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

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

10  
11 **Genetic parameters of linear conformation type traits and their relationship with milk**  
12 **yield throughout lactation in mixed-breed dairy goats.**

13  
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23  
24 **Abstract**

25 Conformation traits are of interest to many dairy goat breeders not only as descriptive traits in  
26 their own right, but also because of their influence on production, longevity and profitability.  
27 If these traits are to be considered for inclusion in future dairy goat breeding programmes,  
28 relationships between them and production traits such as milk yield, must be considered.  
29 With the increased use of regression models to estimate genetic parameters, there is now an  
30 opportunity to investigate correlations between conformation traits and milk yield throughout  
31 lactation in more detail. The aims of this study were therefore to a) estimate genetic

32 parameters for conformation traits in a population of crossbred dairy goats, b) estimate  
33 correlations between all conformation traits and c) assess the relationship between  
34 conformation traits and milk yield throughout lactation. No milk composition information  
35 was available. Data were collected from goats based on 2 commercial goat farms, during  
36 August and September in 2013 and 2014. Ten conformation traits, relating to udder, teat, leg  
37 and feet characteristics, were scored on a linear scale (1-9). The overall dataset comprised of  
38 data available for 4,229 goats, all in their first lactation. The population of goats used in the  
39 study was created using random crossings between 3 breeds: British Alpine, Saanen and  
40 Toggenburg. In each generation, the best performing animals were selected for breeding  
41 therefore leading to the formation of a synthetic breed. The pedigree file used in the analyses  
42 contained sire and dam information for a total of 30,139 individuals. The models used fitted  
43 relevant fixed and random effects. Heritability estimates for the conformation traits were low  
44 to moderate, ranging from 0.02 to 0.38. A range of positive and negative phenotypic and  
45 genetic correlations between the traits were observed, with the highest correlations found  
46 between udder depth and udder attachment (0.78), teat angle and teat placement (0.70), and  
47 back legs and back feet (0.64). The genetic correlations estimated between the conformation  
48 traits and milk yield, across the first lactation, demonstrated changes during this time period.  
49 The majority of correlations estimated between milk yield and both the udder and teat traits  
50 were negative. Therefore, future breeding programmes would benefit from including these  
51 traits in order to ensure that selection for increased productivity is not accompanied by any  
52 unwanted change in functional fitness.

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

## 54 INTRODUCTION

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

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

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

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

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

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

99

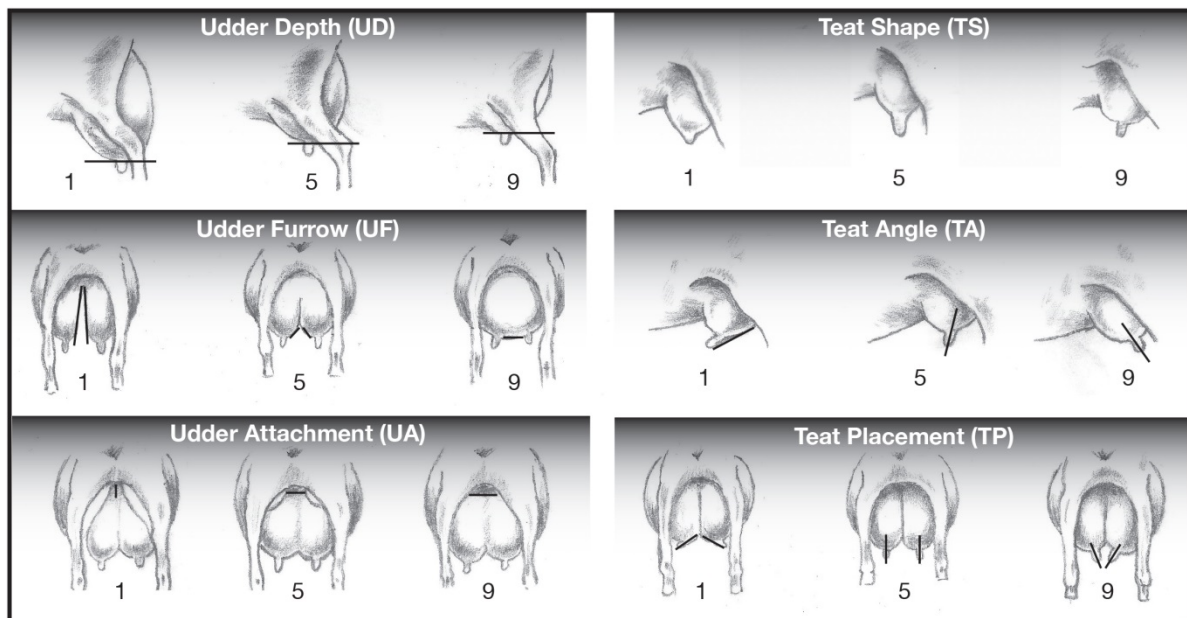
## **MATERIALS AND METHODS**

### ***Conformation Traits***

100 Conformation trait data were collected from goats based on 2 farms, owned by the same  
101 farming business and consisting of related animals, during August and September in 2013  
102 and 2014. The dataset comprised of data available for 4,220 goats all in their first lactation.  
103 The traits recorded for each animal, scored by the same recorder, were linear in form and  
104 scored using a 9-point scale which had many similarities to that developed by the French  
105 dairy goat breeders' association CAPGENES and used by Manfredi et al. (2001) and Rupp et  
106 al. (2011). The data contained information for three udder traits, three teat traits and four  
107 traits relating to legs and feet.  
108

