



Genetic parameters for functional stayability to 24 and 36 months of age and first lactation milk yield in dairy goats



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ABSTRACT

In order to estimate genetic parameters involving functional stayability to 24 and 36 months of age (FST24 and FST36), and first lactation milk yield (MY1) in dairy goats, information obtained in the United States of America (USA) for Alpine, Saanen, Toggenburg, Nubian and LaMancha breeds during the period 1979–2004, was used. The analysis included a total of 40,721 goats from 763 herds daughters to 5777 sires. REML and an animal model was used to estimate (co)variance components, heritabilities, genetic and phenotypic correlations. Statistical models included breed-herd-year and month of birth fixed terms, as well as animal and error random terms. Models for analysis of FST24 and FST36 included also first lactation milk yield as a covariate to correct for voluntary culling. Heritabilities for FST24, FST36, and MY1 were 0.08 ± 0.01 , 0.09 ± 0.02 , and 0.35 ± 0.01 , respectively. Genetic correlations between FST24 and FST36 was 0.69 ± 0.10 , FST24 and MY1 0.83 ± 0.02 , and 0.82 ± 0.03 between FST36 and MY1. Phenotypic correlations between FST24 and FST36 and MY1 were 0.28 ± 0.01 and 0.61 ± 0.001 , respectively, and 0.61 ± 0.01 between FST36 and MY1. As FST24 can be measured early in life and due to favorable selection responses obtained with FST36 and MY1, FST24 could be incorporated as selection criteria in dairy goats breeding programs.

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1. Introduction

In order to increase productivity, genetic improvement programs of dairy goats currently include traits such as milk, fat and protein production (Wiggans and Hubbard, 2001; Rupp et al., 2011). In dairy cattle, direct and indirect evaluation for functional traits are considered as a part of selection criteria in many selection programs worldwide, in pursuit of maximum economic responses for an overall economic index considering longevity, reproduction and health traits (Mark, 2004; VanRaden and Klaaskate, 1993). However, longevity can not be measured easily because of the delayed recording of phenotypic data (De Mello et al., 2014).

In the United States of America (USA) and France, type traits are included in goat breeding programs as selection criteria with a view to increasing longevity and profitability, but almost no research has been conducted on the direct selection of longevity traits in dairy goats (Montaldo and Manfredi, 2002).

One of points to be considered by milk producers is to breed animals that are healthy, fertile at the appropriate age, and able to express their maximum genetic potential for a long productive period (De Mello et al., 2014). Currently there are no studies describing the factors that influence the longevity of dairy goats. However, this could be inferred indirectly through knowledge of the main causes of culling and death of animals. In a recent study related to longevity, Castañeda-Bustos et al. (2014) found that the main criteria that determined the culling of a goat from the herd were low final type score, milk yield and fat yield per lactation; however, authors did not included health or reproduction as possi-

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ble culling causes. In France, the most-frequent exit reasons of the goats from the herd were related to low milk production (36.6%) and health (22.3%), mainly related to udder disorders (Malher et al., 2001); other cause was death due to digestive, nervous and problems during the kidding. High somatic cell score is being used as culling criteria in dairy goats (Bergonier et al., 2003; Leitner et al., 2008) because it is the main factor associated with mastitis and because could propitiate daily losses in milk yield up to 29% (Barrón-Bravo et al., 2013).

Estimates of genetic parameters for traits of economic importance in dairy goats are necessary when implementing efficient animal breeding programs (Hofer, 1998). At present there are few published studies on stayability or longevity in dairy goats worldwide (Pérez-Razo et al., 2004; García-Peniche et al., 2008; Vicencio, 2009; Castañeda-Bustos et al., 2014), but none deals with estimates of genetic parameters with early functional stayability traits and first lactation milk yield using restricted maximum likelihood methodology. Traits used to measure functional longevity have been corrected for the level of milk production in first lactation and other traits that may be used as voluntary culling criterion by including, for example, total milk yield or within-herd milk yield production percentiles as covariates into the models used for analysis (Dekkers, 1993; Mark, 2004; Castañeda-Bustos et al., 2014).

In this respect, Castañeda-Bustos et al. (2014) obtained parameters only for real and functional productive life until 72 months of age and their associations with reproduction and milk-production traits. Early selection may increase the selection response by reducing the generation interval (Pirchner, 1983), lower costs associated with early selection, and permit to making decisions for culling and to directing the mating of animals. Due to high genetic correlations between early and advanced stayabilities some evidence suggests that early selection (Vollema and Groen, 1996; Vollema, 1998; Sasaki, 2013) could also result in indirect improvements to the herd life of animals. The objective of this study was to estimate heritabilities and genetic and phenotypic correlations for first lactation milk yield and stayabilities to 24 and 36 months of age in US dairy goats.

