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Published in:
Journal of Dairy Science

DOI:
10.3168/jds.2015-10269

First published: 01/01/2016

Document Version
Peer reviewed version

Link to publication

Citation for pulished version (APA):
McLaren, A., Mucha, S., Mrode, R., Coffey, MP., & Conington, JE. (2016). Genetic parameters of linear conformation type traits and their relationship with milk yield throughout lactation in mixed-breed dairy goats. *Journal of Dairy Science*, *99*(7), 5516 - 5525. https://doi.org/10.3168/jds.2015-10269

Interpretive summary: Genetic parameters of linear conformation type traits and their relationship with milk yield throughout lactation in mixed-breed dairy goats. By *McLaren et al.* Whilst striving to improve profitability, dairy goat breeders should also consider traits relating to body conformation. In this study, the majority of genetic correlations estimated between milk yield and both udder and teat traits were negative. Farmers should therefore consider these traits when making animal selection decisions to ensure that selection for increased productivity is not accompanied by any potential unwanted deterioration of fitness.

Genetic parameters of linear conformation type traits and their relationship with milk yield throughout lactation in mixed-breed dairy goats.

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Abstract

Conformation traits are of interest to many dairy goat breeders not only as descriptive traits in their own right, but also because of their influence on production, longevity and profitability. If these traits are to be considered for inclusion in future dairy goat breeding programmes, relationships between them and production traits such as milk yield, must be considered. With the increased use of regression models to estimate genetic parameters, there is now an opportunity to investigate correlations between conformation traits and milk yield throughout lactation in more detail. The aims of this study were therefore to a) estimate genetic parameters for conformation traits in a population of crossbred dairy goats, b) estimate correlations between all conformation traits and c) assess the relationship between conformation traits and milk yield throughout lactation. No milk composition information was available. Data were collected from goats based on 2 commercial goat farms, during August and September in 2013 and 2014. Ten conformation traits, relating to udder, teat, leg and feet characteristics, were scored on a linear scale (1-9). The overall dataset comprised of data available for 4,229 goats, all in their first lactation. The population of goats used in the study was created using random crossings between 3 breeds: British Alpine, Saanen and Toggenburg. In each generation, the best performing animals were selected for breeding therefore leading to the formation of a synthetic breed. The pedigree file used in the analyses contained sire and dam information for a total of 30,139 individuals. The models used fitted relevant fixed and random effects. Heritability estimates for the conformation traits were low to moderate, ranging from 0.02 to 0.38. A range of positive and negative phenotypic and genetic correlations between the traits were observed, with the highest correlations found between udder depth and udder attachment (0.78), teat angle and teat placement (0.70), and back legs and back feet (0.64). The genetic correlations estimated between the conformation traits and milk yield, across the first lactation, demonstrated changes during this time period. The majority of correlations estimated between milk yield and both the udder and teat traits were negative. Therefore, future breeding programmes would benefit from including these traits in order to ensure that selection for increased productivity is not accompanied by any unwanted change in functional fitness.

Key Words: dairy goat, conformation, milk yield, random regression

INTRODUCTION

Conformation traits are of interest to many animal breeders not only as descriptive traits in their own right, but also because of their influence on production, longevity and profitability (Brotherstone 1994). In dairy cattle, linear type traits were first recorded in the early 1980's (Meyer et al., 1987; Short and Lawlor, 1992; Brotherstone, 1994). In terms of small ruminants, one of the earliest scales developed was by the American Dairy Goat Association (ADGA), which has been used to score goats across a range of different breeds since 1988 (Luo et al., 1997). The linear traits included in this scale are scored from 1 to 50, with an additional score, based on overall appearance according to a number of weighted criteria, scored between 50 and 99. However, several other scales, which have also been used to assess conformation traits, have been developed based on 9-point linear type scoring systems.

One of the earliest proposed for dairy sheep was by de la Fuente et al. (1996) during the evaluation of Churra ewes, from which a number of other scales, adapted for different breeds, have emerged (Carta et al., 2009). In terms of dairy goats, a 9-point scale has also been developed and is currently used by French dairy goat breeders, as described by Manfredi et al. (2001).

Initially, the most commonly recorded traits were udder and teat type traits, mainly due to their influence on the milking ability, udder health and longevity of animals. More recently a number of studies have also considered additional traits, such as those relating to the legs and feet of the animals (Manfredi et al., 2001; de la Fuente et al., 2011). By improving aspects such as animal mobility and structural correctness, there is the prospect that the productivity and profitability of dairy goat herds could further improve particularly when coincidentally exposed to intense selection pressure for yield traits.

If conformation traits were to be considered for inclusion in future dairy goat breeding programmes, relationships between the conformation traits themselves, as well as with production traits such as milk yield, must be considered. Fernandez et al. (1997) as well as Legarra and Ugarte (2005), while estimating genetic correlations between conformation traits and milk yield in Churra and Laxta sheep respectively, calculated correlations that indicated that selection for improved milk yield could have implications on udder morphology. The depth of the udder and the placement of the teats were particularly affected, leading to a possible decline in the milking ability of animals in machine milking environments. Similar findings were also observed by Manfredi et al. (2001), indicating that to reduce the decline of milking ability, whilst attempting to improve milk yield, the inclusion of conformation traits in breeding programmes would be valuable.