109 The udder traits, as shown in Figure 1 were: Udder furrow (UF), viewed from the rear view  
110 of the udder, indicating the prominence of the medial suspensory ligament. A score of 1  
111 indicates that the ligament is highly prominent, with an extreme cleft in the base of the udder,

112 whereas a score of 9 indicates the ligament is not prominent and there is little/no cleft visible.  
113 Udder depth (UD) is the depth of the udder is measured in comparison to the hocks of the  
114 animal. Udders scored 1 are close to the ground whereas those scored 9 are well above the  
115 hocks. A score of 5 indicates that the cleft of the udder is at the hocks level; Udder  
116 attachment (UA) represents the strength of attachment, based on the perimeter of the insertion  
117 to the abdominal wall. A score of 1 represents udders with a weak and narrow level of  
118 attachment whereas those scored 9 are udders with a large and strong perimeter of  
119 attachment.



120

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

122 The teat traits, also shown in Figure 1 were: Teat shape (TS) indicating the diameter and  
123 shape of the teat ranging from wide and conical for score 1 to small and cylindrical for score  
124 9; Teat angle (TA) describes whether the teat, when looking from the side of the animal, is  
125 pointing forwards (score 1) or towards the rear (score 9). The score of 5 represents teats  
126 pointing straight downwards. Teat placement (TP) is scored using a rear view of the udder  
127 and gives an indication as to placement of the teats in relation to the medial ligament. Teats  
128 pointing outwards, away from each other, would be scored as 1, whereas those pointing

129 inwards, towards each other, would be scored 9. A score of 5 would be given for teats  
130 pointing straight down.

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



143  
144 Figure 2. Scoring criteria used for the leg and feet traits.

### 145 ***Genetic analysis***

146 The population of goats used in the study, as described by Mucha et al. (2014), was created  
147 using random crossings between 3 breeds: British Alpine, Saanen and Toggenburg. In each  
148 generation, the best performing animals were selected for breeding therefore leading to the  
149 formation of a synthetic breed. No information was available in terms of the breed  
150 composition of the animals in the population therefore this could not be included in the

151 analyses. The pedigree file used in the analyses contained sire and dam information for a total  
152 of 30,139 individuals. Estimates of (co)variance components were obtained by the average  
153 information-REML algorithm in the DMU package (Madsen and Jensen, 2008). The model  
154 fitted for the conformation traits was:

$$155 \mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}, \quad [1]$$

156 where  $\mathbf{y}$  is a vector of observations for the analysed conformation score;  $\mathbf{b}$  is a vector of fixed  
157 effects: farm, lactation stage, year of scoring and birth year;  $\mathbf{a}$  is the vector of random  
158 additive animal effects;  $\mathbf{e}$  is the vector of random residual effects, and  $\mathbf{X}$  and  $\mathbf{Z}$  are incidence  
159 matrices relating records to their respective effects. Lactation stage, defined as the number of  
160 days between kidding date and scoring date, was grouped into 7 different levels in order to  
161 achieve an appropriate distribution; i) 100 days or less (939 records), ii) between 101-200  
162 days (2123 records), iii) 201-300 days (536 records), iv) 301-400 days (276 records), v) 401-  
163 500 days (129 records), vi) 501-600 days (114 records) and vii) 601 days and above (103  
164 records). Year of scoring had 2 levels; 2013 (1662 records) and 2014 (2558 records) and birth  
165 year had 5 levels; 2009 (49 records), 2010 (162 records), 2011 (661 records), 2012 (1810  
166 records) and 2013 (1538 records). Only the direct genetic effect (animal) was fitted in each  
167 model due to the fact that the conformation scores were recorded only once on each  
168 individual animal.

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



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

172

173 Where indices 1 and 2 (and so on) indicate the two conformation traits,  $\mathbf{A}$  is the additive  
174 genetic relationship matrix  $\mathbf{I}$  are identity matrices,  $\sigma_g^2$  and  $\sigma_e^2$  are the genetic and residual  
175 variances, respectively.

