ESTIMATION OF THE GENETIC PARAMETERS OF UDDER TRAITS IN SARDA DAIRY SHEEP USING A SIRE MODEL WITH RANDOM CONTEMPORARY GROUPS

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INTRODUCTION

Since recently, the attention of breeders in selection schemes for dairy sheep has focused on traits which could reduce the production costs. Machine milking aptitude has been one of the most important among those, given its relationship with hardness and labour time. Selection on udder morphology is being studied for many sheep breeds, since it has been shown that udder conformation greatly affects the number of manual interventions needed to extract the milk retained in the udder (Marie-Etancelin *et al.*, 2001). In Italy, the selection scheme of the Sarda breed achieves an annual genetic gain on milk yield around 3 litres, by combining artificial insemination and controlled natural mating (Sanna *et al*., 2002). In this context the introduction of new breeding objectives in the breeding program is conceivable. The National Association of Sheep Breeders (ASSONAPA) promoted the establishment of an appraisal method for udder morphology which would be feasible on a large scale. Previous studies had identified basic traits which were able to characterize udder conformation and had proposed a nine point linear scale to score them (Casu Sara *et al*., 2000). Similar appraisal methods have been used in Spain (Fernandez *et al.,* 1997 ; Serrano *et al*., 2001 ; Ugarte *et al.*, 2001) and France (Marie-Etancelin *et al*., 2001). Since 1999 the proposed appraisal method has been applied in the nucleus flocks of the Sarda sheep breed. For technical and economic reasons, farms can only be visited once a year by a single classifier and only primiparous ewes can be scored. All ewes scored in a flock by one classifier in a given year identify a contemporary group, whose components are affected by the management of the flock itself. Schaeffer *et al.* (2001) stated that differences in management should have little effect on conformational traits. This is even more likely when animals are scored only once and early in their productive life. Given this, comparing an animal's score on an overall mean rather than to the mean of the contemporary group, seems more correct and can be achieved by fitting this effect as random. The objective of this work was to assess the impact of this strategy on the estimation of genetic parameters and on the ranking of evaluated animals for udder traits.

MATERIAL AND METHODS

42 245 Sarda primiparous ewes were scored for udder morphology by rear observation of the udders. In 1999, the ewes were scored for two udder traits : the teat placement with respect to the lowest point of the udder (Tp), and the udder depth (Ud). Since 2000, two additional traits have been considered : the udder attachment (Ua), i.e. the ratio between the depth and the width of the udder, and the degree of separation between the two halves (Ds), which indicate the strength of the mammary median ligament. In table 1 the range of variation of the applied

linear scales is summarised. Ewes were scored before the morning or afternoon milking by 28 previously trained classifiers. Milk yield, expressed, as Mature Ewe Equivalent (Mee), and pedigree records were available for all scored ewes. Given that in natural mating rams often serve one or only a few flocks, only ewes from connected flocks (with at least one male having daughters in at least two flocks) were retained for genetic analysis. This gave a 25 973 record dataset. Male relationships were taken into account through the sire-of-sire and the maternal grand sire-of-sire. The final pedigree file included 1 895 males, 1 332 of which were sires of the scored ewes. Heritabilities and genetic correlations between udder traits and with Mee were estimated using a REML algorithm applied to a multi-trait sire model. A sire model was used since udder appraisal has been used for only 3 years and no contribution to additive variance estimates is expected from daughter-dam pairs. The model of analysis for Mee included the fixed effects flock-year (Fy, 775 levels) and year-lambing month (Ym, 15 levels) interaction. For the udder traits two different models were compared : M1, including the fixed effects of lactation stage (16 levels of 10 d) and flock year within classifier (Fyc ; 782 levels) ; M2, including, beside the fixed effects of lactation stage and year-classifier (Yc, 62 levels for Tp and Ud and 44 levels for Ua and Ds) the random effect of flock within year-classifier (Fyc, 782 levels). Covariances between traits for contemporary group effect were neglected. YC takes into account differences among classifiers and slight changes in the scoring scale, which can occur from one year to another, especially in the early period of the appraisal application. Because Fyc were assumed to be random, ewe's scores deviated from the Yc's averages rather than from those of contemporary group's (Schaeffer *et al.*, 2001).