However, while examining the links between conformation traits and milk yield, many of these studies have used cumulated milk yields, produced during lactations of different length, for example 120-day milk yield in sheep (Fernandez et al., 1997; Legarra and Ugarte, 2005) or 250-day milk yield in goats (Manfredi et al., 2001; Rupp et al., 2011). With the increased use of random regression models to estimate genetic parameters in goats (Menendez-Buxadera et al., 2010; Mucha et al., 2014), there is now the opportunity to investigate correlations between conformation traits and milk yield throughout lactation in more detail.

The aims of this study were therefore to a) estimate genetic parameters for conformation traits in a population of crossbred dairy goats, b) estimate correlations between all conformation traits and c) assess the relationship between conformation traits and milk yield throughout lactation.

MATERIALS AND METHODS

Conformation Traits

Conformation trait data were collected from goats based on 2 farms, owned by the same farming business and consisting of related animals, during August and September in 2013 and 2014. The dataset comprised of data available for 4,220 goats all in their first lactation. The traits recorded for each animal, scored by the same recorder, were linear in form and scored using a 9-point scale which had many similarities to that developed by the French dairy goat breeders' association CAPGENES and used by Manfredi et al. (2001) and Rupp et al. (2011). The data contained information for three udder traits, three teat traits and four traits relating to legs and feet.

The udder traits, as shown in Figure 1 were: Udder furrow (UF), viewed from the rear view of the udder, indicating the prominence of the medial suspensory ligament. A score of 1 indicates that the ligament is highly prominent, with an extreme cleft in the base of the udder, whereas a score of 9 indicates the ligament is not prominent and there is little/no cleft visible. Udder depth (UD) is the depth of the udder is measured in comparison to the hocks of the animal. Udders scored 1 are close to the ground whereas those scored 9 are well above the hocks. A score of 5 indicates that the cleft of the udder is at the hocks level; Udder attachment (UA) represents the strength of attachment, based on the perimeter of the insertion to the abdominal wall. A score of 1 represents udders with a weak and narrow level of attachment whereas those scored 9 are udders with a large and strong perimeter of attachment.

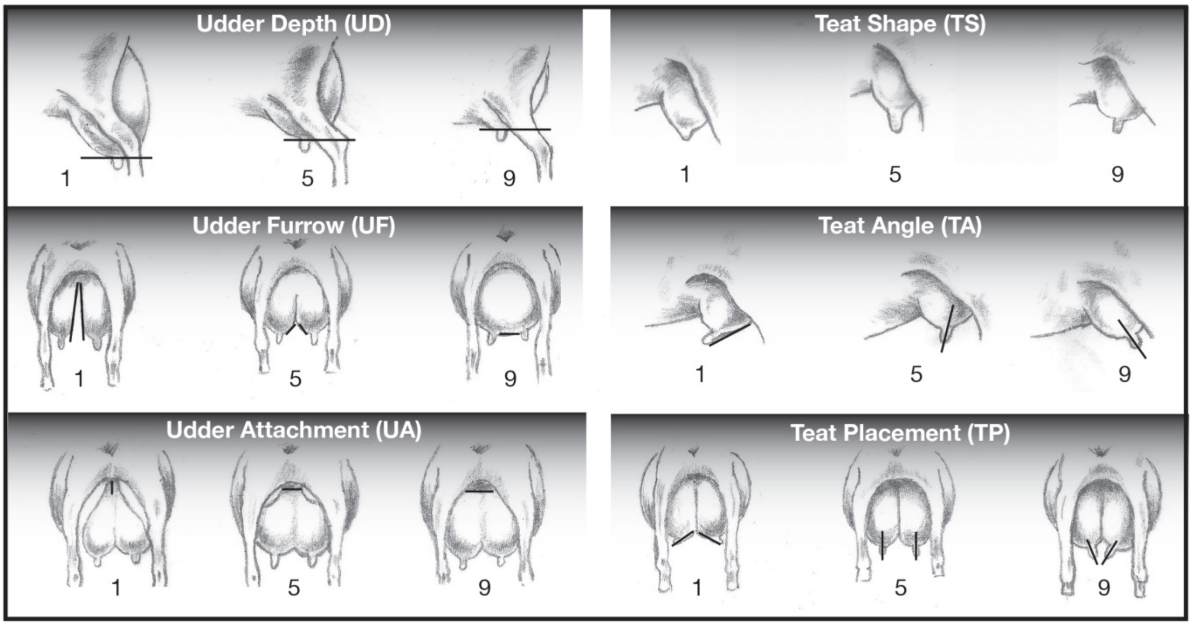

Figure 1. Scoring criteria used for the udder and teat traits.

The teat traits, also shown in Figure 1 were: Teat shape (TS) indicating the diameter and shape of the teat ranging from wide and conical for score 1 to small and cylindrical for score 9; Teat angle (TA) describes whether the teat, when looking from the side of the animal, is pointing forwards (score 1) or towards the rear (score 9). The score of 5 represents teats pointing straight downwards. Teat placement (TP) is scored using a rear view of the udder and gives an indication as to placement of the teats in relation to the medial ligament. Teats pointing outwards, away from each other, would be scored as 1, whereas those pointing inwards, towards each other, would be scored 9. A score of 5 would be given for teats pointing straight down.

