

Genetic parameters for longevity traits in UK dairy goats

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Summary

Genomic selection on UK dairy goats began in 2015. New traits for selection have evolved since that time with the addition of new genotypes for the reference population. The objectives of this study were to define longevity in terms of lifespan and production, to estimate their heritabilities, and calculate phenotypic and genetic correlations. The dataset comprised records on 12,233 female dairy goats based on two genetically linked farm sites. The pedigree contained information on 40,422 individuals. Heritabilities of the longevity traits were found to range from 0.08 to 0.46, with moderate to high phenotypic and genetic correlations between the lifetime longevity and production longevity traits. The results will allow genetic improvement in dairy goats by incorporating longevity into a breeding index with production, health and maintenance traits. The next step following this work is to produce genomic breeding values for longevity traits that will allow genomic selection for use in UK dairy goat breeding programmes.

Keywords: dairy goats, longevity, heritability, genomic evaluation

Introduction

Following an increase in the popularity of goats' milk, much work has been done on UK dairy goat breeding programs, with the focus on milk yield (Mucha *et al.*, 2014). Despite this, dairy goat breeding programmes in the UK are in their early stages compared to the dairy cow, beef and sheep industries, with genomic breeding values being routinely established in 2015. More efficient breeding programs are characterised by incorporating a range of traits that will promote optimum improvement. Therefore additional traits have since been included in routine genomic evaluations to ensure high herd productivity while maintaining good health, conformation and low environmental impact. Longevity is a trait that has significant impact on this industry. Goats with high milk yields and good health which remain in the herd for a long time will reduce both the economic and environmental costs of raising replacement animals per unit of milk produced. Longevity has been studied in sheep and cattle leading to genomic selection in these species, however little work has previously been done defining, evaluating and producing genomic breeding values for this trait in UK dairy goats. The objectives of this study were to estimate the heritability of longevity traits and investigate their genetic and phenotypic correlations with production traits.

Materials and Methods

Phenotypes

Longevity and milk yield data were provided on dairy goats from two genetically linked farm sites in the UK owned by a single farming business. The population was created in 1985 through crossing three breeds; Alpine, Saanen, and Toggenburg. There was no specific crossing strategy, but the best performing animals from each generation were selected for breeding and this resulted in the creation of a synthetic breed. A detailed description of the analysed population can be found in Mucha *et al.* (2014). The dataset comprised of 12,233 female dairy goats with longevity and milk yield information. They were complete records where all animals had either died or been culled. The pedigree file contained records of 40,422 individuals of which 447 were sires and 17,166 were dams. The dataset consisted of milk yield records, birth year (1987 to 2015), farm (2 farms), maximum lactation number (1 to 11) and age at first kidding (246 to 756 days). Previous work investigating clustering based on principle component analysis confirmed that the population was mostly homogeneous therefore breed was not required in the model (Mucha *et al.*, 2015).

Three longevity traits were defined for genetic evaluation. Age at death (AD) was considered the lifetime longevity trait, and was calculated as the number of years from birth to death. A further two traits were considered, which were the number of days in milk over lifetime (LDIM) and the average lifetime daily milk yield (ALDY). The analysis of these traits did not take into account the specific reasons for an animal leaving the herd. This may have been due to culling for commercial practice such as poor health, conformation or reproductive status; due to prior information based on recorded data and performance predictions; or death.

Estimation of variance components

Each longevity trait was fitted in the following univariate mixed animal model in ASReml (Gilmour *et al.*, 2009) to estimate genetic and variance components:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{e}$$

where \mathbf{y} is a column vector of the longevity trait of interest; $\boldsymbol{\beta}$ is the column vector of fixed effects which included birth year, farm, maximum lactation number, age at first kidding, birth year by farm and maximum lactation by farm interactions; \mathbf{a} is the column vector of random animal effects; \mathbf{X} and \mathbf{Z} are the design matrices for the fixed effects and random effects, respectively; \mathbf{e} is the random residual effect. All of the fixed effects were significant ($P < 0.05$) so were included in the model.

Results and Discussion

The mean age at death (AD) was 4.73 ± 2.16 years (\pm standard deviation), the mean lifetime days in milk (LDIM) was 1121.68 ± 677.79 days, and the mean average lifetime daily milk yield (ALDY) was 1.25 ± 0.79 kg. AD was moderately heritable (\pm standard error) at 0.14 ± 0.01 , LDIM was lower at 0.08 ± 0.01 and ALDY was highly heritable at 0.46 ± 0.02 . Low heritabilities are typical of longevity traits and the higher value found for ALDY is likely due to the high heritability of milk yield traits in general. Phenotypic and genetic correlations between the lifetime longevity trait AD and the production longevity traits (LDIM and

ALDMY) were all positive with moderate to high levels of correlation (Table 1.). Phenotypic and genetic correlations between AD and LDIM were high showing that animals with longer lifespans have longer lifetime days in milk, as would be expected. AD was moderately correlated phenotypically and genetically with ALDY, demonstrating that on average, animals with longer lifespans had higher daily yield. This may suggest that selection for increased milk yields in goats' is indirectly selecting on increased animal longevity. However, this is more likely due to farm management strategies where animals with high milk yields remain in the herd longer.

Table 1. Phenotypic (left) and genetic (right) correlations between lifetime (AD) and production (LDIM and ALDMY) longevity traits with standard errors.

| | AD |
|------|----------------------------|
| LDIM | 0.94 (0.001), 0.99 (0.004) |
| ALDY | 0.13 (0.011), 0.25 (0.079) |

Conclusions

Overall, heritability estimates for these longevity traits indicate that they would respond well to selection. The longevity traits were found to have moderate to high correlations with productive longevity traits at both the phenotypic and genetic level. Favourable positive correlations indicate that an increased number of days in milk during the animals' lifetime and an improved average lifetime daily milk yield, have led to longer living dairy goats'. The next step following on from this work is to produce genomic breeding values using the single-step method HBLUP. Currently there are 13,955 animals genotyped with the Illumina 50K caprine chip. Producing GEBVs will provide a good tool to use alongside other traits such as production, health and maintenance traits to ensure good lifetime and production longevity of dairy goats selected in future breeding programmes.

Acknowledgements

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