 1987; Visscher and Goddard, 1993).

The effects of FYC in the FIX model and YC in the RAN model take into account differences among the classifiers and possible changes in the scoring scale between years. In the RAN model, because FYC effects were assumed to be random, the ewes' scores deviated from the YC averages rather than from the overall mean (Schaeffer et al., 2001).



**Table 1.** Estimates of ewe ( $\sigma_a^2$ ), ewe within parity ( $\sigma_{ap}^2$ ), and residual ( $\sigma_e^2$ ) variances; repeatability within ( $r_w$ ) and across ( $r_b$ ) lactation for udder traits; and their linear combinations in experimental farm ewes

Trait	$\sigma_a^2$	$\sigma_{ap}^2$	$\sigma_e^2$	$r_w$	$r_b$
Teat placement	0.494 ± 0.026	0.082 ± 0.004	0.221 ± 0.0035	0.72 ± 0.0096	0.62 ± 0.0131
Degree of suspension of the udder	1.240 ± 0.064	0.186 ± 0.01	0.476 ± 0.007	0.75 ± 0.009	0.65 ± 0.0125
Udder depth	0.607 ± 0.031	0.098 ± 0.005	0.220 ± 0.0035	0.76 ± 0.0087	0.66 ± 0.0124
Degree of separation	0.796 ± 0.042	0.147 ± 0.009	0.401 ± 0.007	0.70 ± 0.0103	0.59 ± 0.0138
Principal component 1	1.318 ± 0.066	0.167 ± 0.008	0.248 ± 0.004	0.86 ± 0.006	0.76 ± 0.010
Principal component 2	0.537 ± 0.028	0.105 ± 0.006	0.296 ± 0.005	0.64 ± 0.011	0.57 ± 0.014

Milk yield on the day of scoring was not included in the models. Legarra and Ugarte (2005) compared models that included or did not include milk yield. They stated that udder fill affected the scoring and that neglecting it could produce a bias in the estimation of genetic parameters. The amount of milk produced on the day of scoring may not reflect the degree of udder fill. Indeed, large udders can produce high milk yields even if udder fill is low, and small udders can produce low milk quantities but with high udder fill. Furthermore, including a genetically correlated trait in the model can lead to a reduction in the estimates of additive genetic variance and covariance for the trait of interest. The results of Legarra and Ugarte (2005) seem to confirm this hypothesis.

In both the FIX and RAN models, heritabilities were calculated as the ratio between the additive genetic variance and the total individual variance. This means that in the RAN model the estimated variance of the FYC random effect was not considered in heritability calculations.

The nonrandom association between sires and flock-year effects was also investigated. In the FIX model, Pearson correlations were calculated between FYC effects and the average sire EBV, that is, the average of the involved sires' EBV weighed for the number of daughters in each FYC.

Afterward, Spearman correlations were calculated between the sires' EBV obtained from the two analyses and between the sires' EBV and the daughters' average scores.

Genetic correlations between udder traits and MEE were estimated by bivariate analyses, because computing limitations prohibited solving for five traits simultaneously. The model of analysis for MEE, also used currently for the genetic evaluation in the Sardinian breed (Carta et al., 1998a), was

$$Y_{ijkm} = \text{FY}_i + \text{YLM}_j + s_k + e_{ijkm} \quad [5]$$

where  $Y_{ijkm}$  was the MEE of ewe  $m$ ;  $\text{FY}_i$  was the fixed effect of flock-year  $i$  (1,752 levels);  $\text{YLM}_j$  was the fixed effect of lambing-year month  $j$  (30 levels for 6 yr and 5 lambing periods);  $s_k$  was the random additive genetic effect of sire  $k$ ; and  $e_{ijkm}$  was the random residual. Variance components were estimated by using the REML method in ASREML (Gilmour et al., 2002).