The leg and feet traits are shown in Figure 2. The scoring for the front legs was similar to that shown for the back legs. A score for both the Front legs (FL) and Back legs (BL) of 5 represented legs that were completely straight. Animals with legs that pointed inwards at a severe angle, resulting in the hocks (BL) or knees (FL) nearly touching, would be given a score of 1 where as those completely the opposite, with the hocks/knees a large distance apart and forming bowed legs, would be scored as a 9. The Front feet (FF) and Back feet (BF) scores describe the direction that the hooves were facing when the animal was standing (Figure 2). A score of 1, considered to be the worst score for both FF and BF, represented hooves that were facing away from each other. A score of 5 represented hooves pointing outwards, but at a less severe angle. The best score for both FF and BF was 9 and was given to animals with both hooves pointing straight forward. In addition to the conformation traits, test day milk yield and cumulative milk yield data, up to day 305, were also available.

Figure 2. Scoring criteria used for the leg and feet traits.

Genetic analysis

The population of goats used in the study, as described by Mucha et al. (2014), was created using random crossings between 3 breeds: British Alpine, Saanen and Toggenburg. In each generation, the best performing animals were selected for breeding therefore leading to the formation of a synthetic breed. No information was available in terms of the breed composition of the animals in the population therefore this could not be included in the analyses. The pedigree file used in the analyses contained sire and dam information for a total of 30,139 individuals. Estimates of (co)variance components were obtained by the average information-REML algorithm in the DMU package (Madsen and Jensen, 2008). The model fitted for the conformation traits was:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}, \qquad [1]$$

where **y** is a vector of observations for the analysed conformation score; **b** is a vector of fixed effects: farm, lactation stage, year of scoring and birth year; **a** is the vector of random additive animal effects; **e** is the vector of random residual effects, and **X** and **Z** are incidence matrices relating records to their respective effects. Lactation stage, defined as the number of days between kidding date and scoring date, was grouped into 7 different levels in order to achieve an appropriate distribution; i) 100 days or less (939 records), ii) between 101-200 days (2123 records), iii) 201-300 days (536 records), iv) 301-400 days (276 records), v) 401-500 days (129 records), vi) 501-600 days (114 records) and vii) 601 days and above (103 records). Year of scoring had 2 levels; 2013 (1662 records) and 2014 (2558 records) and birth year had 5 levels; 2009 (49 records), 2010 (162 records), 2011 (661 records), 2012 (1810 records) and 2013 (1538 records). Only the direct genetic effect (animal) was fitted in each model due to the fact that the conformation scores were recorded only once on each individual animal.

Genetic and phenotypic correlations between each individual conformation trait were estimated using a multivariate analysis including all traits. The covariance structure for the multivariate analyses was:

$$\mathrm{Var}\begin{bmatrix} a_1 \\ a_2 \\ \vdots \\ a_{10} \\ e_1 \\ e_2 \\ \vdots \\ e_{10} \end{bmatrix} = \begin{bmatrix} \mathrm{A}\sigma^2_{g1} & \mathrm{A}\sigma_{g1,2} & \cdots & \mathrm{A}\sigma_{g1,10} & 0 & 0 & 0 & 0 \\ & \mathrm{A}\sigma^2_{g2} & \cdots & \mathrm{A}\sigma_{g2,10} & 0 & 0 & 0 & 0 \\ & & \cdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ & & & \mathrm{A}\sigma^2_{g10} & 0 & 0 & 0 & 0 \\ & & & & \mathrm{I}\sigma^2_{e1} & \mathrm{I}\sigma_{e1,2} & \cdots & \mathrm{I}\sigma_{e1,10} \\ & & & & & \mathrm{I}\sigma^2_{e2} & \cdots & \mathrm{I}\sigma_{e2,10} \\ & & & & & & \cdots & \vdots \\ symm & & & & & & & \mathrm{I}\sigma^2_{e10} \end{bmatrix}$$

Where indices 1 and 2 (and so on) indicate the two conformation traits, **A** is the additive genetic relationship matrix **I** are identity matrices, σ_g^2 and σ_e^2 are the genetic and residual variances, respectively.

Milk yield was modelled with a random regression animal model developed in a previous study (Mucha et al., 2014):

y = Xb + Za + Wp + e, [2]

where **y** is the vector of test-day observations; **b** the vector of fixed effects, consisting of age at kidding, herd test day, year-season, and fixed lactation curves modeled by fitting Legendre polynomials (Kirkpatrick et al., 1990) of fourth order; **a** is a 1 × 3 vector of random regression coefficients (Legendre polynomials of second order) for the animal effect; **p** is the 1 × 3 vector of random regression coefficients (Legendre polynomials of second order) for the permanent environment effect; and **e** is the vector of random residual effect. The matrix **X** is the incidence matrix for fixed effects; **Z** and **W** are matrices of Legendre polynomials of DIM of second order for random animal and permanent environment effect, respectively.

Random effects were assumed to be normally distributed with zero means and the following covariance structure:

$$\mathrm{Var}\begin{bmatrix}\mathbf{a}\\ \mathbf{p}\\ \mathbf{e}\end{bmatrix}=\begin{bmatrix}\mathbf{A}\otimes\mathbf{G} & 0 & 0\\ & \mathbf{I}\otimes\mathbf{P} & 0\\ symm & & \mathbf{I}\sigma_e^2\end{bmatrix}$$

where **G** and **P** are 3 × 3 (co)variance matrices of the random regression coefficients for the animal and permanent environment effects, respectively.

