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Genetic and phenotypic parameters of milk yield, milk composition and age at first kidding in Saanen goats from Mexico

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ABSTRACT

A total of 4007 lactation records from 1520 Saanen goats kidding from 1999 to 2006 and obtained from 10 herds in Guanajuato, Mexico, were analyzed to estimate the heritabilities, repeatabilities, as well as genetic, environmental and phenotypic correlations for milk yield (MILK), fat yield (FAT), protein yield (PROT), fat content (%FAT), protein content (%PROT) and age at fist kidding (AFK). A five-trait repeatability model was used to estimate (co)variances for milk traits, and a four-trait animal model for first lactation records was used to estimate (co) variances involving AFK. For MILK, FAT, PROT, %FAT, %PROT and AFK, heritability estimates were 0.17 ± 0.04, 0.19 ± 0.05, 0.17 ± 0.04, 0.32 ± 0.06, 0.38 ± 0.07 and 0.31 ± 0.09, respectively. Repeatabilities for MILK, FAT, PROT, %FAT and %PROT were 0.43 ± 0.02, 0.42 ± 0.02, 0.42 ± 0.02, 0.64 ± 0.02, and 0.63 ± 0.02, respectively. The genetic correlations between MILK and FAT, and between MILK and PROT, were high and positive (0.72 ± 0.08 and 0.87 ± 0.04, respectively). Genetic correlations between MILK and %FAT, between MILK and %PROT and between MILK and AFK, were -0.24 ± 0.16, -0.30 ± 0.15 and -0.18 ± 0.23, respectively. Genetic correlations between AFK and FAT and between AFK and PROT were -0.09 ± 0.24 and -0.17 ± 0.25, respectively; and genetic correlations between AFK and %FAT and between AFK and %PROT were 0.29 ± 0.35 and 0.14 ± 0.27, respectively. Selection for milk traits is possible using a repeatability animal model. Selection for milk production traits would probably not increase AFK, but more precise estimates of the genetic correlations are required. Selection to lower AFK is possible. These (co)variance estimates would make it possible to predict the selection responses from different economic indices in order to maximize the economic responses for the local markets.

1. Introduction

In many countries, including those of the Mediterranean basin and several in Latin America, goat milk is used mainly for making cheese. In Mexico, goat milk is used for making cheese and candy. Under these circumstances, besides milk yield, the economic value of goat milk depends to a great extent on fat and protein contents (Montaldo and Manfredi, 2002).

Genetic parameters for economically important traits are needed for accurate and unbiased prediction of genetic values, to predict direct and correlated selection responses, and to develop economic multi-trait selection indices (Van Vleck, 1993; Hofer, 1998). Multi-trait animal models are preferable to

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single-trait models for unbiased (co)variance and genetic parameter estimation in animal populations (Thompson, 2008).

Studies on genetic parameters estimation in milk goats are very scarce in Latin American countries, and most of these studies are limited to milk production, usually with low sample sizes and data from few herds (Ribeiro et al., 1998; Gonçalves et al., 2002; Valencia et al., 2007). In Mexico, Montaldo et al. (1982) estimated repeatabilities for some milk productive traits in goats using single-trait models and ANOVA methods. Valencia et al. (2007), estimated heritabilities, repeatabilities and correlations for total milk production, cumulated milk production to 120 days and for lactation length in Saanen goats in Mexico using data from one herd.

Published estimates of genetic parameters for milk yield and content traits in goats are scarce. Few multi-trait animal model-REML estimates of (co)variance matrices are available for yield and content traits (Analla et al., 1996; Gonçalves et al., 2002; Valencia et al., 2007). Information regarding genetic parameters for age at first kidding and their relationships with milk yield traits is also scarce in goats (Bagnicka et al., 2007).

The aim of this study was to estimate heritabilities, repeatabilities, as well as genetic, environmental and phenotypic correlations for milk, fat, and protein yields, in addition to fat and protein contents and age at fist kidding, in Saanen herds from Guanajuato in the central region of Mexico using multi-trait animal repeatability models and REML methodology. Data used were part of a genetic improvement program of dairy goats for the State of Guanajuato (Valencia and Montaldo, 2006). Also, a method to project incomplete records to 305-day records for milk traits was developed in this population.