The correlated response of the selection for milk yield on udder morphology was studied by calculating genetic trends for udder traits as the average EBV of ewes by year of birth. Breeding values were estimated by applying single-trait BLUP animal models and using the MTDFREML software (Boldman et al., 1993). The analysis included 76,984 records for TP and UD and 63,945 for SU and DS. Pedigree files based on 3 generations of ancestors included 145,637 animals for TP and UD and 126,593 for SU and DS.

## RESULTS AND DISCUSSION

### Repeatability of Udder Traits in the Experimental Flock

In the experimental flock, from the first to fourth parity, cistern height increased (TP mean values in-

**Table 2.** Eigenvectors and eigenvalues of principal components and proportion of the total variability explained by each principal component (individually and cumulatively) in experimental farm ewes

Principal component	Eigenvectors					Proportion of variation	
	Teat placement	Degree of suspension of the udder	Udder depth	Degree of separation	Eigenvalues	Individual	Cumulative
1	-0.54	0.60	0.55	0.22	2.15	0.54	0.54
2	-0.04	-0.20	-0.21	0.96	0.96	0.24	0.78
3	0.77	0.07	0.60	0.18	0.57	0.14	0.92
4	0.33	0.77	-0.53	0.06	0.32	0.08	1.00

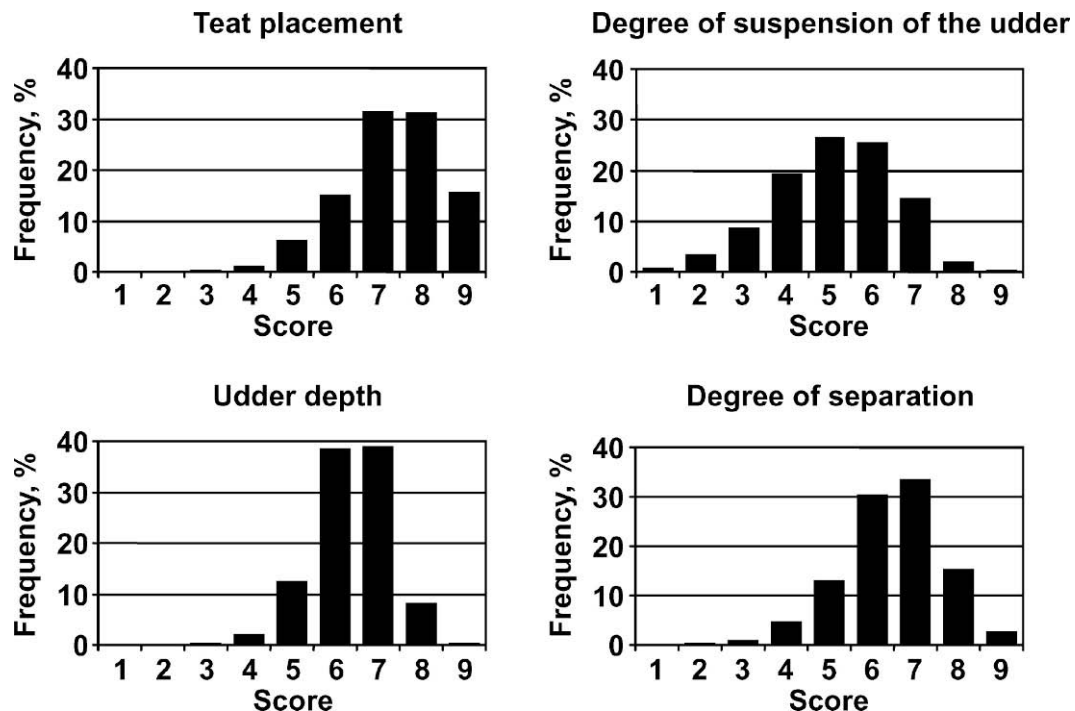
**Table 3.** Raw correlation matrix between linear udder traits and correlations between these and their first two linear combinations from a principal component analysis of experimental farm ewes

