Estimation of genetic parameters for milk yield across lactations in mixed-breed dairy goats

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ABSTRACT

Currently, breeding values for dairy goats in the United Kingdom are not estimated and selection is based only on phenotypes. Several studies from other countries have applied various methodologies to estimate breeding values for milk yield in dairy goats. However, most of the previous analyses were based on relatively small data sets, which might have affected the accuracy of the parameter estimates. The objective of this study was to estimate genetic parameters for milk yield in crossbred dairy goats in lactations 1 to 4. The research was based on data provided by 2 commercial goat farms in the United Kingdom comprising 390,482 milk yield records on 13,591 dairy goats kidding between 1987 and 2012. The population was created by crossing 3 breeds: Alpine, Saanen, and Toggenburg. In each generation, the best-performing animals were selected for breeding and, as a result, a synthetic breed was created. The pedigree file contained 28,184 individuals, of which 2,414 were founders. The data set contained test-day records of milk yield, lactation number, farm, age at kidding, and year and season of kidding. Data on milk composition was unavailable. Covariance components were estimated with the average information REML algorithm in the ASReml package (VSN International Ltd., Hemel Hempstead, UK). A random regression animal model for milk yield with fixed effects of herd test day, year-season, and age at kidding was used. Heritability was the highest at 200 and 250 d in milk (DIM), reaching 0.45 in the first lactation and between 0.34 and 0.25 in subsequent lactations. After 300 DIM, the heritability started decreasing to 0.23 and 0.10 at 400 DIM in the first and subsequent lactations, respectively. Genetic correlation between milk yield in the first and subsequent lactations was between 0.16 and 0.88. This study found that milk yields in first and subsequent lactations are highly correlated, both at the genetic and phenotypic level. Estimates of heritability for milk yield were higher than most of the values reported in the literature, although they were in the range reported in this species. This should facilitate genetic improvement for the population studied as part of a broader multi-trait breeding program.

Key words: milk yield, dairy goat, random regression

INTRODUCTION

Currently, breeding values for dairy goats in the United Kingdom (**UK**) are not estimated and selection is based only on phenotypes. Unlike in dairy cattle, no centralized recording system exists. Most goat farms are small, with only several animals. Many hobby breeders also exist, who are not interested in production improvement. Few large herd goat breeders conduct their breeding programs independently of each other with hardly any exchange of data. Therefore, estimates of genetic parameters for the UK dairy goats are unknown. Estimation of heritability of milk yield along with correlations with other traits is essential to set up an effective breeding program. It is essential to predict both the direct and correlated response to selection, and to develop a selection index that includes traits of economic importance. Moreover, it is important to raise awareness and benefits of genetic indices among breeders who currently use only raw yields. Routine breeding value estimation is performed, for instance, in such countries as Canada, France, the United States, and Norway (Bélichon et al., 1999; Montaldo and Manfredi, 2002). Unfortunately in the UK, no organized selection program exists, which may negatively affect the genetic level of the population and reduce its profitability compared with goat populations from other countries.

Several other studies have applied various methodologies to estimate breeding values for milk yield in dairy goats. These include models for lactation total milk yield (Valencia et al., 2005) and 250-d cumulated milk yield (Rupp et al., 2011) as well as the repeatability of milk yield and random regression models using test-day records (Zumbach et al., 2008). Random regression models have been proven as good tools for estimation of genetic parameters in dairy goats (Zumbach et al., 2008; Menéndez-Buxadera et al., 2010). The use of a random regression model allows better insight into the relation-

ship between the traits under investigation compared with a single-point estimate of heritability from lactation yield models. Random regression test-day models are more flexible compared with test-day models with a fixed lactation curve, as it seems to better account for the shape of the lactation curves, allowing each animal to have a different shape of lactation as determined at the genetic level (Jamrozik et al., 1997).