The variance-covariance structures for the bivariate analyses of milk yield and conformation traits were as follows:

$$\mathrm{Var}\begin{bmatrix}\mathbf{a}_1\\ \mathbf{a}_2\\ \mathbf{p}_2\\ \mathbf{e}_1\\ \mathbf{e}_2\end{bmatrix}=\begin{bmatrix}\mathbf{AG}_1 & \mathbf{AG}_{12} & 0 & 0 & 0\\ & \mathbf{AG}_2 & 0 & 0 & 0\\ & & \mathbf{IP}_2 & 0 & 0\\ & & & \mathbf{I}\sigma_{e1}^2 & \mathbf{I}\sigma_{e12}^2\\ symm & & & & \mathbf{I}\sigma_{e2}^2\end{bmatrix}$$

Where indices 1 and 2 indicate the two traits. The first trait was one of the conformation traits (following model 1), and the second trait was milk yield (following model 2). $\mathbf{G}_1$ contained only one value, $\mathbf{G}_{12}$ contained one row (1x3), whereas $\mathbf{G}_2$ and $\mathbf{P}_2$ were 3x3 (co)variance matrices as defined for model 2. Because the first trait was modelled with model 1 it had no permanent environment, thus $\mathbf{P}_1$ and $\mathbf{P}_{12}$ do not exist.

The genetic covariances between milk yield and conformation traits on the *i*th DIM were calculated as $\hat{\sigma}_{gi12}=\mathbf{L}'(\mathrm{DIM}_i)\hat{\mathbf{G}}_{12}$ where $\mathbf{L}(\mathrm{DIM}_i)$ is the row vector of Legendre polynomials for DIM_i (Kirkpatrick et al., 1990), of size 3. The phenotypic covariance was the sum of genetic and residual covariance. An additional analysis with cumulative 305 day milk yield was also performed, using the following model:

$$\mathbf{y} = \mathbf{Xb} + \mathrm{Za} + \mathbf{e},\quad [3]$$

where **y** is a vector of observations for the 305 day milk yield; **b** is a vector of fixed effects: age at kidding, farm, year-season; **a** is the vector of random additive animal effects; **e** is the vector of random residual effects, and **X** and **Z** are incidence matrices relating records to their respective effects. Subsequently bivariate analyses of milk and conformation were performed where conformation traits were modelled using model 1 and 305 day milk yield with model 3. The covariance structure for the bivariate analyses was:

$$\mathrm{Var}\begin{bmatrix}\mathbf{a}_1\\ \mathbf{a}_2\\ \mathbf{e}_1\\ \mathbf{e}_2\end{bmatrix}=\begin{bmatrix}\mathbf{A}\sigma_{g1}^2 & \mathbf{A}\sigma_{g12} & 0 & 0\\ & \mathbf{A}\sigma_{g2}^2 & 0 & 0\\ & & \mathbf{I}\sigma_{e1}^2 & \mathbf{I}\sigma_{e12}\\ \mathit{symm} & & & \mathbf{I}\sigma_{e2}^2\end{bmatrix}$$

Where indices 1 and 2 indicate the two traits. The first trait was one of the conformation traits, and the second trait was 305d milk yield, **A** is the additive genetic relationship matrix, **I** are identity matrices, σ_g^2 and σ_e^2 are the genetic and residual variances, respectively.

The standard errors for heritability and genetic and phenotypic correlations were calculated using the methodology proposed by Fischer et al. (2004), with the interpretation proposed by Frigo et al. (2010). Fat and protein content was not included in the analysis as no data was available from either of the farms contributing data to the study.

RESULTS & DISCUSSION

A summary of traits included in the analyses are shown in Table 1. The average scores recorded on both farms were similar for all traits. The front legs trait had the lowest overall standard deviation (0.37) which was a reflection that 88% of records were a score of 5. The average daily milk yield, during the first lactation, was 3.32 +0.003 kg. The additional summary statistics for this trait are provided by Mucha et al. (2014).

Table 1. Summary of conformation traits included in the analyses.

Trait	Count	Minimum	Maximum	Average	S. Dev.
Udder Furrow (UF)	4153	2	9	6.42	±0.99
Udder Depth (UD)	4220	2	9	5.93	±0.94
Udder Attachment (UA)	4220	3	9	7.69	±0.68
Teat Shape (TS)	4198	1	8	4.17	±1.00
Teat Angle (TA)	4216	1	6	4.24	±0.81
Teat Placement (TP)	4216	1	8	3.37	±0.81
Front Legs (FL)	4216	2	9	4.88	±0.37
Back Legs (BL)	4219	2	9	4.60	±0.62
Front Feet Set (FF)	4213	3	9	8.23	±0.74
Back Feet Set (BF)	4217	4	9	7.78	±0.77
305 day milk yield (kg)	4170	157.05	3002.50	1151.75	±325.88