Trait	Degree of suspension of the udder	Udder depth	Degree of separation	Principal component 1	Principal component 2
Teat placement	-0.57	-0.42	-0.21	-0.79	-0.04
Degree of suspension of the udder	—	0.64	0.12	0.88	-0.19
Udder depth		—	0.12	0.81	-0.20
Degree of separation			—	0.32	0.94

creasing from  $7.56 \pm 1.09$  to  $8.13 \pm 0.81 \pm \text{SD}$ ). The means for UD and SU decreased from  $6.40 \pm 0.90$  to  $5.25 \pm 0.96$  and from  $4.91 \pm 1.58$  to  $3.65 \pm 1.24$ , respectively. Lower variations were observed for DS (from  $6.0 \pm 1.07$  in first to  $6.35 \pm 1.30$  in fourth lactation). These patterns correspond to a worsening of milkability and to a relaxation of the suspensory system of the udder. This finding agrees with previous results (De la Fuente et al., 1996; Marie et al., 1999)

Repeatabilities of udder traits during the productive lives of the animals were from moderate to high (Table 1). Within-lactation repeatabilities were greater than 0.70 for all scored traits and were higher than those found for similar traits in the Churra (Fernandez et al., 1997), Lacaune (Marie et al., 1999), and Latxa breeds (Ugarte et al., 2001). Their values suggest that a single scoring per lactation is reasonably accurate for ranking

ewes for selection purposes. As expected, repeatabilities across lactations were lower, ranging from 0.59 for DS to 0.66 for UD. In Holstein cattle, Meyer et al. (1987) found lower repeatabilities by estimating phenotypic correlations between first and second lactation for udder traits. Principal component analysis showed that the first 2 eigenvalues of the correlation matrix between udder traits explained, respectively, 54 and 24% of the total common variability (Table 2). In the eigenvector associated with the first eigenvalue, the weight of TP was negative and the weights of UD and SU were positive, and these were twice the weight of DS (Table 2). Thus, principal component 1 was highly correlated with TP, UD, and SU (Table 3). The weight of DS was predominant and positive in the eigenvector associated with the second eigenvalue of the correlation matrix, whereas the loadings of the three other traits were

**Figure 2.** Frequency of scores for linear udder traits of primiparous ewes of the Sardinian breed in registered flocks.

**Table 4.** Estimates of genetic additive ( $\sigma_a^2$ ), residual ( $\sigma_e^2$ ), and flock within-year classifier ( $\sigma_{\text{FYC}}^2$ ), variances and heritability for udder traits in a single-trait analysis for models fitting the contemporary group effect as fixed (FIX) or random (RAN) in registered flocks

Trait	FIX			RAN			
	$\sigma_a^2$	$\sigma_e^2$	$h^2$	$\sigma_{\text{FYC}}^2$	$\sigma_a^2$	$\sigma_e^2$	$h^2$
Teat placement	0.29 ± 0.019	0.66 ± 0.016	0.30 ± 0.019	0.14 ± 0.067	0.29 ± 0.018	0.66 ± 0.015	0.31 ± 0.018
Degree of suspension of the udder	0.29 ± 0.024	1.01 ± 0.021	0.23 ± 0.018	0.15 ± 0.0084	0.33 ± 0.025	0.98 ± 0.0210	0.25 ± 0.018
Udder depth	0.12 ± 0.0097	0.47 ± 0.0082	0.20 ± 0.016	0.11 ± 0.053	0.13 ± 0.0098	0.46 ± 0.0083	0.22 ± 0.016
Degree of separation	0.18 ± 0.016	0.74 ± 0.014	0.20 ± 0.017	0.17 ± 0.086	0.19 ± 0.016	0.73 ± 0.014	0.21 ± 0.017

small (Table 2). Within-lactation repeatability was high for both principal components 1 and 2 (Table 1). Furthermore, although across-lactation repeatability of principal component 2 was similar to that of DS, across-lactation repeatability of principal component 1 was high (Table 1), indicating that a single lifetime score may be sufficient to rank the animals correctly for overall udder morphology. This result is of particular interest for selection, as it permits a quite accurate and early genetic evaluation of the animals. Similar conclusions were drawn by Snowden et al. (2001), Meyer et al. (1987), and Legarra and Ugarte (2005), who estimated that there were high genetic correlations for udder traits between first and second lactation in both cattle and ewes.