2. Materials and methods

2.1. Population and data

The original data were obtained from 2000 to 2006, and consisted of 5772 lactations from 2230 goats, from 10 herds located in the villages of Apaseo el Grande, Guanajuato, Mexico (in the central region of the country). This area has a semidry temperate weather with rains in the summer. Herds are approximately at 1780 m above mean sea level with an average temperature of 19 °C. Goats are maintained in an intensive production system, fed with alfalfa hay, commercial concentrate and are supplemented with vitamins and minerals.

Monthly information of fat and protein contents was obtained with an infrared milk analyzer Bentley 150. The official milk recording system was the A4 of the International Committee for Animal Recording (ICAR, 2007); therefore, the total test-day milk production, fat percentage and protein percentage of each goat were evaluated monthly. Total fat and protein yields were obtained from milk yield and percentages for each monthly test-day.

The original information was edited to guarantee the quality of the data to be analyzed. Records with incomplete information were eliminated. Records with less than 3 test-day measurements per goat for milk traits or records of less than 100 days in milk (DIM) were discarded. For age at first kidding, records with values of less than 10 months were discarded. Only records of Saanen breed were kept for analysis.

The 305-day yields from complete records (i.e., records with at least 305 DIM) for milk, fat, and protein yields were calculated using the Test Interval Method (Norman et al., 1999). In order to obtain the 305-day yields from records with 100–304 DIM the following equation was used:

$$305\text{–}day\,yield = CYn + (RYn[305 - DIM]) \tag{1}$$

where: CYn is the cumulative yield to day n; RYn is the average remaining yield from day n to 305 obtained through projection factors for last production.

To estimate projection factors for incomplete lactations, lactation records with at least 8 monthly measurements and with 280–320 DIM were used. A total of 2197 lactations from 950 goats were used for milk production, 1058 lactations from 663 goats for fat production and 1045 lactations from 652 goats for protein production. Two kidding seasons were defined, Autumn–Winter (October to March), and Spring–Summer (April to September). Three age groups were defined (≤2, 3–4 and ≥5 years). The projection factors were obtained within combinations of kidding season and age. The regression equation (Wiggans and Van Vleck, 1979) for estimating the projection factors was:

$$RYn = b_1(LSPn) + b_2(n*LSPn) + b_3\left(\frac{1}{LSPn}\right) + b_4\left(\frac{\sqrt{\text{DIM}}}{LSPn}\right) \tag{2}$$

where: RYn is the average remaining yield from day n; LSPn is the last-sample production in n days. The regression coefficients, LSPn and DIM were used to predict RYn for incomplete records using Eq. (2).

The final data analyzed consisted of 4007 305-day lactation records belonging to 1520 Saanen goats and the pedigree file consisted of 1773 total animals with 101 sires and 637 dams. The final data file included 305-day milk yield (MILK), fat yield (FAT), protein yield (PROT), fat content (%FAT), protein content (%PROT) and age at first kidding (AFK). Numbers of observations for each trait are displayed in Table 1.

Table 1
Descriptive statistics for milk yield, milk composition and age at fist kidding in Saanen goats.

Trait	n [a]	Average	Min	Max	SD	CV (%)
Milk yield (kg)	4007	1095	297	2242	292	26.63
Fat yield (kg)	2080	33.50	8.18	64.74	8.95	26.71
Protein yield (kg)	2087	28.05	8.27	53.58	7.10	25.31
Fat content (%)	2080	3.24	2.38	4.24	0.35	10.89
Protein content (%)	2087	2.72	2.12	3.32	0.17	6.42
Age at first kidding (months) [b]	773	16.59	10.03	29.36	4.40	26.52

Min is the minimum value; Max is the maximum value; SD is the standard deviation; CV is the coefficient of variation.

[a] Number of observations for the five-trait repeatability model.

[b] Number of observations for the four-trait animal model, with first kidding information only, were 1190 for MY; 561 for FY and FC; 552 for PY and PC; and 773 for AFK.