Genetic Parameters

The univariate heritability estimates for each trait, across both farms, ranged from 0.02 to 0.38 (Table 2). The highest estimates were generally associated with the udder and teat related traits, where as those estimated for the legs and feet were lower. The individual traits with the overall highest and lowest heritability estimates were UD (0.38) and FL (0.02) respectively. Manfredi et al. (2001) also observed generally higher estimates for the udder and teat traits when compared with the legs and feet. However, although a similar scale and scoring system was used, some of the traits considered by Manfredi et al. (2001), differed from those in the present study. The leg and feet traits similar between both studies were those relating to hock distance (similar to BL in the present study) and feet angle, although no indication was given as to whether this was relating to the angle of all feet, or just the front/back ones. Nonetheless, heritability estimates for the hock distance (0.16 and 0.12 for the Alpine and Saanen breeds respectively), were reasonably similar to the present study (0.13). In dairy sheep, de la Fuente et al. (2011) estimated a heritability of 0.18 for rear legs, scored in the same manner but with a slight difference in score definitions. The very low heritability estimate observed for FL is likely due to the lack of variation in the scores given for this trait, perhaps influenced by previous selection criteria on the farms which may have only selected animals with straight front legs to remain in the herd. The heritability of milk yield in this population was 0.56, as estimated by Mucha et al. (2015). The authors suggest that this relatively high estimate could be influenced by the reduction in “noise” due to the automated recording equipment used and the fact that the data originates from just two farms.

Considering the udder and teat traits in more detail, the estimates observed in the present study for UD, UF, TS, were in close agreement to those observed by both Manfredi et al. (2001) and Rupp et al. (2011), despite some differences between the individual breeds. However, estimates observed for UA (0.15) and TP (0.23) were lower than the values estimated by Manfredi et al. (2001) and Rupp et al. (2011), who both referred to these traits as the rear udder and teat placement respectively. The estimates given by these two authors ranged from 0.23-0.29 for UA and 0.25-0.38 for TP. Additionally, the heritability of 0.36 observed for TA was higher than previous estimates, which ranged from 0.15-0.22 (Manfredi et al., 2001; Rupp et al., 2011). When compared to the estimates given by Luo et al. (1997) for TP and UD, all of the estimates observed in the current study were low, although some similarities were seen between the UF and TS estimates (referred to as suspensory ligament and teat diameter respectively).

Many of these differences may be related to the number of data records available (n=4,220) and the breed composition of animals used in this study. The three studies discussed above all had data available from just less than 19,000 up to just over 43,000 animals recorded over a number of different years. It is likely that as more data becomes available future estimates may become more accurate, particularly in terms of the standard errors associated with the estimates observed. The lower estimates observed for the feet and leg traits in general could be influenced by farm selection policies already in place as individuals with undesirable conformation for these traits can become visible from an early age and therefore can be removed before becoming established in the herd. The synthetic nature of the population structure in the current study, based on a history of crossbreeding, also differed from the pure-bred populations previously referred to. This could also influence the heritability values estimated due to the expected increase in the additive genetic variance in mixed populations when compared to pure-bred populations. Luo et al. (1997) mention data available from crossbred goats, which they refer to as ‘experimentals’, but unfortunately data from these animals was not used in their final analyses to keep consistency with additional data they were using in the study.

Relationships between Conformation Traits

The genetic and phenotypic correlations estimated between all of the conformation traits are shown in Table 2. A range of positive and negative genetic correlations were observed, with the highest estimated between UD and UA (0.77) and the lowest between FL and TS and between BF and TP (both -0.01). The standard errors associated with the genetic correlations were relatively high, with the highest generally associated with the leg and feet traits. The phenotypic correlations were low to medium, ranging from 0.003 to 0.38 with standard errors between 0.01 and 0.02.

Among the udder traits, the genetic correlations ranged from 0.12 – 0.77, with the highest observed between UD and UA. The relationships between the teat traits were similar to those observed among the udder traits, ranging from -0.10 – 0.69, with negative values estimated between TS and both TA and TP. The moderately high positive correlation between TA and TP (0.69) indicated that selection for improved teat placement would also result in the improved angle of the teats. The relationships between the udder and teat traits followed a similar pattern to those observed by Manfredi et al. (2001), in both Alpine and Saanen breeds, in terms of direction of the relationships. All were positive, with the exceptions of those observed between UF and both TA and TP, indicating that as the strength of the medial ligament changed, there was a negative knock-on effect on the angle and placement of the teats.

Genetic correlations estimated between the leg and feet traits ranged from 0.05 to 0.64. The highest estimate, estimated between BL and BF (0.64), suggests that improvements made in back leg conformation would also have a positive effect on the conformation of the back feet. In general, relatively high standard errors were also observed between these traits and the other conformation traits which, in part, are most likely influenced by the low heritability estimates associated with these traits, particularly those relating to FL.

Table 2. Univariate heritabilities (on diagonal in bold), genetic (below diagonal) and phenotypic (above diagonal) correlations between conformation traits, during first lactation only. Standard errors in parenthesis.

