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Genetic aspects of conformation in dairy goats

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Introduction

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. It is important to include conformation traits in the consideration of selection of replacement females, as their functionality and longevity in the herd is dependent on their ability to produce milk without incurring problems associated with structural weakness.

Conformation (or 'linear type') traits refer to aspects of physical attributes such as udder and teat type that affect milking ability, udder health and longevity, as well as feet and legs which are important for improved mobility and structural correctness, stature and other traits such as body depth and chest width. If these traits are to be considered for inclusion in future dairy goat breeding programmes, the genetic and phenotypic relationships amongst them and with production traits such as milk yield, must be considered.

The recording of conformation scores is considered in detail by the International Committee on Animal Recording (ICAR), which is the recognised authority for setting standards of individual animal recording across different nations involved in genetic improvement of livestock. An ideal linear scoring system is one that is easy to implement, is repeatable and reflects the biological extremes for that trait within the population that is being scored. In France, a 9-point scale has been developed and is currently used by French dairy goat breeders, as described by Manfredi et al. (2001).

The UK does not yet have a formal nationwide breeding programme for dairy goats. Instead, it is up to individual farms and companies to undertake their own recording protocols. However, being able to standardise the recording so that animals across herds can be equitably compared would greatly accelerate the rate at which milking goat herds could improve performance and efficiency.

The aim of this paper is to describe a conformation assessment scoring system appropriate for UK dairy goats and to discuss the implications of its use for genomic selection.

Methods

A composite goat population was used for this study, as described by Mucha et al., (2014). Goats on two farms were assessed in their 1st lactation for 10 conformation traits on a linear 9-point scale and the genetic and phenotypic relationships with these and milk yield were estimated. A total of 5,026 goats were scored once by a single assessor and these records were matched with 131,579 individual milk yield records. The information in the pedigree comprised 34,391 animals over 15 generations from 296 sires and 12,468 dams.

The conformation traits include udder depth (UD), udder furrow (UF), udder attachment (UA), teat shape (TS), teat angle (TA), teat placement (TP), front legs (FL), back legs (BL), front feet (FF) and back feet (BF), as described by McLaren et al., 2016. Each trait was scored on a 9-point scale that describe the extremes of the phenotypes possible in the population being scored. The measurements were taken on digital images of the rear and side view of each animal taken when it was in a rotary milking parlour.

A full description of the statistical methodology used for the study is described by McLaren et al., 2016.

The model fitted for the conformation traits was:

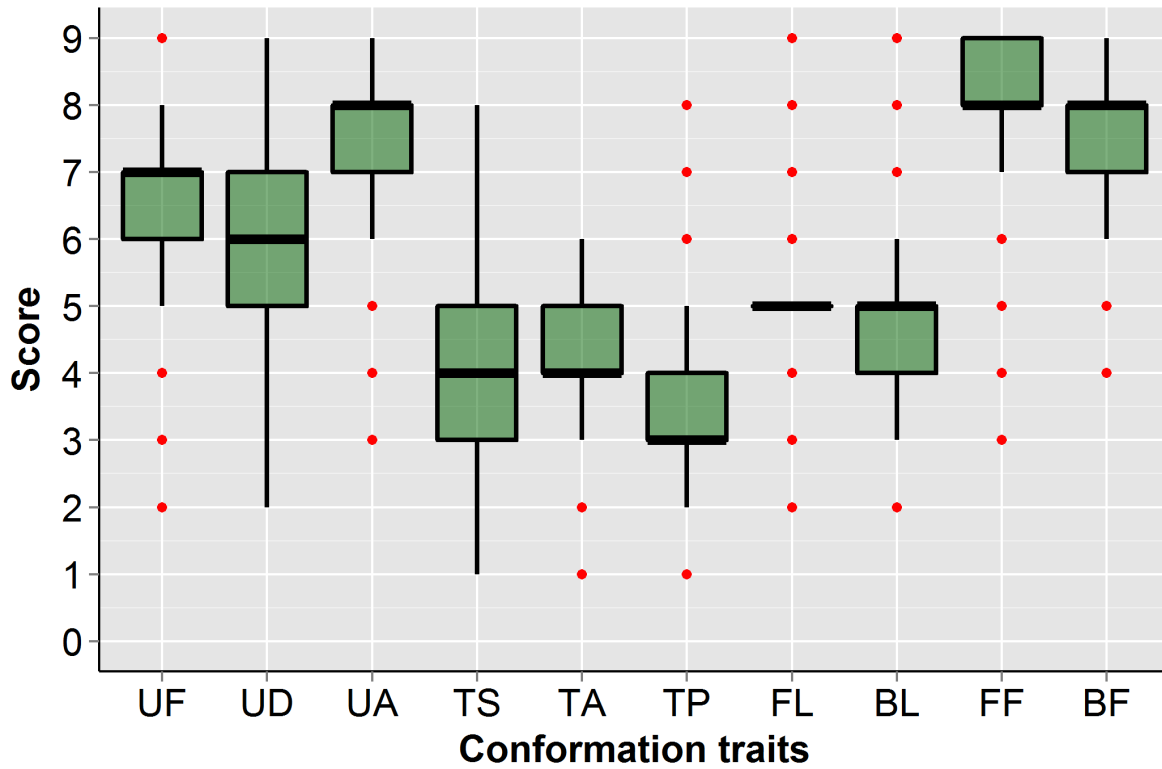
$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}, \quad [1]$$