DIM averages for all analyzed data were 277, 276 and 274 for MILK, FAT and PROT respectively. Percentages of records with 200 or less DIM were 7.6% for MILK, 9.3% for FAT and 10.0% for PROT. Estimated correlation coefficients between projected and total (305-day) productions using the data set used to develop the projection factors for MILK, FAT and PROT varied from 0.934 to 0.939 for 100–150 DIM; from 0.969 to 0.972 for 151–200 DIM; from 0.988 to 0.990 for 201–250 DIM, and 0.999 for 251–304 DIM. Projections from incomplete data were unbiased because the average estimation errors for 100–150 DIM were <0.03%, and even lower for DIM>150. Therefore, the impact of projected data on genetic parameter estimation in this study is likely to be small.

Four parity groups were defined (1, 2, 3 and 4 or more lactations). Reproductive year and birth year effects were defined as the period from October of the previous year to September of the current year. Two kidding seasons and two birth seasons were defined, Autumn–Winter (October to March), and Spring–Summer (April to September).

2.2. Estimation of (co)variance components and genetic parameters

Data were analyzed with linear mixed models using AI-REML methodology implemented in the software ASReml (Gilmour et al., 2006). To estimate variance components for milk traits (MILK, FAT, %FAT, PROT and %PROT) a five-trait repeatability model was used. Starting values for each trait were initially obtained with similar single-trait repeatability models. The models for the analysis of milk traits included fixed effects of season of kidding, lactation number, and herd-reproductive year (a total of 63 combinations were made). Animal, permanent environment and residual effects were included as random effects.

Only for the estimation of (co)variance components involving AFK, separate analyses of first kidding information using animal models were made. These analyses lead to the use of two four-trait animal models, because the simultaneous inclusion of FAT, PROT together with %FAT and %PROT (plus AFK and MILK) lead to no convergence. Therefore, two four-trait animal models were used to allow convergence; one for the analysis of AFK, MILK, FAT and PROT and another that included AFK, MILK, %FAT and %PROT. These models included the fixed effects of season of kidding and herd-reproductive year effects (a total of 57 combinations were made) for the milk traits and the fixed effects of season of birth and herd-birth year effects (a total of 59 combinations were made) for AFK. Animal and residual effects were included as random effects. Significance testing of fixed effects in all models was made from equivalent single-trait models using partial *F* test statistics.

The five-trait repeatability model was:

$$\mathbf{Y} = \mathbf{X}b + \mathbf{Z}a + \mathbf{W}p + \mathbf{e}$$

where $\mathbf{Y}$ = vector of records for the traits; $\mathbf{X}$, $\mathbf{Z}$ and $\mathbf{W}$ are incidence matrices that relate fixed, animal, and permanent environmental effects, respectively to data; $\mathbf{b}$ = vector of fixed effects for the traits analyzed; $\mathbf{a}$ = vector of the animal random effects; $\mathbf{p}$ = vector of the permanent environmental effects; $\mathbf{e}$ = vector of residual effects for the analyzed traits.

Expectations and covariance matrices of random vectors are described in the following equations:

$$\mathbf{E}\begin{bmatrix}\mathbf{Y}\\ \mathbf{a}\\ \mathbf{p}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{X}b\\ 0\\ 0\\ 0\end{bmatrix};$$

$$\mathbf{V}\begin{bmatrix}\mathbf{a}\\ \mathbf{P}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{G} & 0 & 0\\ 0 & \mathbf{P} & 0\\ 0 & 0 & \mathbf{R}\end{bmatrix} = \begin{bmatrix}\mathbf{A}\otimes\mathbf{G}_0 & 0 & 0\\ 0 & \mathbf{I}_1\otimes\mathbf{P}_0 & 0\\ 0 & 0 & \mathbf{I}_2\otimes\mathbf{R}_0\end{bmatrix}$$

$\mathbf{G}_0$, $\mathbf{P}_0$ and $\mathbf{R}_0$ denote 5×5 matrices containing additive genetic, permanent environmental and residual (co)variance components respectively. $\mathbf{A}$ is the numerator relationship matrix; $\mathbf{I}_1$ and $\mathbf{I}_2$ were identity matrices and $\otimes$ is the Kronecker product.