### Genetic Analysis in Registered Flocks

**Linear Score Distribution.** The frequencies of udder trait scores are reported in Figure 2. The average udder of Sardinian primiparous ewes showed teats implanted at a quite high level (7.32), an average depth above the hocks (6.38), a well-balanced ratio between width and depth [i.e., a quite high SU (5.11)], and udder halves markedly separated (6.46). Low scores (1 to 3) were infrequent or absent, especially for TP and UD. The linear scales were indeed designed to cover the biological extremes of the traits, whether they actually existed. The extreme values of the linear scales were more often found for SU, whose distribution showed the highest variability. On the whole, these results showed

that the Sardinian breed should be improved for udder morphology traits, with major emphasis on TP.

**Estimation of Genetic Parameters.** Table 4 reports variance components and heritability estimates obtained with the single-trait analysis for the FIX and RAN models. Heritability estimates ranged from 0.20 for DS and UD in the FIX model to 0.31 for TP in the RAN model. These results agree with estimates found in several Spanish breeds for the linear scores proposed by De la Fuente et al. (1996). Indeed, heritability estimates in Churra ranged from 0.16 for UD to 0.24 for udder attachment (Fernandez et al., 1997). Legarra and Ugarte (2005) reported higher heritabilities in Latxa first-lactation ewes, ranging from 0.22 for UD to 0.38 for TP. Only for the Manchega breed did Serrano et al. (2002) report very low heritability estimates, especially for udder attachment (0.06). The authors argued that this was because the classifiers had difficulty in scoring that particular trait.

Heritabilities and additive genetic variances of all udder traits estimated with the RAN model were as high as (TP and DS) or higher (UD and SU) than those of the FIX model (Table 4). Residual variance estimates were similar or smaller in RAN than in FIX. Variance of the FYC random effect ranged from 10 (SU) to 16% (UD) of the total variance. These values were moderate but not negligible and reflected differences between flocks in management, environment, and probably in the genetic merit of the dams. The latter cannot be estimated directly because the scoring system has only recently been implemented. Correlations between the

**Table 5.** Spearman correlations between sires' EBV ( $r_{\text{EBV}}$ ) from the FIX and RAN models and Pearson correlations of average score of daughters with sires' EBV estimated with the 2 models ( $r_{\text{FIX}}$ ,  $r_{\text{RAN}}$ ) for rams with more than 10 daughters (n) in registered flocks<sup>1</sup>

Trait	n	$r_{\text{EBV}}$	$r_{\text{FIX}}$	$r_{\text{RAN}}$
Teat placement	1,792	0.94	0.44	0.57
Degree of suspension of the udder	1,522	0.92	0.35	0.49
Udder depth	1,792	0.91	0.36	0.57
Degree of separation	1,522	0.94	0.38	0.50

<sup>1</sup>FIX = Model with the contemporary group included as a fixed effect; RAN = model with the contemporary group included as a random effect.

**Table 6.** Genetic parameters of udder traits and milk yield estimated with a bivariate analysis considering the random contemporary group<sup>1</sup>

Trait	Teat placement	Degree of suspension of the udder	Udder depth	Degree of separation	Mature ewe equivalent
Teat placement	0.31–0.33 <sup>2</sup>	–0.69 ± 0.03	–0.55 ± 0.03	–0.20 ± 0.05	0.15 ± 0.04
Degree of suspension of the udder	–0.39 ± 0.01	0.26–0.29 <sup>2</sup>	0.82 ± 0.02	0.11 ± 0.05	–0.10 ± 0.05
Udder depth	–0.32 ± 0.01	0.47 ± 0.01	0.22–0.23 <sup>2</sup>	–0.01 ± 0.06	–0.48 ± 0.04
Degree of separation	–0.08 ± 0.05	0.06 ± 0.01	0.03 ± 0.01	0.21–0.21 <sup>2</sup>	0.13 ± 0.05
Mature ewe equivalent	0.07 ± 0.02	–0.07 ± 0.02	–0.13 ± 0.02	0.08 ± 0.02	0.40–0.40 <sup>2</sup>

<sup>1</sup>On the diagonal = range of heritabilities; above the diagonal = genetic correlations; below the diagonal = environmental correlations in registered flocks.