One problem in the estimation of genetic parameters for dairy goats is the availability of sufficient high-quality data. Many of the reports present in the literature were based on relatively small data sets, which might have affected the accuracy of the parameter estimates. Moreover, previous analyses were mostly limited to 305 DIM, which is based on dairy cattle evaluations. In the case of goats, they are often milked for lactations that extend past 400 d. However in the UK, no previous study has been done on the estimation of genetic parameters for goat milk production.

Therefore, the objective of this study was to estimate heritability for milk yield, across 400 d of lactation, in a synthetic population of crossbred dairy goats for lactations 1 to 4. Genetic and phenotypic correlations between milk yield in the first and subsequent lactations were estimated. This information will provide the basis for development of routine breeding value estimation for UK dairy goats.

MATERIALS AND METHODS

Data

The lactation data were from 2 separate farm units in the UK, owned by a single farming business. The herds used for this study are larger than other units operating in the UK, although several herds exist with 400+ dairy goats undertaking routine milk recording and using electronic identification to facilitate data recording. The business is considered to be the most technically advanced in the UK, although it works closely with other milk producers that supply milk into the same commercial milk processing enterprise. The data set comprised 390,482 records on 13,591 dairy goats kidding between 1987 and 2012. The population was created in 1985 by crossing 3 breeds: Alpine, Saanen, and Toggenburg. No particular crossing strategy existed. In each generation, the best-performing animals were selected for breeding and, as a result, a synthetic breed was created. The breed composition of the animals was not recorded and, thus, could not be included in the analysis. To mitigate this problem, SNP information was used to asses breed composition of the animals. A total of 1,961 goats from the same population were genotyped with the Illumina Caprine 50K BeadChip (Illumina Inc., San Diego, CA;

Tosser-Klopp et al., 2012). Clustering based on principal components analysis, performed with SNP & Variation Suite v7.7.8 (Golden Helix Inc., Bozeman, MT), did not reveal any major distinct groups. This suggests that the analyzed population is mostly homogeneous and, therefore, breed was not included as a factor in the analysis. The pedigree file contained 28,184 individuals, of which 2,414 were considered as founders. There were 318 sires and 10,781 dams in the pedigree. The data set contained test-day records of milk yield, along with information about lactation number (1 to 4), farm (2 farms), age at kidding (12 to 90 mo), and year (1987 to 2012) and season of kidding [summer (June to August), autumn (September to November), winter (December to February), and spring (March to May)]. Fat and protein content was not included in the analysis, as it had not yet been recorded on either of the 2 farms that contributed data. Litter size was recorded only for some of the animals and, as a result, only 170,710 milk records could be matched with litter size records. Only goats with more than 3 test-day observations were used for analysis. Additionally, the data set was restricted to have at least 10 records per level of herd-test-day, year-season, and age at kidding. Test-day milk records below 0.5 and above 12 kg were removed from the data as error records. Lactation length was restricted to between 4 and 400 DIM because goats from the 2 farms are milked for long lactations. The target age for first kidding is 12 mo and average lactation length is 18 mo. Animals are milked 3 times per day in the first stage of lactation and twice when milk production decreases. Unfortunately, the number of milking occasions associated with each daily yield was not recorded. Goats are fed with high-DM grass silage. Metabolizable energy content of the diet was around 11.1 to 11.4 MJ/kg of DM at 16% CP.

Estimation of (Co)Variance Components

Covariance components were estimated with the average information REML algorithm in the ASReml package (Gilmour et al., 2009). The following random regression animal model for milk yield was used:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wp} + \mathbf{e},$$

where $\mathbf{y}$ is the vector of test-day observations; $\mathbf{b}$ the vector of fixed effects, consisting of herd test day, year-season, and fixed lactation curves modeled by fitting Legendre polynomials (Kirkpatrick et al., 1990) of fourth order nested within age at kidding; $\mathbf{a}$ is a 1 × 3 vector of random regression coefficients (Legendre polynomials of second order) for the animal effect; $\mathbf{p}$ is the 1 × 3 vector of random regression coefficients