The four-trait animal models for the estimation of (co) variances involving AFK were:

$$\mathbf{Y} = \mathbf{X}b + \mathbf{Z}a + \mathbf{e}$$

where $\mathbf{Y}$ = vector of records for the traits; $\mathbf{X}$ and $\mathbf{Z}$ are incidence matrices that relate fixed and animal effects, respectively to data; $\mathbf{b}$ = vector of fixed effects for the traits analyzed; $\mathbf{a}$ = vector of the animal random effects; $\mathbf{e}$ = vector of residual effects for the analyzed traits.

Expectations and covariance matrices of random vectors are described in the following equations:

$$\mathbf{E}\begin{bmatrix}\mathbf{Y}\\ \mathbf{a}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{X}b\\ 0\\ 0\end{bmatrix};\ \mathbf{V}\begin{bmatrix}\mathbf{a}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{G} & 0\\ 0 & \mathbf{R}\end{bmatrix} = \begin{bmatrix}\mathbf{A}\otimes\mathbf{G}_0 & 0\\ 0 & \mathbf{I}\otimes\mathbf{R}_0\end{bmatrix}$$

$\mathbf{G}_0$, and $\mathbf{R}_0$ denote 4×4 matrices containing additive genetic, and residual (co)variance components respectively. $\mathbf{A}$ is the numerator relationship matrix; $\mathbf{I}$ is an identity matrix and $\otimes$ is the Kronecker product.

3. Results

3.1. General statistics and fixed effects

The descriptive statistics of the studied variables are presented in Table 1. From the single-trait analyses using the repeatability model, all fixed effects were significant ($P<0.01$) for MILK, FAT and PROT. For %FAT, season of kidding and herd-reproductive year effects were significant ($P<0.01$). For % PROT, lactation number and herd-reproductive year effects were significant ($P<0.01$). From single-trait analysis for AFK, herd-birth year effect was significant ($P<0.01$). The fixed effects accounted jointly for 6.80 to 51.98% of total variation of each trait. The highest percentages were for MILK (51.98%), PROT (46.09%), FAT (44.53%) and AFK (40.01%). The lowest were for %FAT (6.80%) and %PROT (8.13%).

3.2. Variance components, heritabilities and repeatabilities

Variance components, heritabilities and repeatabilities are presented in Table 2. The larger heritabilities were observed for %PROT (0.38 ± 0.07), %FAT (0.32 ± 0.06) and AFK (0.31 ± 0.09). The smaller heritabilities were estimated for FAT (0.19 ± 0.05), MILK (0.17 ± 0.04) and PROT (0.17 ± 0.04). The larger

Table 2
Variance components, heritabilities (h^2) and repeatabilities (re) for milk yield, milk composition and age at first kidding in Saanen goats.

Trait	σ^2_a	σ^2_{pe}	σ^2_e	σ^2_p	h^2	re
Milk yield [a]	6895	10,550	23,380	40,830	0.17 ± 0.04	0.43 ± 0.02
Fat yield [a]	8.51	10.14	25.74	44.39	0.19 ± 0.05	0.42 ± 0.02
Protein yield [a]	4.66	6.79	15.72	27.17	0.17 ± 0.04	0.42 ± 0.02
Fat content [a]	0.038	0.037	0.042	0.116	0.32 ± 0.06	0.64 ± 0.02
Protein content [a]	0.011	0.007	0.011	0.028	0.38 ± 0.07	0.63 ± 0.02
Age at first kidding [b]	3.62		8.00	11.62	0.31 ± 0.09	

σ^2_a is the additive genetic variance; σ^2_{pe} is the permanent environmental variance; σ^2_e is the residual variance; σ^2_p is the phenotypic variance; h^2 is the heritability; re is the repeatability.

[a] The estimates were obtained by using a five-trait repeatability model.

[b] The estimates were obtained by using a four-trait animal model with first kidding information.

repeatabilities were for %FAT (0.64 ± 0.02) and %PROT (0.63 ± 0.02). The smaller repeatabilities were estimated for MILK (0.43 ± 0.02), FAT (0.42 ± 0.02) and PROT (0.42 ± 0.02).