where \mathbf{y} is a vector of observations for the analysed conformation score; \mathbf{b} is a vector of fixed effects: farm, lactation stage, year of scoring and birth year; \mathbf{a} is the vector of random additive animal effects; \mathbf{e} is the vector of random residual effects, and \mathbf{X} and \mathbf{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 as described by McLaren et al., 2016. Milk yield was estimated with a random regression animal ('test day') model developed in a previous study (Mucha et al., 2014). A bivariate analysis was used to estimate the variance-covariance structures of conformation and milk yield using the method described in McLaren et al 2016 and the standard errors for the heritability and genetic and phenotypic correlations were calculated using the methodology proposed by Fischer et al 2004.

Results

The distribution of the conformation traits are shown in Figure 1. The box plots indicate that median (as indicated by the thick line), upper 75th and lower 25th quartile ranges, (therefore 50% of all observations are within the boxes). The 'tails' on the boxes for each trait indicate the distribution of the remaining lower 25% and top 25% and the dotted line are outliers.

Figure 1: Trait distribution of conformation scores



UF=Udder furrow, UD=udder depth, UA=udder attachment, TS=Teat size, TA=teat angle, TP=teat placement, FL=front legs, BL=black legs, FF=front feet, BF=back feet

The genetic parameters are shown in Figure 2 below. The estimates are colour-coded as indicated in the legend, with stronger colours indicating higher estimates. Heritability estimates are on the diagonal, phenotypic correlations are above, and genetic correlations are below the diagonal. Note that the correlations describe the direction and strength of the relationship amongst the conformation traits and not necessarily whether they are 'good' or 'antagonistic'. Figure 3 indicates this point.

