ANALYSIS OF UDDER HEALTH IN DAIRY EWES

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SUMMARY

Somatic cell scores were recorded in a population of 160 dairy ewes during consecutive lactations. Udder scores and udder health traits including mastitis, blood in milk and udder problems were also available from some of these animals as well as milking behaviour. The Wood model was previously used to model lactation curves and to estimate cumulative milk and somatic cell yields and lactation persistency. The effects of udder score, blood in milk and mastitis were tested. Udder scores showed a moderate positive correlation with milk yield, but not somatic cell score. Animals were also genotyped using 189 microsatellites for genome-wide linkage analysis. We identified 3 different linkage regions for udder scores which lined up with QTL for other milk production traits.

INTRODUCTION

It has been shown that selection for milk yield improves milk ejection traits even though the relationships between individual milk flow traits and udder type traits are very weak (Bruckmaier *et al.* 1997). Selection for milk yield would have a deleterious effect on udder depth and teat placement, which could have an economic impact on milking ability (Legarra and Ugarte 2005). Problems in milking, for example due to udder confirmation, may lead to milk contamination and mastitis (Marie-Etancelin *et al.* 2001). Breeders are increasingly interested in improving the machine milkability of Sardinian dairy sheep by selection for udder morphology, and as a trait with a high repeatability, animal's udders can be scored by a single, early lifetime score (Casu *et al*. 2006). Udder type traits show genetic variation and moderate heritability estimates suggest that improvement by selection is feasible but estimates of genetic correlations of udder type traits with milk yield varied among breeds. An introduction of udder traits in the breeding program should also consider the relationships shown with somatic cell score (SCS), perhaps forming a selection index for SCS based on udder traits. In this study we report on QTL for udder health traits and their relationship with milk production traits.

MATERIALS AND METHODS

Lactation data from 160 Awassi-Merino ewes were used in this study. Animals were part of a QTL mapping population based on a cross between Awassi rams and Australian Merino ewes (Raadsma *et al.* 2009a). All animals were kept in feed lot conditions at the University of Sydney research farm 'Mayfarm' at Camden, New South Wales, Australia. Ewes were milked once or twice daily, milk yield and milk composition were regularly recorded as described previously (Raadsma *et al.* 2009b). Additional udder health traits including blood in the milk and mastitis (binary) and udder scores (1: smallest to 5: largest) were evaluated. The Wood model (Wood 1968) was used to model lactation curves and to estimate milk and somatic cell yields and lactation persistency, the description of the fitting of this model to the data is described previously (Raadsma *et al*. 2009b). Persistency of milk and somatic cell yields were derived from the Wood model parameters as the yield at day 100 relative to the yield at the peak. Analyses were performed using the R (version 2.12.0) and the GenStat (13th edition) packages (R Development Core Team team, VSN international). Animals were genotyped using 189 microsatellites covering all autosomes. A detailed description of the genotyping procedure and marker positions is given in

Raadsma *et al*. (2009a). A linkage analysis was performed using QTL Express (Seaton *et al.* 2002) and QTL MLE (Raadsma *et al.* 2009a).

RESULTS AND DISCUSSION

The summary statistics for the lactation performance data are shown in Table 1. Modelling using the Wood models showed that the persistency of the somatic cell yield (a measure from zero to one reflecting increasing persistency) was higher (0.48) compared to persistency of milk yield (0.29).

Table 1. Summary of lactation performance, shown are average (mean), standard deviation (SD), minimum (min) and maximum (max) values

Trait	N	mean	SD	min	max
Milk yield [ml] (MY)	160	702	322	32	1514
Protein percent [%] (PP)	147	5.30	0.54	4.36	8.68
Fat percent [%] (FP)	147	5.15	1.18	2.77	9.20
Lactose percent [%] (LP)	147	5.49	0.29	3.94	5.92
Somatic cell score (SCS)	147	2.01	0.41	1.29	3.37
Somatic cell persistency (SCPersit)	159	0.47	0.07	0.23	0.63
Milk persistency (MYPersist)	149	0.28	0.15	0.05	0.77
Udder score	156	2.44	0.65	1.00	5.00

Udder scores were available from a total of 156 animals, eight animals had small udders (score = 1), and only nine animals had large udders (score = 4 and 5), while most animals had udder scores of 2 (N = 76) and 3 (N = 63). Among the 156 ewes, only four were diagnosed with clinical mastitis and 11 animals showed an occurrence of blood in the milk for at least one milking.

The udder score showed significant correlations with milk yield and protein percent, whereas somatic cell score was negatively correlated with milk yield and lactose percent (Table 2).