Trait	UF	UD	UA	TS	TA	TP	FL	BL	FF	BF
Udder Furrow (UF)	**0.28 (0.04)**	0.24 (0.02)	0.09 (0.02)	0.32 (0.02)	-0.13 (0.02)	-0.20 (0.02)	0.02 (0.02)	0.01 (0.02)	-0.03 (0.02)	-0.01 (0.02)
Udder Depth (UD)	0.23 (0.10)	**0.38 (0.05)**	0.38 (0.01)	0.23 (0.02)	0.23 (0.02)	0.17 (0.02)	-0.06 (0.02)	0.05 (0.02)	-0.06 (0.02)	-0.02 (0.02)
Udder Attachment (UA)	0.12 (0.13)	0.77 (0.08)	**0.15 (0.04)**	0.07 (0.02)	0.15 (0.02)	0.19 (0.02)	-0.04 (0.02)	0.03 (0.02)	-0.04 (0.02)	-0.01 (0.02)
Teat Shape (TS)	0.41 (0.10)	0.30 (0.10)	0.25 (0.13)	**0.32 (0.05)**	-0.10 (0.02)	-0.07 (0.02)	-0.01 (0.02)	0.01 (0.02)	-0.02 (0.02)	-0.01 (0.02)
Teat Angle (TA)	-0.25 (0.11)	0.29 (0.10)	0.35 (0.13)	-0.14 (0.11)	**0.36 (0.05)**	0.38 (0.01)	-0.07 (0.02)	0.08 (0.02)	0.04 (0.02)	0.04 (0.02)
Teat Placement (TP)	-0.25 (0.11)	0.25 (0.11)	0.57 (0.11)	-0.10 (0.12)	0.69 (0.08)	**0.23 (0.04)**	-0.05 (0.02)	0.04 (0.02)	0.02 (0.02)	0.003 (0.02)
Front Legs (FL)	0.14 (0.25)	-0.33 (0.24)	-0.30 (0.28)	-0.01 (0.26)	-0.55 (0.24)	-0.26 (0.26)	**0.02 (0.02)**	0.02 (0.02)	0.16 (0.02)	0.01 (0.02)
Back Legs (BL)	-0.10 (0.15)	0.02 (0.14)	0.24 (0.17)	0.12 (0.15)	0.11 (0.15)	0.13 (0.15)	0.19 (0.30)	**0.13 (0.04)**	0.04 (0.02)	0.40 (0.01)
Front Feet Set (FF)	-0.08 (0.15)	-0.07 (0.14)	-0.02 (0.18)	-0.09 (0.15)	0.26 (0.15)	0.02 (0.16)	-0.37 (0.31)	-0.18 (0.19)	**0.13 (0.04)**	0.22 (0.02)
Back Feet Set (BF)	-0.07 (0.12)	-0.16 (0.11)	-0.09 (0.15)	-0.08 (0.12)	0.17 (0.12)	-0.01 (0.13)	0.05 (0.27)	0.64 (0.11)	0.08 (0.16)	**0.25 (0.05)**

Relationships between Conformation Traits and Milk Yield throughout lactation

To our knowledge, this is the first time that correlations between conformation traits and milk yield have been estimated throughout lactation in this manner. As many dairy goats herds strive to make improvements in milk yields, it is important to consider the relationship and effects that this may have on other traits such as those associated with conformation. The genetic correlations observed between each conformation trait and milk yield during the first lactation are shown in Figure 3. Phenotypic correlations estimated were all close to zero, with the exception of UD, which ranged from -0.35 to -0.07.