2. Material and methods

Data were obtained from the American Dairy Goat Association from 1978 to 2004, and include information from Alpine, Saanen, Toggenburg, Nubian and LaMancha breeds.

Traits included in this study were functional stayability to 24 and 36 months of age (FST24 and FST36) and first lactation milk yield (MY1). MY1 was previously corrected to 305 days, mature equivalent basis (Wiggans and Hubbard, 2001). For each herd, the year of beginning and ending on production recording was obtained. We retained for analysis only data from herds with at least three continuous years on record. Through the use of birth dates and kidding dates into the herd, a procedure was performed to verify that goats had the opportunity to reach 24 and 36 months to define FST24 and FST36, respectively. If any of these criteria was not fulfilled for a goat, her record was removed from the final data file. A binary value (0, 1) was defined for goats, assigning a one when the goat reached 24 months, or a zero when the final age was less than 24 months (FST24 variable); FST36 was estimated similarly as with FST24 but to 36 months. In this way, zeros were assigned to stayability variables when the goats did not reach this age because of death or culling and not because the herd disappeared from the database or the goat did not have the opportunity to reach that age.

In order to obtain more accuracy estimates of the parameters, records of goats without a birth date were removed because it was not possible to estimate any of the stayability traits. In addition, ani-

Table 1

Descriptive statistics for stayabilities and first lactation milk yield (MY1) in US goats.

Trait	Number of observations	Average	Standard deviation	CV%
FST24	40721	0.50	0.50	100.0
FST36	20191	0.24	0.43	179.2
MY1 (kg)	40721	1035.5	315.5	30.5

FST24: functional stayability to 24 months of age; FST36: functional stayability to 36 months of age; CV%: coefficient of variation.

mals ages less than 11 months at first kidding were also eliminated as that age was considered to be the lower biological limit. Additionally, records without first lactation information were removed as well as those with missing information on the lactation number because it was not possible to estimate the stayability traits. Only records with at least 60 days in lactation, with at least 150 kg of milk yield, goats with information on milk yield and those who had a first or first and second lactation were used. Herds with at least thirty goats and sires with at least three daughters were retained for analysis. The percentage of records deleted by using all these criteria was less than 4%. In order to maintain an adequate number of data per year, records from 1978 and 1979 were grouped together. The minimum and maximum number of data was 757 for 1980 and 2117 for 1987.

The final data file included a total of 40,721 goats, daughters to 5777 sires from 763 herds. The number of data for Alpine breed was 13,452, for Saanen 5356, Toggenburg 5693, Nubian 11,947 and for LaMancha was 4273, and levels by year ranged from 1979 to 2004. Herds were required to have ≥ 2 breeds. Thus, different number of data were available for each trait (Table 1) and after final edits, 998 breed-flock-year were used for the analysis, with a mean of 40.8 records, and a range of 10–164 records per class.

Univariate animal models were used to estimate animal and error variance components for all traits. The model included the fixed effects of breed-herd-year and month of birth, and animal and error as random effects. The models used for univariate analysis, represented in matrix notation were as follows, based on Henderson (1984):

$$y = Xb + Zu + e$$

where: y = vector of record observations; X = incidence matrix accounting for the fixed effects breed-flock-year and month of kidding; b = vector of unknown fixed effects; Z = incidence matrix for random animal effect; u = vector of unknown random animal effects; and e = vector of unobservable random residual effects.

In the models used to analyze FST24 and FST36, MY1 was included as a fixed covariate in order to consider a functional definition of FST24 and FST36, instead of a raw stayability. Bivariate mixed models were used to estimate genetic and phenotypic correlations for yield and stayability traits, with the following structure:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} = \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Where the subscripts 1 and 2 show the traits to evaluate and the other terms in the model were as previously described. Variance components were obtained using the ASReml program (Gilmour et al., 2006). Expectation (E) and covariance matrices (V) of random vectors for the model are described in the following equations:

$$E \begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix} \text{ and } V \begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix},$$

where $G = A \otimes G_0$ (A is the numerator additive relationship matrix; G_0 is the genetic (co)variance matrix; and \otimes is Kronecker product

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