Table 2. Phenotypic correlations between milk yield, milk composition and udder score

Trait	MY	PP	FP	LP	SCS	SCPersist	MYPersist	Udder	Blood
Protein percent	0.08								
Fat percent	-0.31	0.24							
Lactose percent	0.45	-0.43	-0.21						
SCS	-0.30	0.30	0.18	-0.60					
SCPersist	-0.02	-0.08	-0.18	0.03	-0.09				
MYPersist	0.33	-0.02	-0.02	0.33	-0.19	0.18			
Udder	0.47	0.47	0.08	-0.11	0.13	-0.20	0.13		
Blood	-0.11	0.01	0.06	0.02	0.13	-0.10	-0.10	-0.03	
Mastitis	0.00	0.08	0.06	-0.09	0.03	-0.04	0.04	0.05	-0.04

Phenotypic correlation between traits, MY= milk yield, PP = protein percent, FP = fat percent, LP = lactose percent, SCS = somatic cell score, SCPersist = somatic cell yield persistency, MYPersist = persistency milk yield; all correlations > 0.13 are significant $P < 0.05$

Genetic correlations among milk yield and different udder confirmation traits have varied among studies, but some studies revealed that selection based on teat placement and degree of suspension of the udder should produce an improvement of the overall udder morphology without negatively affecting milk production (Casu *et al.* 2006). Low phenotypic correlations were

reported between milk production and udder score in cattle, which differed from our finding (MacNeil and Mott 2006).

No significant association between udder health (blood, mastitis) and lactation performance was observed, whilst the udder scores (udder scores 1 and 2 versus 3 to 5) had a significant effect on milk yield and protein percent (Table 3).

Table 3. Results of the *t*-test between binary traits and lactation parameters; shown are *P*-values

Trait	Milk yield	Protein percent	Fat percent	Lactose percent	Somatic cell score	SCPersist	MYPersist
Udder score	0.00	0.01	0.29	0.26	0.37	0.10	0.10
Mastitis	0.50	0.34	0.31	0.21	0.39	0.24	0.19
Blood in milk	0.08	0.40	0.22	0.47	0.15	0.25	0.06

Analysis of variance (one way) showed that the udder score (scores 1 to 5) had an effect on milk yield, protein, fat and lactose percent ($P \leq 0.01$) and somatic cell score ($P \leq 0.05$). Animals with a larger udder (score > 3) had the higher protein and fat percent and somatic cell score compared to animals with small udders (score = 1), while animals with an average sized udder (score = 3) had the highest milk yield and lactose percent.

The QTL analysis using QTL Express showed suggestive QTL for blood in the milk on chromosome 6 and 24, for mastitis on chromosome 8 and for udder score on chromosomes 11, 23 and 26 (Figure 1).

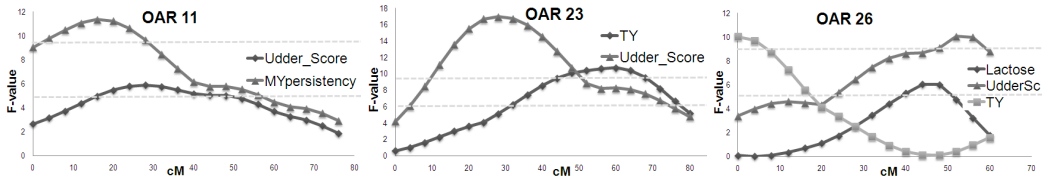

Figure 1. QTL mapping results of the linkage analysis for udder score and milk persistency on chromosome 11, udder score and milk yield on chromosome 23 and for udder score milk yield and lactose percent on chromosome 26; dashed grey lines indicate 5% suggestive and 1% significance threshold.

QTL were previously identified on chromosomes 7, 14, 15, 20 and 26 for five linear udder traits including udder depth, udder attachment, teat placement, teat size, and udder shape (Gutiérrez-Gil *et al.* 2008). Some of these QTL could be verified by bovine studies (Schrooten *et al.* 2000, Hiendleder *et al*. 2003, Ashwell *et al.* 2005). Other QTL for udder shape and quality were identified on all bovine chromosomes except chromosomes 3, 8 and X (Hu *et al*. 2010). The QTL for udder scores on OAR 11 was not located within the comparative region of the bovine QTL for udder depth, udder attachment or udder height, while most of the QTL for udder characteristics summarized in the QTLdb (http://www.animalgenome.org/cgi-bin/QTLdb/index) on BTA 24 were located in the comparative region to the identified locus on OAR 23 (Hu *et al*. 2010). One QTL for udder depth on BTA 27 is also located within the comparative region to the QTL identified on OAR 26.

Gutiérrez-Gil *et al.* (2008) pointed out the importance of further characterization of genetic variability involved in udder traits. Most markers linked or associated with mammary gland and lactation related traits as reviewed in a database for cattle candidate genes and genetic markers for milk production and mastitis were found on bovine chromosomes 6, 14 and 19 (Ogorevc *et al*. 2009). QTL for clinical mastitis were summarized on bovine chromosomes 3 to 6, 8 to 11, 14, 15, 18, 21, and 25 to 27 in the animal QTLdb (Hu *et al*. 2010). The low incidence of clinical mastitis in our study makes it difficult to identify QTL therefore more animals are needed to validate the results before comparing it to other studies.

CONCLUSIONS

A moderate positive phenotypic correlation between udder scores and milk yield and protein percent was found, while the association with other traits was low. We could identify a number of QTL for udder scores in an sheep population, but such findings need to be confirmed given the relatively low power of the study. Future studies will further investigate some of the traits using SNP information for a better genome coverage and fine-mapping of the regions.

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