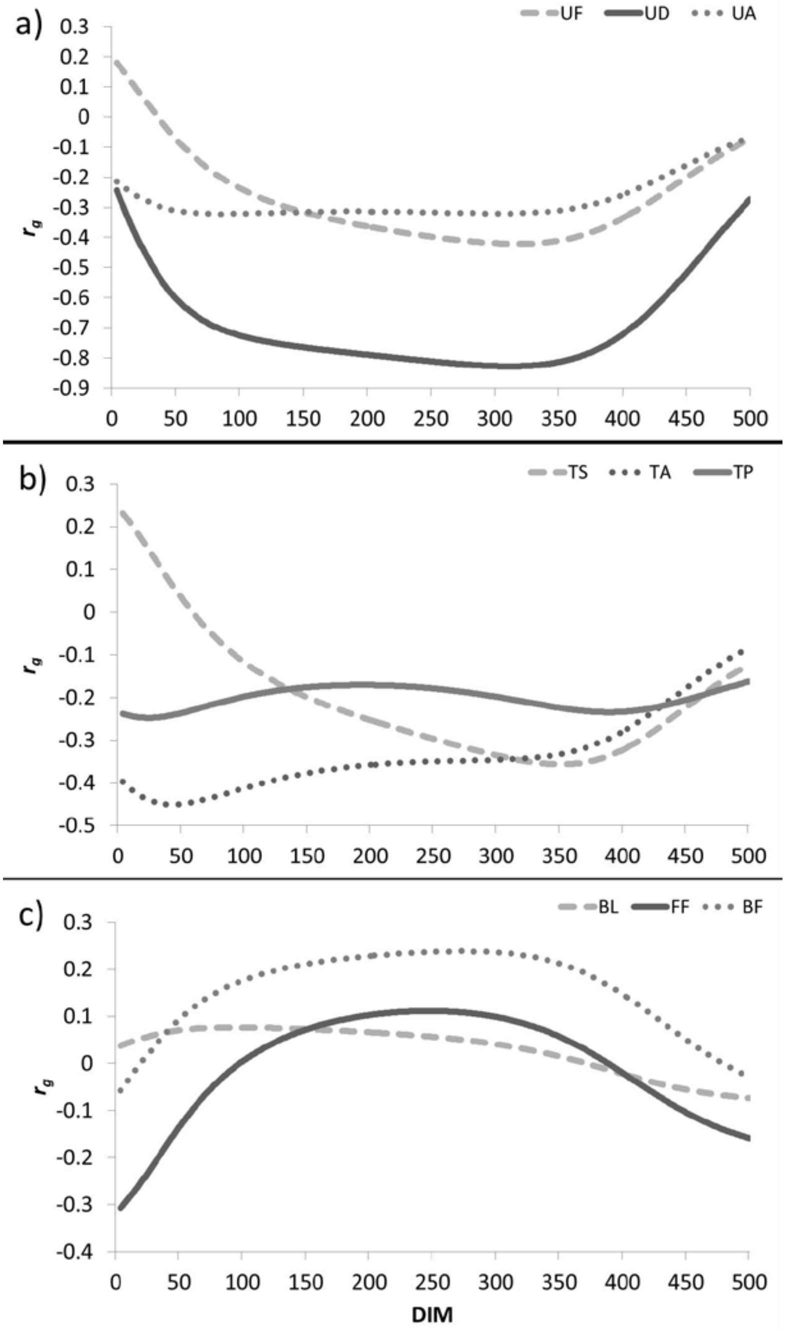

Figure 3. Genetic correlations (r_g) between milk yield and conformation traits; Udder traits (3a) of Udder Furrow (UF), Udder Depth (UD), Udder Attachment (US); Teat traits (3b) of Teat Shape (TS), Teat Angle (TA), Teat Placement (TP); Feet and leg traits (3c) of Back Legs (BL), Front Feet (FF) and Back Feet (BF); during 500 days of lactation, based on a random regression model.

Genetic correlations associated with the udder traits (UF, UD and UA) are shown in Figure 3a. The correlations estimated between milk yield and UF ranged from -0.42 and 0.18.

Positive values were found up to approximately 50 DIM after which the values became negative and remained negative throughout the remainder of the lactation. The size of the correlations increased up to around 300 DIM (-0.42) after which they began to steadily fall back towards zero. Standard errors ranged from 0.05 to 0.07. The correlations observed between milk yield and UD followed a similar pattern, however unlike UF, all values were negative ranging from -0.24 and -0.83. The absolute correlation values increased sharply during the first 100 DIM before continuing to increase, at a slower rate, between 100 DIM and 350 DIM. From 350 DIM onwards the correlations fell back to around -0.27 at 500 DIM. Standard errors were between 0.03 and 0.06 with the lowest occurring mid-lactation between approximately 200 and 300 DIM. Correlation values observed for UA were also all negative ranging from -0.07 to -0.32. There was a gradual increase in the strength of the correlation during the first 70 DIM from a value of -0.21 to -0.32, after which values remained approximately -0.32 until 350 DIM. Standard errors were between 0.06 and 0.09 with the lowest found during mid-lactation. When compared with the genetic correlations estimated with the cumulative milk yield at 305 days, the udder traits all behaved consistently in the fact that all correlations observed were negative (-0.25 ±0.13, -0.71 ±0.08 and -0.28 ±0.17) for UF, UD and UA respectively). Manfredi et al. (2001), when estimating correlations between udder traits and milk yield at 250-days also observed negative correlations ranging from -0.51 to -0.19 whereas Barillet (2000) comments that, across a number of different studies in both dairy goats and sheep, correlations between milk yield and UD, although to varying degrees, were always antagonistic. Similar relationships between UD and milk yield have also been observed in dairy cattle (Brotherstone, 1994). The correlations that we have observed in the current study therefore seem to be in agreement with those estimated previously. Another method of udder scoring, relating to UD, was investigated by Casu et al. (2006) using the degree of suspension of the udder, calculated using the ratio between the udder attachment width and udder height. They suggested this trait as a possible alternative due to the fact that in their study it had a similar heritability as UD, it was highly correlated with UD (0.82) and it had a low and unfavourable genetic correlation with milk yield. In addition, although not investigated in the present study, results reported by Marie-Entacelin et al. (2005) and Rupp et al. (2011) suggest the possibility that selection for improved udder conformation can reduce lactation somatic cell counts in both sheep and goats respectively. Overall, the results found in the present study, particularly the highly negative correlations observed between milk yield and UD, suggest that future breeding programmes would benefit by taking into account udder traits so that selection for productivity is not accompanied by the possible deterioration in udder conformation, especially in the absence of detailed measures of mastitis.

The genetic correlations associated with the teat traits (TS, TA and TP) varied throughout the first lactation (Figure 3b). Correlations between milk yield and TS had a similar pattern as the udder traits in that the values became increasingly negative in the early stage of lactation and began to decrease and approach zero towards the end. The values ranged from -0.36 to 0.23 and followed a similar pattern to those observed for UF. Standard errors ranged from 0.05 to 0.07. The correlations estimated between milk yield and both TA and TP followed a different pattern, when compared with TS, with all estimates remaining negative throughout the lactation. During the first 50 days in milk, the correlations associated with TA changed from -0.40 to -0.45. From this point onwards, the correlation values began to decrease again steadily, levelling off at -0.35 for a period after 250 DIM before falling again after 350 DIM to -0.05. The standard errors ranged from 0.04 to 0.07. The correlation values observed for TP ranged from -0.15 and -0.25 and were therefore relatively more stable across lactation when compared to the other teat traits. The overall standard errors ranged from 0.05 to 0.08. The relationship with the cumulative milk yield at 305 days were in general agreement, particularly for TS and TP with genetic correlations of -0.35 (0.13) and -0.05 (0.15) respectively observed. However, the magnitude of the correlation associated with TA (0.03 ±0.13), which is essentially zero given the standard error, is different to the estimate from the random regression analyses in early lactation but not very different to the very low, negative, estimates towards the end of lactation. The relationship between TP and milk yield, as reported by Manfredi et al. (2001) was low, with absolute values below 0.2, similar to the values observed in the present study between 100 and 300 DIM. Correlations of a similar magnitude between these two traits were also observed by Fernandez et al. (1997) and Legarra and Ugarte (2005) in different breeds of dairy sheep. Manfredi et al. (2001) reports that there was an extremely small relationship between TS and milk yield with a correlation of just 0.03 in the Saanen breed, which is very different to the values observed in the present study which went to -0.36. Although moderate, the size of the correlations observed for both TS and TA indicate that increased milk yield will affect the size and angle of the teats which, depending on the milking equipment used, may prove problematic. Rupp et al. (2011), also observed favourable correlations between some teat conformation characteristics and somatic cell count, although this was much more evident in the Saanen breed than the Alpine, suggesting that individual breed differences would need to be taken into consideration. The inclusion therefore of teat conformation information, in addition to the udder traits mentioned previously, would further benefit future breeding programmes, particularly in terms of milking ability but possibly also, after further investigation, milk quality and udder health.