<sup>2</sup>SE of heritability estimates were always <0.023.

FYC effects and the average sire EBV obtained from the FIX model were close to zero and not significant for all the 4 linearly scored traits. A nonrandom association among sires and flock-years and bias in the breeding value estimation can thus be excluded when the contemporary group effect is treated as random.

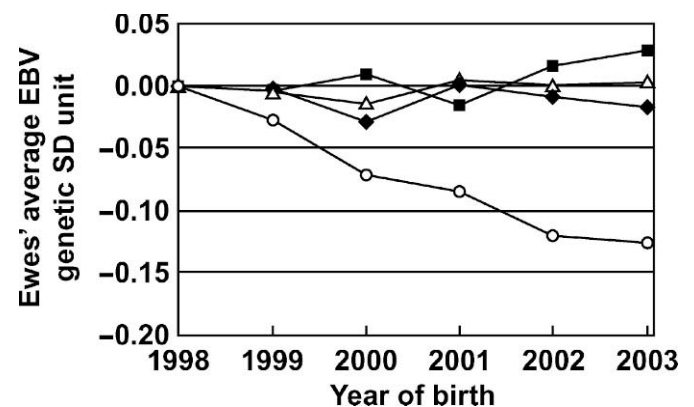
Spearman correlations between the EBV of sires from the FIX and RAN models (Table 5) indicated important differences in the ranking of the animals. Correlations between the sires' EBV and the average scores of daughters were significantly higher with the RAN model (Table 5). Thus, using contemporary groups as a random effect had a positive impact on the genetic evaluation of udder traits. Indeed, this approach produced a slight increase in heritability estimates. Moreover, the stronger correlations between the sires' EBV and the average scores of their daughters agree with breeders' expectations, particularly with regard to natural-mating sires, which have daughters in a single flock or a few flocks and can be directly evaluated by the farmers themselves.

The RAN model was thus used for estimating genetic and environmental correlations among udder traits and among these and MEE (Table 6), as well as for estimating genetic trends (Figure 3). Single-trait heritability estimates were always included in the range of the bivariate results (Table 6), and differences reached a maximum value of 11% for SU. Most of the genetic correlations between udder traits had moderate to high values. In general, results from the current study agree with those reported for the Churra (Fernandez et al., 1997) and Latxa (Legarra and Ugarte, 2005) breeds. The differences found in the sign were attributable to the linear scales having TP and UD in the opposite direction. The lowest genetic correlations were those involving DS (Table 6). The DS and UD in particular were not genetically correlated. Genetic correlations between UD and SU and between TP and SU were larger than those estimated between udder attachment and UD and between TP and udder attachment in the Latxa breed (Legarra and Ugarte, 2005). By contrast, Serrano

et al. (2002), when working on the Manchega breed, found very low genetic correlations between UD and udder attachment (0.13) and between UD and TP (0.06).

On the whole, genetic correlations estimated in the Sardinian breed showed that whatever basic trait is considered as a selection goal, it will result in a positive evolution of the overall udder morphology.