3.3. Correlations

The genetic, phenotypic and environmental correlations are presented in Table 3. The genetic correlations between MILK and FAT, between MILK and PROT, were high and positive (0.72 ± 0.08 and 0.87 ± 0.04, respectively); the genetic correlations between MILK and %FAT, between MILK and %PROT were all negative (−0.24 ± 0.16 and −0.30 ± 0.15, respectively). The genetic correlations between FAT and %FAT, and PROT with %PROT were positive (0.49 ± 0.13 and 0.21 ± 0.16, respectively). The genetic correlation between AFK and MILK, was moderate and negative (−0.18 ± 0.23). The genetic correlations between AFK and FAT, and AFK with PROT were close to zero with high standard errors (−0.09 ± 0.24 and −0.17 ± 0.25, respectively); the genetic correlations between AFK and %FAT, and AFK with %PROT were 0.29 ± 0.35 and 0.14 ± 0.27, respectively.

The phenotypic correlations between MILK and FAT and between MILK and PROT were high and positive (0.85 ± 0.01 and 0.95 ± 0.01, respectively); and the phenotypic correlations between MILK and %FAT, and between MILK and %PROT were negative (−0.23 ± 0.02 and −0.29 ± 0.02, respectively). Phenotypic correlations between AFK and MILK, between AFK and FAT, and between AFK and PROT, were close to zero (0.04 ± 0.04, 0.08 ± 0.05, and 0.05 ± 0.04, respectively). The phenotypic correlations between AFK and %FAT, and between AFK and %PROT were low (0.14 ± 0.06 and 0.07 ± 0.06, respectively).

The environmental correlations between MILK and PROT, between FAT and PROT, between MILK and FAT were the highest and positive (0.97 ± 0.01, 0.91 ± 0.01, and 0.90 ± 0.01, respectively); the environmental correlations between MILK and %FAT, and between MILK and %PROT were negative (−0.15 ± 0.03 and −0.29 ± 0.03, respectively). The Environmental correlations between AFK and MILK, between AFK and FAT, and between AFK and PROT, were 0.13 ± 0.08, 0.16 ± 0.09, and 0.14 ± 0.08, respectively. The environmental correlations between AFK and %FAT and between AFK and %PROT were positive and close to zero with high standard errors (0.09 ± 0.11 and 0.04 ± 0.11, respectively).

4. Discussion

4.1. Heritabilities and repeatabilities

Our MILK heritability estimate (0.17 ± 0.04) (Table 2), although in its lower part, was within the range of the published values using REML (0.09 to 0.46) for different goat populations (Analla et al., 1996; Ribeiro et al., 1998; Hermiz et al., 2002; Andonov et al., 2007; Valencia et al., 2007).

Hermiz et al. (2002) using REML, estimated the heritability for MILK as 0.46 in Iraqi local goats. Kala and Prakash (1990) using ANOVA and a sire model, estimated heritabilities for milk yield as 0.40 in Jamunapari goats, and as 0.36 in Barbari goats. In Brazil, Ribeiro et al. (1998) estimated the heritability for this trait using REML and an animal model as 0.09 for Saanen goats.

Table 3
Genetic, phenotypic and environment correlations for milk yield, milk composition and age at first kidding in Saanen goats.