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

$$178 \mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wp} + \mathbf{e}, \quad [2]$$

179 where  $\mathbf{y}$  is the vector of test-day observations;  $\mathbf{b}$  the vector of fixed effects, consisting of age  
180 at kidding, herd test day, year-season, and fixed lactation curves modeled by fitting Legendre  
181 polynomials (Kirkpatrick et al., 1990) of fourth order;  $\mathbf{a}$  is a  $1 \times 3$  vector of random  
182 regression coefficients (Legendre polynomials of second order) for the animal effect;  $\mathbf{p}$  is the  
183  $1 \times 3$  vector of random regression coefficients (Legendre polynomials of second order) for  
184 the permanent environment effect; and  $\mathbf{e}$  is the vector of random residual effect. The matrix  $\mathbf{X}$   
185 is the incidence matrix for fixed effects;  $\mathbf{Z}$  and  $\mathbf{W}$  are matrices of Legendre polynomials of  
186 DIM of second order for random animal and permanent environment effect, respectively.

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

$$189 \quad \text{Var} \begin{bmatrix} \mathbf{a} \\ \mathbf{p} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{A} \otimes \mathbf{G} & 0 & 0 \\ & \mathbf{I} \otimes \mathbf{P} & 0 \\ \text{symm} & & \mathbf{I}\sigma_e^2 \end{bmatrix}$$

190 where  $\mathbf{G}$  and  $\mathbf{P}$  are  $3 \times 3$  (co)variance matrices of the random regression coefficients for the  
191 animal and permanent environment effects, respectively.

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

$$194 \quad \text{Var} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \mathbf{p}_2 \\ \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{A}\mathbf{G}_1 & \mathbf{A}\mathbf{G}_{12} & 0 & 0 & 0 \\ & \mathbf{A}\mathbf{G}_2 & 0 & 0 & 0 \\ & & \mathbf{I}\mathbf{P}_2 & 0 & 0 \\ & & & \mathbf{I}\sigma_{e1}^2 & \mathbf{I}\sigma_{e12}^2 \\ \text{symm} & & & & \mathbf{I}\sigma_{e2}^2 \end{bmatrix}$$

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

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

$$205 \quad \mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{e}, [3]$$

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

$$212 \quad \text{Var} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma_{g1}^2 & \mathbf{A}\sigma_{g12} & 0 & 0 \\ & \mathbf{A}\sigma_{g2}^2 & 0 & 0 \\ & & \mathbf{I}\sigma_{e1}^2 & \mathbf{I}\sigma_{e12} \\ \text{symm} & & & \mathbf{I}\sigma_{e2}^2 \end{bmatrix}$$

213 Where indices 1 and 2 indicate the two traits. The first trait was one of the conformation  
 214 traits, and the second trait was 305d milk yield,  $\mathbf{A}$  is the additive genetic relationship matrix,  
 215  $\mathbf{I}$  are identity matrices,  $\sigma_g^2$  and  $\sigma_e^2$  are the genetic and residual variances, respectively.

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

## 220 RESULTS & DISCUSSION

221 A summary of traits included in the analyses are shown in Table 1. The average scores  
 222 recorded on both farms were similar for all traits. The front legs trait had the lowest overall  
 223 standard deviation (0.37) which was a reflection that 88% of records were a score of 5. The  
 224 average daily milk yield, during the first lactation, was 3.32 +0.003 kg. The additional  
 225 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	$\pm 0.99$
Udder Depth (UD)	4220	2	9	5.93	$\pm 0.94$
Udder Attachment (UA)	4220	3	9	7.69	$\pm 0.68$
Teat Shape (TS)	4198	1	8	4.17	$\pm 1.00$
Teat Angle (TA)	4216	1	6	4.24	$\pm 0.81$
Teat Placement (TP)	4216	1	8	3.37	$\pm 0.81$
Front Legs (FL)	4216	2	9	4.88	$\pm 0.37$
Back Legs (BL)	4219	2	9	4.60	$\pm 0.62$
Front Feet Set (FF)	4213	3	9	8.23	$\pm 0.74$
Back Feet Set (BF)	4217	4	9	7.78	$\pm 0.77$
305 day milk yield (kg)	4170	157.05	3002.50	1151.75	$\pm 325.88$

226

### 227 *Genetic Parameters*

228 The univariate heritability estimates for each trait, across both farms, ranged from 0.02 to  
229 0.38 (Table 2). The highest estimates were generally associated with the udder and teat  
230 related traits, where as those estimated for the legs and feet were lower. The individual traits  
231 with the overall highest and lowest heritability estimates were UD (0.38) and FL (0.02)  
232 respectively. Manfredi et al. (2001) also observed generally higher estimates for the udder  
233 and teat traits when compared with the legs and feet. However, although a similar scale and  
234 scoring system was used, some of the traits considered by Manfredi et al. (2001), differed  
235 from those in the present study. The leg and feet traits similar between both studies were  
236 those relating to hock distance (similar to BL in the present study) and feet angle, although no  
237 indication was given as to whether this was relating to the angle of all feet, or just the  
238 front/back ones. Nonetheless, heritability estimates for the hock distance (0.16 and 0.12 for  
239 the Alpine and Saanen breeds respectively), were reasonably similar to the present study  
240 (0.13). In dairy sheep, de la Fuente et al. (2011) estimated a heritability of 0.18 for rear legs,  
241 scored in the same manner but with a slight difference in score definitions. The very low  
242 heritability estimate observed for FL is likely due to the lack of variation in the scores given