The correlations estimated for BL, FF and BF are shown in Figure 3c. The values estimated between milk yield and FL are not shown due to the unreliable nature of the results from the low heritability of FL and the lack of variation in the scores associated with this trait. The correlations associated with BL were associated with high standard errors (0.06-0.10) and not significantly different to zero ($p<0.05$). The correlations with the feet traits both became increasingly positive, at different rates, during the early stages of lactation before beginning to fall again towards 500 DIM. Both were also associated with standard errors ranging from 0.05 to 0.08. The FF correlations became more positive during early lactation, moving from -0.31 at the beginning to 0.11 at 250 DIM. The values then fell again to -0.16 at 500 DIM. Although following a similar pattern to FF, the strength of the correlations observed for BF were higher. Positive correlations were observed between approximately 20 DIM and 480 DIM. The highest correlation was 0.24 at 250. Like the previous correlations estimated between the conformation traits and milk yield at 305 days, the standard errors were relatively high. The relationship with FF (0.08 ±0.18) and BF (-0.09 +0.15), were again both essentially zero. This was similar to the majority of correlations observed throughout mid-lactation in the random regression analyses for FF but only for the correlations associated with BF during early and late lactation. The correlation observed with 305 day milk yield for BL was 0.33 (+0.17) which was quite different to the low correlations estimated in the random regression analyses (close to zero). This can be interpreted as a reflection of the product of the relative contribution of each daily milk yield to the 305 yield and the genetic correlations of the trait with daily milk. However, as mentioned previously, the addition of more data records for these traits may improve the reliability of results in the future. In terms of other estimates available in the literature, which are comparable with the ones presented here, there are very few, due to the investigation of differently defined traits relating to the legs and feet or the fact that many focus on udder and teat related traits. De la Fuente et al. (2011), estimated a small genetic correlation of -0.09 between the back legs and milk yield of Churra ewes which was markedly different to when compared with our estimate of 0.33 with milk yield at 305 days.

The results presented have improved our knowledge of this population in terms of both the conformation traits themselves and their relationship with milk yield. It is unfortunate that no information was available with regards to the milk composition such as fat, protein and somatic cell counts as these are also economically important traits to consider. Future studies would therefore benefit from recording this data as well. Additionally, further investigation into the economic values of these traits and the effects of any changes in conformation on aspects such as udder health and the longevity of the animals in the herd would be also worthwhile. The impact of the different scores will depend on aspects such as the environments in which goats such as these are being milked. For example the milking machines used may influence which teat and udder scores are the most (and least) desirable. Nonetheless, the heritability and correlation estimates observed for the majority of traits in our study, indicate that genetic change can be achieved using conventional quantitative selection methods. In addition however, the development over recent years in genomic selection provides further opportunities for this population and indeed dairy goats worldwide. Although becoming increasingly popular in species such as dairy and beef cattle, genomic selection in dairy goats is still relatively new. A recent study by Mucha et al. (2015), using the same sample population as this study, found that genomic breeding values could be estimated using a single-step approach. Using such methodology offers potential to identify animals, at a very early age, with favourable conformation characteristics and milk yield, thus improving the efficiency and production of the herd further.

CONCLUSIONS

Conformation traits investigated in the present study had a low to moderate range of heritabilities, with those relating to the udders and teats providing the highest estimates. The traits relating to the feet and legs were less heritable and less reliable, although this could potentially be improved in the future with the collection of more data records from the population studied. The genetic correlations estimated between the conformation traits and milk yield, across the first lactation, demonstrate the changes that occur during this time period. The majority of the correlations estimated between milk yield and both the udder and teat traits were negative, therefore future breeding programmes would benefit from including these traits in order to ensure that selection for increased productivity is not accompanied by the unwanted deterioration of functional fitness.

ACKNOWLEDGEMENTS

This paper is part of a 3-year project co-funded by the UK innovation agency, the Technology Strategy Board (Swindon, UK). The authors gratefully acknowledge cooperation with Angus Wielkopolski and Mark De Hamel from Yorkshire Dairy Goats (Seaton Ross, York, UK) and Marta Rus for her technical assistance in scoring all of the animals used in the study. Many thanks also to David McNeil (SRUC) for his drawings depicting the different conformation scores.

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