Figure 2: Heritability (diagonal), and correlations amongst conformation traits

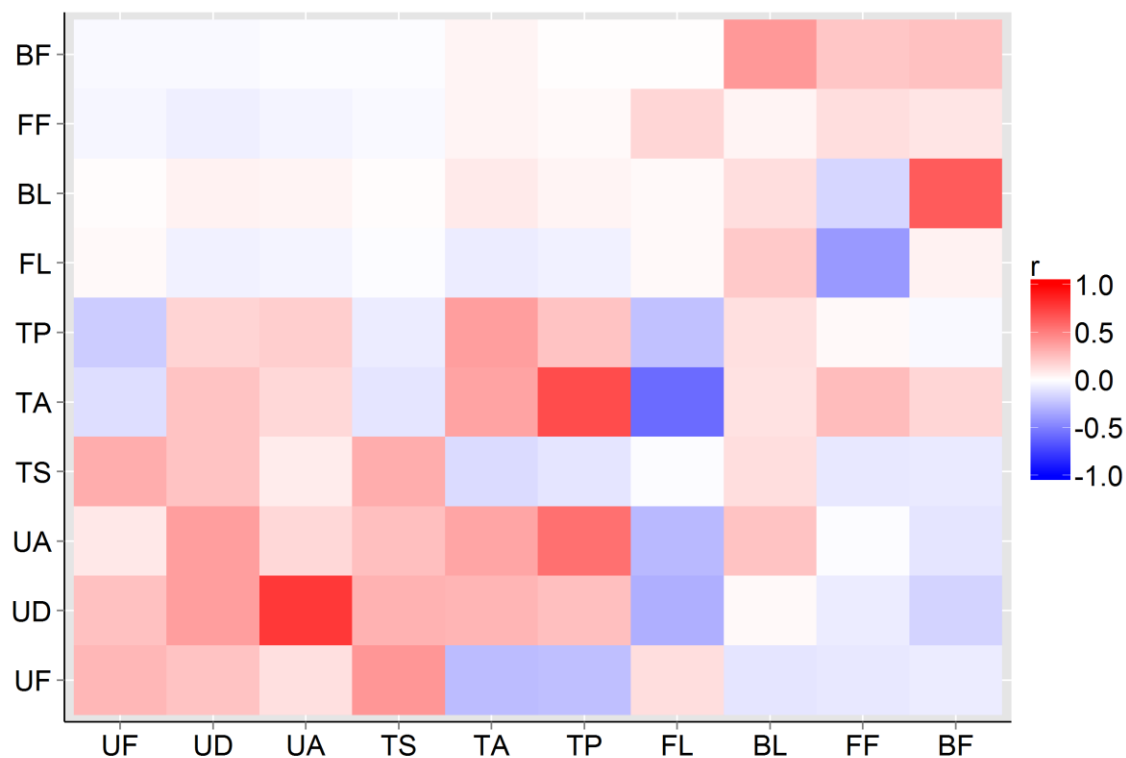


Figure 3: Example of 9-point conformation scores for front and back legs



A full description of the relationships (genetic and phenotypic correlations) among conformation traits and milk yield is in McLaren et al., 2016. To summarise, the genetic relationship of udder depth and udder attachment with milk yield were negative (and antagonistic) at all stages of the lactation. This means that higher yielding goats are more likely to have deeper udders and with weaker attachment to the abdominal wall, which is in agreement with several other studies in sheep, goats and dairy cattle. The genetic relationship between udder furrow and milk yield was positive at the start of lactation but became negative (deteriorated) during peak lactation before becoming positive again towards the end of lactation. The genetic correlation between teat placement and milk yield was more or less unchanged throughout lactation although that between teat shape (indicating the diameter and shape of the teat ranging from wide and conical for score 1 to

small and cylindrical for score 9) and milk yield 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. Overall, the results found in the present study, suggest that future breeding programmes would benefit by taking into account udder traits so that selection for productivity is not accompanied by the deterioration in udder conformation, especially in the absence of detailed measures of mastitis.

Discussion

The study has quantified the genetic basis to conformation traits in a composite breed of dairy goats in the UK. Conformation traits are largely low to moderately heritable and are sufficient to warrant their inclusion into goat breeding programmes. The method by which conformation scoring is undertaken is labour intensive and laborious. Having an automated way of assessing conformation (e.g. by image analysis) would enable more animals to be assessed and reduce the costs associated with it.

Evidence from McLaren et al 2016, which is summarised here, indicates the importance of including conformation into formal breeding programmes which cannot be stressed highly enough. As it is likely that some of these conformation traits will be directly linked to mastitis susceptibility, and as higher yielding dairy goats tend to be more susceptible to mastitis, the inclusion of conformation scoring will ensure that selection for milk yield is not undertaken at the expense of animal health and welfare.

A new era of genomic selection has recently been introduced in the UK. This involves a combination of records on animal pedigree, phenotype and genotype combined, to provide predictions of genomic merit, based on Single Nucleotide Polymorphism (SNP 'chip') technology into a 'single step' evaluation method (Mucha et al., 2015). The potential of this technology for dairy goat herds is impressive, as it enables sires to be selected based on their genomic estimated breeding value (GEBV) at an earlier age, reducing the need to wait until their daughters are lactating to predict their genetic worth. This saves considerable time and money by reducing the costs associated with progeny testing and improves the accuracy of selection. It also enables related animals to be screened and ranked on their genomic worth without the need for phenotyping. That means farmers can submit DNA from sires and dams for testing, and the animals can be ranked on their genomic potential for the trait of interest, without having to undertake milk recording themselves. This is a major step for the UK goat milk industry that offers considerable scope to improve the efficiency and sustainability of the national herd.

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