243 for this trait, perhaps influenced by previous selection criteria on the farms which may have  
244 only selected animals with straight front legs to remain in the herd. The heritability of milk  
245 yield in this population was 0.56, as estimated by Mucha et al. (2015). The authors suggest  
246 that this relatively high estimate could be influenced by the reduction in “noise” due to the  
247 automated recording equipment used and the fact that the data originates from just two farms.

248 Considering the udder and teat traits in more detail, the estimates observed in the present  
249 study for UD, UF, TS, were in close agreement to those observed by both Manfredi et al.  
250 (2001) and Rupp et al. (2011), despite some differences between the individual breeds.  
251 However, estimates observed for UA (0.15) and TP (0.23) were lower than the values  
252 estimated by Manfredi et al. (2001) and Rupp et al. (2011), who both referred to these traits  
253 as the rear udder and teat placement respectively. The estimates given by these two authors  
254 ranged from 0.23-0.29 for UA and 0.25-0.38 for TP. Additionally, the heritability of 0.36  
255 observed for TA was higher than previous estimates, which ranged from 0.15-0.22 (Manfredi  
256 et al., 2001; Rupp et al., 2011). When compared to the estimates given by Luo et al. (1997)  
257 for TP and UD, all of the estimates observed in the current study were low, although some  
258 similarities were seen between the UF and TS estimates (referred to as suspensory ligament  
259 and teat diameter respectively).

260 Many of these differences may be related to the number of data records available (n=4,220)  
261 and the breed composition of animals used in this study. The three studies discussed above all  
262 had data available from just less than 19,000 up to just over 43,000 animals recorded over a  
263 number of different years. It is likely that as more data becomes available future estimates  
264 may become more accurate, particularly in terms of the standard errors associated with the  
265 estimates observed. The lower estimates observed for the feet and leg traits in general could  
266 be influenced by farm selection policies already in place as individuals with undesirable

267 conformation for these traits can become visible from an early age and therefore can be  
268 removed before becoming established in the herd. The synthetic nature of the population  
269 structure in the current study, based on a history of crossbreeding, also differed from the  
270 pure-bred populations previously referred to. This could also influence the heritability values  
271 estimated due to the expected increase in the additive genetic variance in mixed populations  
272 when compared to pure-bred populations. Luo et al. (1997) mention data available from  
273 crossbred goats, which they refer to as ‘experimentals’, but unfortunately data from these  
274 animals was not used in their final analyses to keep consistency with additional data they  
275 were using in the study.

#### 276 *Relationships between Conformation Traits*

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

284 Among the udder traits, the genetic correlations ranged from 0.12 – 0.77, with the highest  
285 observed between UD and UA. The relationships between the teat traits were similar to those  
286 observed among the udder traits, ranging from -0.10 – 0.69, with negative values estimated  
287 between TS and both TA and TP. The moderately high positive correlation between TA and  
288 TP (0.69) indicated that selection for improved teat placement would also result in the  
289 improved angle of the teats. The relationships between the udder and teat traits followed a  
290 similar pattern to those observed by Manfredi et al. (2001), in both Alpine and Saanen breeds,

291 in terms of direction of the relationships. All were positive, with the exceptions of those  
292 observed between UF and both TA and TP, indicating that as the strength of the medial  
293 ligament changed, there was a negative knock-on effect on the angle and placement of the  
294 teats.