Traits [a]	Genetic correlations	Environmental correlations	Phenotypic correlations
Milk yield–fat yield	0.72 ± 0.08	0.90 ± 0.01	0.85 ± 0.01
Milk yield–protein yield	0.87 ± 0.04	0.97 ± 0.01	0.95 ± 0.01
Milk yield–fat content	−0.24 ± 0.16	−0.15 ± 0.03	−0.23 ± 0.02
Milk yield–protein content	−0.30 ± 0.15	−0.29 ± 0.03	−0.29 ± 0.02
Milk yield–age at first kidding	−0.18 ± 0.23	0.13 ± 0.08	0.04 ± 0.04
Fat yield–protein yield	0.80 ± 0.06	0.91 ± 0.01	0.88 ± 0.01
Fat yield–fat content	0.49 ± 0.13	0.26 ± 0.03	0.30 ± 0.02
Fat yield–protein content	0.10 ± 0.16	−0.16 ± 0.03	−0.04 ± 0.03
Fat yield–age at first kidding	−0.09 ± 0.24	0.16 ± 0.09	0.08 ± 0.05
Protein yield–fat content	0.03 ± 0.17	−0.08 ± 0.03	−0.09 ± 0.03
Protein yield–protein content	0.21 ± 0.16	−0.06 ± 0.03	0.02 ± 0.03
Protein yield–age at first kidding	−0.17 ± 0.25	0.14 ± 0.08	0.05 ± 0.04
Fat content–protein content	0.50 ± 0.11	0.34 ± 0.03	0.46 ± 0.02
Fat content–age at first kidding	0.29 ± 0.35	0.09 ± 0.11	0.14 ± 0.06
Protein content–age at first kidding	0.14 ± 0.27	0.04 ± 0.11	0.07 ± 0.06

[a] Estimates between milk traits obtained using a five-trait repeatability model. Estimates involving age at first kidding were obtained using a four-trait animal model with first kidding data only.

The repeatability for MILK (0.43 ± 0.02) was within the range estimated by other authors (0.20 to 0.56) for different goat populations using REML (Analla et al., 1996; Ribeiro et al., 1998; Hermiz et al., 2002; Valencia et al., 2007).

The heritability for FAT (0.19 ± 0.05) was within the range estimated in previous studies (0.16 to 0.39) using REML (Boichard et al., 1989; Muller et al., 2002; Bagnicka et al., 2004; Bömkes et al., 2004; Delgado et al., 2006). The repeatability for FAT (0.42 ± 0.02) was high when compared to the range found in the published studies (0.19 to 0.28) in several goat populations (Bagnicka et al., 2004; Bömkes et al., 2004; Delgado et al., 2006).

The heritability estimated for PROT (0.17 ± 0.04) was within the range of values estimated by other authors (0.13 to 0.36) for different goat populations using REML (Boichard et al., 1989; Muller et al., 2002; Bagnicka et al., 2004; Bömkes et al., 2004; Delgado et al., 2006). The repeatability for PROT (0.42 ± 0.02) was above the range of values estimated by other authors (0.15 to 0.34) for different goat populations using REML (Bagnicka et al., 2004; Bömkes et al., 2004; Delgado et al., 2006).

The heritability for %FAT (0.32 ± 0.06) was within the range of values estimated by other authors with REML (0.14 to 0.50) for different dairy goat populations (Boichard et al., 1989; Analla et al., 1996; Andonov et al., 2007). The repeatability for %FAT (0.64 ± 0.02) was within the range estimated for this trait in different goat populations (0.25 to 0.36) with REML (Analla et al., 1996; Bagnicka et al., 2004; Andonov et al., 2007).

For %PROT, the heritability estimated in our study (0.38 ± 0.07) was within the range of values estimated with REML by other authors (0.14 to 0.52) (Boichard et al., 1989; Analla et al., 1996; Bömkes et al., 2004; Andonov et al., 2007). On the other hand, our repeatability for %PROT (0.63 ± 0.02) was above the range (0.32 to 0.47) estimated by other authors (Analla et al., 1996; Bagnicka et al., 2004; Andonov et al., 2007).

In France, Ilahi et al. (1998) using an animal model and REML in Alpine goats, estimated the highest heritability and repeatability that have been observed for %FAT as 0.72 and 0.80, respectively, and the highest heritability and repeatability for %PROT too as 0.73 and 0.83, respectively.

The heritability for AFK was 0.31 ± 0.09. Bagnicka et al. (2007) estimated the heritability as 0.13 ± 0.04 using REML and an animal model in Polish goats. Our estimate is within the range of estimates obtained in dairy cattle (0.10 and 0.47) (Grosshans et al., 1997; Ruiz-Sánchez et al., 2007).