Table 1. Description of the linear scales applied to the udder traits

Trait / score	1	9
Tp	Teats implanted vertically at the lowest point of the udder [B]	Teats implanted horizontally at a very high level [A]
Ud	Udder close to the ground [A]	Udder close to the abdominal wall [B]
Ua	Udder of rectangular form with depth much greater than width [A]	Udder of rectangular form with width greater than depth[B]
Ds	Separation between halves not marked [A]	Separation between halves very marked[B]

(A) worst score ; (B) best score

RESULTS AND DISCUSSION

As shown in table 2, estimates of genetic correlations were not affected by the model. On the whole, they were quite high and favorable, i.e. selection for an udder trait implies a positive evolution of the global udder morphology. Genetic correlations between Mee and udder traits were quite low, except for the negative correlation with Ud. These results agree with those previously obtained by Carta *et al*. (2001) on a reduced dataset. Whatever the model used, udder traits heritabilities, calculated as the ratio between 4*V(s) and [V(s) + V(e)], were of the same magnitude of those reported for the Laxta breed by Ugarte *et al*. (2001) but higher than those found by Fernandez *et al*. (1997) for similar traits in the Churra breed. Heritability of Tp and Ua estimated with M2 were higher than those obtained with M1, due to an increase in

estimated sire variance (table 3). The estimates of residual variances were very similar in the two models for all traits. Fyc variances ranged from 8 (Ua) to 16 % (Ud) of the total variance. Their values may reflect differences between flocks in management, environment and, in this specific case, in the average dam genetic merit, which is not taken into account by a sire model.

Table 2. h^2(diag), M1 (below diag.) and M2 (above diag.) genetic correlations

Traits	Tp	Ud	Ua	Ds	Mee
Tp	0.32 / 0.35	-0.58	-0.7	-0.17	0.18
Ud	-0.53	0.24 / 0.25	0.82	0.11	-0.53
Ua	-0.65	0.78	0.25 / 0.29	0.1	-0.2
Ds	-0.19	0.11	0.13	0.19 / 0.19	-0.02
Mee	0.16	-0.52	-0.16	0.09	0.40

Table 3. Estimates of sire, residual and Fyc variances for M1 and M2

Traits	M1		M2		
	V(s)	V(e)	V(s)	V(FYC)	V(e)
Tp	0.080	0.923	0.088	0.155	0.924
Ud	0.037	0.592	0.040	0.119	0.593
Ua	0.093	1.386	0.109	0.130	1.388
Ds	0.045	0.902	0.045	0.174	0.902

Table 4 Spearman correlations between M1 and M2 EBV and Pearson correlations of average score of daughters with BV estimated with the 2 models (r1, r2)

Traits	N	EBV corr.	r1	r2
Tp	826	0.92	0.45	0.58
Ud	826	0.91	0.39	0.56
Ua	607	0.88	0.29	0.44
Ds	607	0.95	0.43	0.54

Table 4 shows Spearman correlations between sire breeding values estimated with M1 and M2 and their correlations with the average scores of daughters, calculated on a subset of sires with at least 10 daughters. Important re-ranking of evaluated animals occurred between the two models and correlations with average score of daughters were significantly higher for BV estimated with M2. The inclusion of contemporary groups as a random effect has a greater impact than that found for similar traits in dairy cattle (Moll and Casanova, 1999).

CONCLUSION

Using contemporary group as a random effect seems to have a positive impact on the genetic evaluation for udder traits in Sarda breed. Not only did this strategy produce a significant increase in heritability for at least two of the scored traits, but it also determined a stronger

correspondence between estimated breeding values of sires and average scores of their daughters. This agrees with breeder's expectations, particularly with regard to sires of natural mating, whose daughters are grouped either in a single, or in a small number, of flocks. This study confirms that the proposed appraisal method of udder morphology can be applied on a large scale by well-trained classifiers. Heritability estimates and genetic correlations with milk yield support the hypothesis that a global udder index should be used in the selection program of the Sarda breed. This global index should be mainly based on teat placement and udder attachment, which show quite high heritabilities and low unfavourable genetic correlations with milk yield.

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