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

301

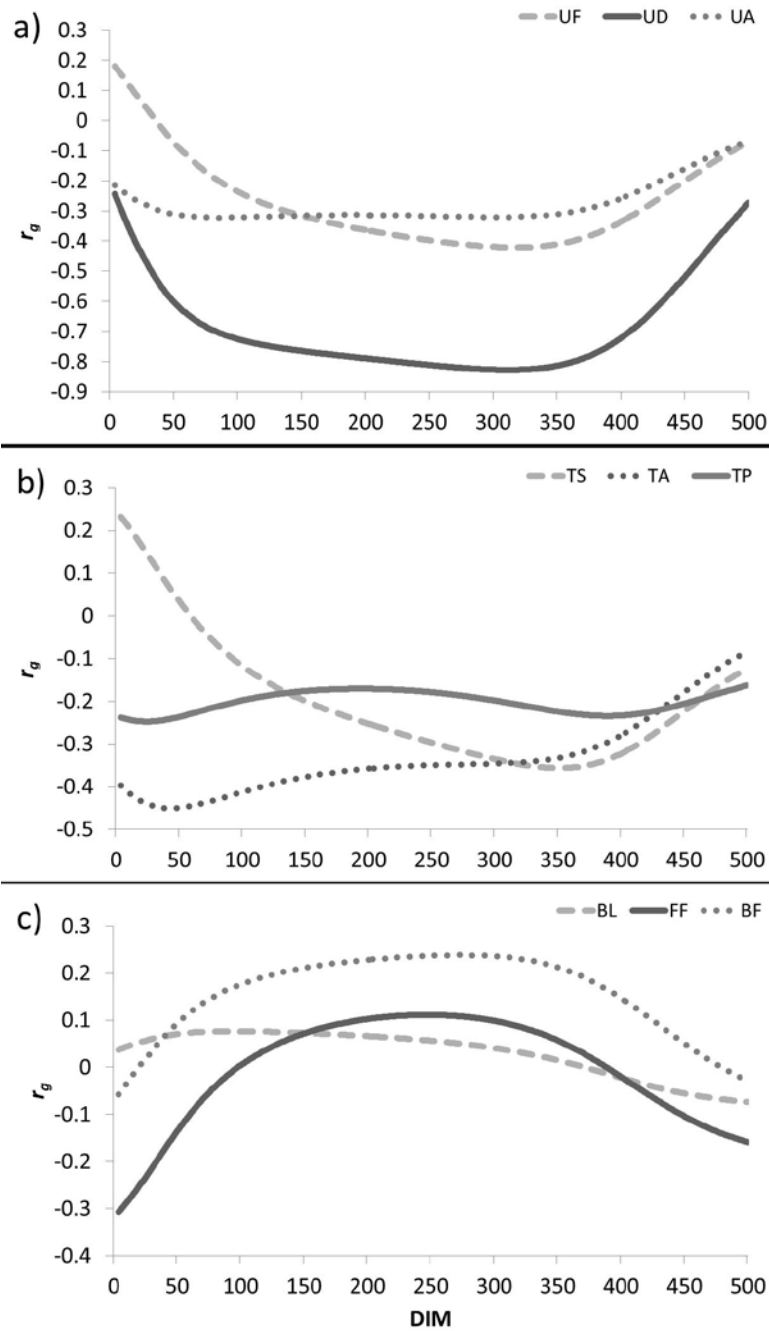
Table 2. Univariate heritabilities (on diagonal in bold), genetic (below diagonal) and phenotypic (above diagonal) correlations between conformation traits, during first lactation only. Standard errors in parenthesis.

Trait	UF	UD	UA	TS	TA	TP	FL	BL	FF	BF
Udder Furrow (UF)	<b>0.28 (0.04)</b>	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)	<b>0.38 (0.05)</b>	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)	<b>0.15 (0.04)</b>	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)	<b>0.32 (0.05)</b>	-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)	<b>0.36 (0.05)</b>	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)	<b>0.23 (0.04)</b>	-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)	<b>0.02 (0.02)</b>	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)	<b>0.13 (0.04)</b>	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)	<b>0.13 (0.04)</b>	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)	<b>0.25 (0.05)</b>



303 *Relationships between Conformation Traits and Milk Yield throughout lactation*

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



311

312 Figure 3. Genetic correlations ( $r_g$ ) between milk yield and conformation traits; Udder traits  
 313 (3a) of Udder Furrow (UF), Udder Depth (UD), Udder Attachment (US); Teat traits (3b) of  
 314 Teat Shape (TS), Teat Angle (TA), Teat Placement (TP); Feet and leg traits (3c) of Back  
 315 Legs (BL), Front Feet (FF) and Back Feet (BF); during 500 days of lactation, based on a  
 316 random regression model.

317 Genetic correlations associated with the udder traits (UF, UD and UA) are shown in Figure

318 3a. The correlations estimated between milk yield and UF ranged from -0.42 and 0.18.