4.2. Genetic correlations

The genetic correlations between MILK and FAT (0.72 ± 0.08), and between MILK and PROT (0.87 ± 0.04) (Table 3) were within the range of values estimated by several authors with REML methodology (0.37 to 0.97) in different dairy goat populations (Boichard et al., 1989; Muller et al., 2002; Bagnicka et al., 2004; Bömkes et al., 2004; Delgado et al., 2006).

The genetic correlations between MILK and %FAT (−0.24 ± 0.16), and between MILK and %PROT (−0.30 ± 0.15) were similar to previously estimated values (−0.89 to −0.02) with REML in dairy goats (Boichard et al., 1989; Analla et al., 1996; Ilahi et al., 1998; Muller et al., 2002; Bagnicka et al., 2004; Bömkes et al., 2004). For these traits, the genetic correlations were very close to phenotypic correlations (Table 3).

The genetic correlations between FAT and PROT (0.80 ± 0.06), between FAT and %FAT (0.49 ± 0.13), and between FAT and %PROT (0.10 ± 0.16), were also approximately within the range of values estimated, by several authors (0.69 to 0.96, 0.28 to 0.48, and 0.01 to 0.08, respectively) with REML in different dairy goat populations (Boichard et al., 1989; Muller et al., 2002; Bagnicka et al., 2004; Bömkes et al., 2004; Delgado et al., 2006).

Our genetic correlation between PROT and %PROT (0.21 ± 0.16) was similar to that observed by Muller et al. (2002) using REML and an animal model (0.23). This genetic correlation has been estimated in dairy goats as low as 0.12 by Bagnicka et al. (2004) and as high as 0.59 by Bömkes et al. (2004).

The genetic correlation between %FAT and %PROT (0.50 ± 0.11) was within the range estimated by other authors with REML in different goat populations (0.25 to 0.93) (Boichard et al., 1989; Analla et al., 1996; Ilahi et al., 1998; Brežnik et al., 2000; Muller et al., 2002; Bagnicka et al., 2004; Bömkes et al., 2004).

The genetic correlation between MILK and AFK was favorable (−0.18 ± 0.23). Using MINQUE, Kennedy et al. (1982) estimated this correlation for first lactation dairy goats in a range that varied from −0.05 to −0.06 with data adjusted for age–season of kidding, and from 0.24 to 0.38 for non adjusted data. Nonetheless our estimates should only be compared with those obtained with REML. In dairy cattle, several authors have also estimated favorable genetic correlations between these traits in a range varying from −0.20 to −0.44 (cited by Ruiz-Sánchez et al., 2007).

4.3. Phenotypic correlations

The phenotypic correlations between MILK and FAT (0.85 ± 0.01) and between MILK and PROT (0.95 ± 0.01) were high and positive, in agreement with other authors who have estimated these in a range varying from 0.80 to 0.96 (Boichard et al., 1989; Rabasco et al., 1993; Muller et al., 2002; Bagnicka et al., 2004; Delgado et al., 2006).

The phenotypic correlations between MILK and %PROT (−0.29 ± 0.02), between FAT and PROT (0.88 ± 0.01), between FAT and %FAT (0.30 ± 0.02), between FAT and % PROT (−0.04 ± 0.03), between %FAT and %PROT (0.46 ± 0.02) and between PROT and %PROT (0.02 ± 0.03) were within the ranges estimated by different authors in different goat populations (−0.47 to −0.12, 0.81 to 0.94, 0.29 to 0.45, −0.14 to 0.02, 0.25 to 0.54, and −0.06 to 0.17, respectively) using REML. The phenotypic correlation between PROT and %FAT (−0.09 ± 0.03) was also close to the range estimated in several studies (−0.05 to 0.01) (Boichard et al., 1989; Analla et al., 1996; Ilahi et al., 1998; Muller et al., 2002; Bagnicka et al., 2004; Bömkes et al., 2004; Delgado et al., 2006).

The phenotypic correlation between MILK and AFK was low (0.04 ± 0.04). In an old study, Kennedy et al. (1982) estimated phenotypic correlations between AFK and MILK in dairy goat's fist lactation using MINQUE adjusting data to age–season of kidding (0.00 to 0.04) and without adjusting data (0.21 to 0.22). In dairy cows, the phenotypic correlations have ranged from −0.20 to 0.16 (cited by Ruiz-Sánchez et al., 2007).