The genetic correlations among milk yield and TP, SU, and DS were weak. Stronger and more unfavorable genetic correlations were estimated between TP and milk yield in both the Churra (–0.34; Fernandez et al., 1997) and Latxa (–0.24; Legarra and Ugarte, 2005) breeds. The only udder trait with a noticeable and unfavorable genetic correlation with milk yield in Sardinian sheep was UD. In Latxa sheep, the genetic correlation between these 2 traits was also unfavorable—0.43 or 0.54, depending on whether milk yield on the day of scoring was included in the model (Legarra and Ugarte, 2005). In the Manchega (Serrano et al., 2002) and Churra (Fernandez et al., 1997) breeds, the genetic correlation between UD and 120-d milk yield was even higher (0.82 and 0.64, respectively). Environmental correlations had the same trends as genetic ones, but with



**Figure 3.** Genetic trends of udder traits in registered flocks. Teat placement (—■—); udder depth (—○—); degree of suspension of the udder (—△—); degree of separation of the 2 halves (—◆—).



**Table 7.** Variances (on the diagonal), covariances (above the diagonal), and correlations (below the diagonal) of the flock within-year classifier random effect estimated for udder trait and between udder traits in registered flocks

Trait	Teat placement	Degree of suspension of the udder	Udder depth	Degree of separation
Teat placement	0.14–0.14 <sup>1</sup>	–0.074 ± 0.006	–0.018 ± 0.004	0.009 ± 0.006
Degree of suspension of the udder	–0.50 ± 0.03	0.15–0.16 <sup>1</sup>	0.040 ± 0.005	0.004 ± 0.006
Udder depth	–0.15 ± 0.03	0.31 ± 0.03	0.11–0.11 <sup>1</sup>	–0.021 ± 0.005
Degree of separation	0.06 ± 0.03	0.02 ± 0.04	–0.15 ± 0.03	0.17–0.18 <sup>1</sup>

<sup>1</sup>SE of variance estimates were between 0.003 and 0.009.

lower absolute values (Table 6). Correlations between traits for the FYC random effect were in the same direction as the genetic ones and were generally lower (Table 7).

The analysis of genetic trends of udder traits agreed with the genetic correlation estimates (Figure 3). The average genetic progress of MEE was approximately 2 L/yr. At the same time, UD showed an annual genetic trend that was constant, negative, and equal to 2.5%. From 1998 to 2003, the average TP value increased by 0.016 linear points, with variations between years. This corresponded to an average annual genetic trend of 0.58% of the genetic SD. The DS did not show any particular trend. Finally, there was a slightly increasing trend in the SU average genetic merit.

These results confirm that the udder morphology of Sardinian sheep can be improved by selection. Particular emphasis should be given to improving TP and UD, as these have the strongest negative relationship with machine milkability. At present, the average TP value is unsuitable for machine milking, whereas UD has a negative genetic trend because of selection based on milk yield. The TP can be directly improved, as it is quite heritable and has a low genetic correlation with milk yield. The UD can only be directly improved with difficulty because of its highly unfavorable genetic correlation with milk yield. However, the genetic improvement of UD can be efficiently achieved by selecting for SU, which had a higher heritability estimate than UD, a highly favorable genetic correlation with UD, and a low and unfavorable genetic correlation with milk yield. Direct selection for SU should also lead to animals with well-suspended udders.

On this basis, a first genetic evaluation was carried out in 2004 for TP and SU on a limited sample of the ewes of the herdbook. Only 30% of 34,694 primiparous ewes and 348 out of 831 flocks recorded for milk yield were also evaluated for their udder traits. However, despite the small size of the sample, most of the AI rams in the herdbook were evaluated for both TP and SU.

## CONCLUSIONS

This study confirms that the machine milkability of Sardinian sheep can be improved by selection for udder morphology. Research carried out since 1998 has enabled the development of an appraisal method for udder morphology that is suitable for a large-scale evaluation of Sardinian ewes. Results from repeatability estimates showed that a genetic evaluation based on a single score in the productive life of a ewe was sufficiently reliable. Estimated heritabilities and genetic correlations between udder traits and milk yields showed that a selection based on TP and SU should produce an improvement of the overall udder morphology without negatively affecting milk production. In the near future, udder scoring will be extended to the entire registered population to conduct a more accurate and efficient genetic evaluation.

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