319 Positive values were found up to approximately 50 DIM after which the values became  
320 negative and remained negative throughout the remainder of the lactation. The size of the  
321 correlations increased up to around 300 DIM (-0.42) after which they began to steadily fall  
322 back towards zero. Standard errors ranged from 0.05 to 0.07. The correlations observed  
323 between milk yield and UD followed a similar pattern, however unlike UF, all values were  
324 negative ranging from -0.24 and -0.83. The absolute correlation values increased sharply  
325 during the first 100 DIM before continuing to increase, at a slower rate, between 100 DIM  
326 and 350 DIM. From 350 DIM onwards the correlations fell back to around -0.27 at 500 DIM.  
327 Standard errors were between 0.03 and 0.06 with the lowest occurring mid-lactation between  
328 approximately 200 and 300 DIM. Correlation values observed for UA were also all negative  
329 ranging from -0.07 to -0.32. There was a gradual increase in the strength of the correlation  
330 during the first 70 DIM from a value of -0.21 to -0.32, after which values remained  
331 approximately -0.32 until 350 DIM. Standard errors were between 0.06 and 0.09 with the  
332 lowest found during mid-lactation. When compared with the genetic correlations estimated  
333 with the cumulative milk yield at 305 days, the udder traits all behaved consistently in the  
334 fact that all correlations observed were negative ( $-0.25 \pm 0.13$ ,  $-0.71 \pm 0.08$  and  $-0.28 \pm 0.17$ )  
335 for UF, UD and UA respectively). Manfredi et al. (2001), when estimating correlations  
336 between udder traits and milk yield at 250-days also observed negative correlations ranging  
337 from -0.51 to -0.19 whereas Barillet (2000) comments that, across a number of different  
338 studies in both dairy goats and sheep, correlations between milk yield and UD, although to  
339 varying degrees, were always antagonistic. Similar relationships between UD and milk yield  
340 have also been observed in dairy cattle (Brotherstone, 1994). The correlations that we have  
341 observed in the current study therefore seem to be in agreement with those estimated  
342 previously. Another method of udder scoring, relating to UD, was investigated by Casu et al.  
343 (2006) using the degree of suspension of the udder, calculated using the ratio between the

344 udder attachment width and udder height. They suggested this trait as a possible alternative  
345 due to the fact that in their study it had a similar heritability as UD, it was highly correlated  
346 with UD (0.82) and it had a low and unfavourable genetic correlation with milk yield. In  
347 addition, although not investigated in the present study, results reported by Marie-Entacelin et  
348 al. (2005) and Rupp et al. (2011) suggest the possibility that selection for improved udder  
349 conformation can reduce lactation somatic cell counts in both sheep and goats respectively.  
350 Overall, the results found in the present study, particularly the highly negative correlations  
351 observed between milk yield and UD, suggest that future breeding programmes would benefit  
352 by taking into account udder traits so that selection for productivity is not accompanied by  
353 the possible deterioration in udder conformation, especially in the absence of detailed  
354 measures of mastitis.

355 The genetic correlations associated with the teat traits (TS, TA and TP) varied throughout the  
356 first lactation (Figure 3b). Correlations between milk yield and TS had a similar pattern as the  
357 udder traits in that the values became increasingly negative in the early stage of lactation and  
358 began to decrease and approach zero towards the end. The values ranged from -0.36 to 0.23  
359 and followed a similar pattern to those observed for UF. Standard errors ranged from 0.05 to  
360 0.07. The correlations estimated between milk yield and both TA and TP followed a different  
361 pattern, when compared with TS, with all estimates remaining negative throughout the  
362 lactation. During the first 50 days in milk, the correlations associated with TA changed from -  
363 0.40 to -0.45. From this point onwards, the correlation values began to decrease again  
364 steadily, levelling off at -0.35 for a period after 250 DIM before falling again after 350 DIM  
365 to -0.05. The standard errors ranged from 0.04 to 0.07. The correlation values observed for  
366 TP ranged from -0.15 and -0.25 and were therefore relatively more stable across lactation  
367 when compared to the other teat traits. The overall standard errors ranged from 0.05 to 0.08.  
368 The relationship with the cumulative milk yield at 305 days were in general agreement,

369 particularly for TS and TP with genetic correlations of -0.35 (0.13) and -0.05 (0.15)  
370 respectively observed. However, the magnitude of the correlation associated with TA (0.03  
371  $\pm$ 0.13), which is essentially zero given the standard error, is different to the estimate from the  
372 random regression analyses in early lactation but not very different to the very low, negative,  
373 estimates towards the end of lactation. The relationship between TP and milk yield, as  
374 reported by Manfredi et al. (2001) was low, with absolute values below 0.2, similar to the  
375 values observed in the present study between 100 and 300 DIM. Correlations of a similar  
376 magnitude between these two traits were also observed by Fernandez et al. (1997) and  
377 Legarra and Ugarte (2005) in different breeds of dairy sheep. Manfredi et al. (2001) reports  
378 that there was an extremely small relationship between TS and milk yield with a correlation  
379 of just 0.03 in the Saanen breed, which is very different to the values observed in the present  
380 study which went to -0.36. Although moderate, the size of the correlations observed for both  
381 TS and TA indicate that increased milk yield will affect the size and angle of the teats which,  
382 depending on the milking equipment used, may prove problematic. Rupp et al. (2011), also  
383 observed favourable correlations between some teat conformation characteristics and somatic  
384 cell count, although this was much more evident in the Saanen breed than the Alpine,  
385 suggesting that individual breed differences would need to be taken into consideration. The  
386 inclusion therefore of teat conformation information, in addition to the udder traits mentioned  
387 previously, would further benefit future breeding programmes, particularly in terms of  
388 milking ability but possibly also, after further investigation, milk quality and udder health.

389 The correlations estimated for BL, FF and BF are shown in Figure 3c. The values estimated  
390 between milk yield and FL are not shown due to the unreliable nature of the results from the  
391 low heritability of FL and the lack of variation in the scores associated with this trait. The  
392 correlations associated with BL were associated with high standard errors (0.06-0.10) and not  
393 significantly different to zero ( $p < 0.05$ ). The correlations with the feet traits both became

394 increasingly positive, at different rates, during the early stages of lactation before beginning  
395 to fall again towards 500 DIM. Both were also associated with standard errors ranging from  
396 0.05 to 0.08. The FF correlations became more positive during early lactation, moving from -  
397 0.31 at the beginning to 0.11 at 250 DIM. The values then fell again to -0.16 at 500 DIM.  
398 Although following a similar pattern to FF, the strength of the correlations observed for BF  
399 were higher. Positive correlations were observed between approximately 20 DIM and 480  
400 DIM. The highest correlation was 0.24 at 250. Like the previous correlations estimated  
401 between the conformation traits and milk yield at 305 days, the standard errors were  
402 relatively high. The relationship with FF ( $0.08 \pm 0.18$ ) and BF ( $-0.09 + 0.15$ ), were again both  
403 essentially zero. This was similar to the majority of correlations observed throughout mid-  
404 lactation in the random regression analyses for FF but only for the correlations associated  
405 with BF during early and late lactation. The correlation observed with 305 day milk yield for  
406 BL was  $0.33 (+0.17)$  which was quite different to the low correlations estimated in the  
407 random regression analyses (close to zero). This can be interpreted as a reflection of the  
408 product of the relative contribution of each daily milk yield to the 305 yield and the genetic  
409 correlations of the trait with daily milk. However, as mentioned previously, the addition of  
410 more data records for these traits may improve the reliability of results in the future. In terms  
411 of other estimates available in the literature, which are comparable with the ones presented  
412 here, there are very few, due to the investigation of differently defined traits relating to the  
413 legs and feet or the fact that many focus on udder and teat related traits. De la Fuente et al.  
414 (2011), estimated a small genetic correlation of -0.09 between the back legs and milk yield of  
415 Churra ewes which was markedly different to when compared with our estimate of 0.33 with  
416 milk yield at 305 days.

417 The results presented have improved our knowledge of this population in terms of both the  
418 conformation traits themselves and their relationship with milk yield. It is unfortunate that no

419 information was available with regards to the milk composition such as fat, protein and  
420 somatic cell counts as these are also economically important traits to consider. Future studies  
421 would therefore benefit from recording this data as well. Additionally, further investigation  
422 into the economic values of these traits and the effects of any changes in conformation on  
423 aspects such as udder health and the longevity of the animals in the herd would be also  
424 worthwhile. The impact of the different scores will depend on aspects such as the  
425 environments in which goats such as these are being milked. For example the milking  
426 machines used may influence which teat and udder scores are the most (and least) desirable.  
427 Nonetheless, the heritability and correlation estimates observed for the majority of traits in  
428 our study, indicate that genetic change can be achieved using conventional quantitative  
429 selection methods. In addition however, the development over recent years in genomic  
430 selection provides further opportunities for this population and indeed dairy goats worldwide.  
431 Although becoming increasingly popular in species such as dairy and beef cattle, genomic  
432 selection in dairy goats is still relatively new. A recent study by Mucha et al. (2015), using  
433 the same sample population as this study, found that genomic breeding values could be  
434 estimated using a single-step approach. Using such methodology offers potential to identify  
435 animals, at a very early age, with favourable conformation characteristics and milk yield, thus  
436 improving the efficiency and production of the herd further.

## 437 **CONCLUSIONS**

438 Conformation traits investigated in the present study had a low to moderate range of  
439 heritabilities, with those relating to the udders and teats providing the highest estimates. The  
440 traits relating to the feet and legs were less heritable and less reliable, although this could  
441 potentially be improved in the future with the collection of more data records from the  
442 population studied. The genetic correlations estimated between the conformation traits and

443 milk yield, across the first lactation, demonstrate the changes that occur during this time  
444 period. The majority of the correlations estimated between milk yield and both the udder and  
445 teat traits were negative, therefore future breeding programmes would benefit from including  
446 these traits in order to ensure that selection for increased productivity is not accompanied by  
447 the unwanted deterioration of functional fitness.

448

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- 457 Barillet, F. 2007. Genetic improvement for dairy production in sheep and goats. *S. Rum. Res.*  
458 70:60-75.
- 459 Brotherstone, S. 1994. Genetic and phenotypic correlations between linear type traits and  
460 production traits in Holstein-Friesian dairy cattle. *Anim. Prod.* 59:183-187.
- 461 Casu, S., I. Pernazza, and A. Carta. 2006. Feasibility of a linear scoring method of udder  
462 morphology for the selection scheme of Sardinian sheep. *J. Dairy Sci.* 89:2200-2209.
- 463 Carta, A., S. Casu, and S. Salaris. 2009. Invited Review: Current state of genetic  
464 improvement in dairy sheep. *J. Dairy. Sci.* 92:5814-5833.
- 465 de la Fuente, L. F., G. Fernandez, and F. San Primitivo. 1996. A linear evaluation system for  
466 udder traits of dairy ewes. *Liv. Prod. Sci.* 45:171-178.
- 467 de la Fuente, L. F., C. Gonzalo, J. P. Sanchez, R. Rodriguez, J. A. Carriedo, and F. San  
468 Primitivo. 2011. Genetic parameters of the linear body conformation traits and genetic  
469 correlations with udder traits, milk yield and composition, and somatic cell count in dairy  
470 ewes. *Can. J. Anim. Sci.* 91:585-591.
- 471 Fernandez, G., J. A. Baro, L. F. de la Fuente, and F. San Primitivo. 1997. Genetic parameters  
472 for linear udder traits of dairy ewes. *J. Dairy Sci.* 86:601-605.
- 473 Fischer, T. M., A. R. Gilmour, and J. H. J. van der Werf. 2004. Computing approximate  
474 standard errors for genetic parameters derived from random regression models fitted by  
475 average information REML. *Genet. Sel. Evol.* 36:363-369.
- 476 Frigo, E., C. D. Dechow, O. Pedron, and B. G. Cassell. 2010. The genetic relationship of  
477 body weight and early-lactation health disorders in two experimental herds. *J. Dairy Sci.*  
478 93:1184-1192.
- 479 Kirkpatrick, M., D. Lofsvold, and M. Bulmer. 1990. Analysis of the inheritance, selection  
480 and evolution of growth trajectories. *Genetics* 124:979-993.
- 481 Legarra, A., and E. Ugarte. 2005. Genetic parameters of udder traits, somatic cell score, and  
482 milk yield in Latxa sheep. *J. Dairy Sci.* 88:2238-2245.
- 483 Luo, M. F., G. R. Wiggans, and S. M. Hubbard. 1997. Variance component estimation and  
484 multitrait genetic evaluation for type traits of dairy goats. *J. Dairy Sci.* 80:594-600.
- 485 Madsen, P., and J. Jensen. 2008. A user's guide to DMU. University of Aarhus, Tjele,  
486 Denmark.
- 487 Manfredi, E., A. Piacere, P. Lahaye, and V. Ducrocq. 2001. Genetic parameters of type  
488 appraisal in Saanen and Alpine goats. *Liv. Prod. Sci.* 70:183-189.

- 489 Marie-Entacelin, C., J. M. Astruc, D. Porte, H. Larroque, and C. Robert-Granié. 2005.  
490 Multiple-trait genetic parameters and genetic evaluation of udder-type traits in Lacuane dairy  
491 ewes. *Live. Prod. Sci.* 97:211-218.
- 492 Menéndez-Buxadera, A., A. Molina, F. Arrebola, M. J. Gil, and J. M. Serradilla. 2010.  
493 Random regression analysis of milk yield and milk composition in the first and second  
494 lactations of Murciano-Granadina goats. *J. Dairy Sci.* 93:2718-2726.
- 495 Meyer, K., S. Brotherstone, W. G. Hill, and M. R. Edwards. 1987. Inheritance of linear type  
496 traits in dairy cattle and correlations with milk production. *Anim. Prod.* 44:1-10.
- 497 Mucha, S., R. Mrode, M. Coffey, and J. Conington. 2014. Estimation of genetic parameters  
498 for milk yield across lactations in mixed-breed dairy goats. *J. Dairy Sci.* 97:2455-2461.
- 499 Mucha, S., R. Mrode, M. Coffey, and J. Conington. 2015. Estimation of genomic breeding  
500 values for milk yield in UK dairy goats. *J. Dairy Sci.* 98:8201-8208.
- 501 Rupp, R., V. Clément, A. Piacere, C. Robert-Granié, and E. Manfredi. 2011. Genetic  
502 parameters for milk somatic cell score and relationship with production and udder type traits  
503 in dairy Alpine and Saanen primiparous goats. *J. Dairy Sci.* 94:3629-3634.
- 504 Short, T. H., and T. J. Lawlor. 1992. Genetic parameters of conformation traits, milk yield,  
505 and herd life in Holsteins. *J. Dairy Sci.* 75:1987-1998.
- 506