4.4. Environmental correlations

Environmental correlations between milk and fat and protein yields were positive (0.90 to 0.97) and negative between milk yield and fat and protein percentages (−0.15 to −0.29) (Table 3). These estimates agree with the findings of Analla et al. (1996) and Muller et al. (2002). Environmental correlations follow the same pattern as phenotypic correlations; these similarities are partially a consequence of the low additive genetic variances in MILK, FAT and PROT. A favorable environmental association exists between AFK and MILK, FAT and PROT (0.13 to 0.16); these estimates show that the environment can strongly influence the expression of these traits. Environmental correlations between AFK and fat and protein percentages were positive but low with high standard errors, leading to inconclusive results; hence new studies to explore this relationship in dairy goats need to be addressed.

4.5. General discussion

The multi-trait repeatability model used in this study allowed us to disentangle, in general terms, the relative influences of additive, genetic and environmental effects on the (co)variation of the main milk production traits in this population. Estimates obtained here are the basis for calculating the selection response to different selection indices, designing breeding strategies, and for the genetic evaluation of this population.

The use of this model (Wiggans and Hubbard, 2001) together with well proven methodology for projecting incomplete lactations to 305-day records in goats (Wiggans and Van Vleck, 1979; Sahlu et al., 2009), confirmed in this study, may lead to an efficient identification of superior animals for breeding purposes in this population. However, repeatability models are not ideal for either the estimation of genetic parameters nor for genetic evaluation purposes, because the assumptions that underlie their use, such as homogeneous correlations between records of different lactations, are rarely fulfilled. This fact has stimulated the development of other options for genetic evaluation of dairy cows and goats such as considered within animal lactations as correlated traits, and also the use of methods that allow for a more flexible use of incomplete data by using random regression test-day methodology (Andonov et al., 2007; Zumbach et al., 2008). Random regression test-day methods are however not free of numerical problems (Meyer, 2005). Moreover, from the practical point of view, implementation of multi-trait selection methodology is more difficult by use of test-day approaches, because of highly parameterized models (Andonov et al., 2007), and the need of better data sets (large and structured) for estimating the required genetic parameters and predicting the genetic values of the animals.

In dairy cattle the correlations between the predicted breeding values obtained using test-day and 305-day methodology have been high (e.g. Schaeffer et al., 2000). An additional consideration regarding the use of test-day vs. total lactation data is the existence of a patent on the test-day method (Mark, 2004). From the practical point of view, there is also the need to maintain a balance between an increased complexity in evaluation procedures and the need for a larger number of parameters to be estimated with the amount of data available, and the resources available for the operation of the breeding program. Therefore, 305-day lactation records together with a multi-trait repeatability model have been adopted for the genetic evaluation in this population.

The use of AFK as a selection criterion seems to be possible because it is heritable; moreover, there are no evidence for genetic antagonisms with MILK, FAT or PROT, although these genetic correlation estimates showed large standard errors (Table 3).

5. Conclusion

This is the first study in Latin America where genetic parameters (heritabilities and correlations) are estimated simultaneously for milk, fat and protein yields, fat and protein content and age at first kidding, in a dairy goat population. The heritabilities estimated in the present study, were within the range of estimates obtained in diverse goat populations worldwide, but our heritabilities for production traits were closer to the lower limit of the range of previous estimates.

Compared to previous Latin American studies, the genetic parameters obtained in our study are probably more precise, because of our larger number of observations and the use of multi-trait animal repeatability models together with AI-REML methodology.

Heritability estimates for AFK and its correlations indicate that selection for lower AFK is possible but also that favorable correlated responses for milk, fat and protein yields may be expected, although estimates of these genetic correlations involving AFK have large standard errors.

The heritabilities obtained show that selection for milk yield and content is possible in this population. Genetic correlations between milk and fat production, and between milk and protein production, were both high and positive, which indicate that favorable genetic correlated response will occur for fat and protein production if the selection was practiced only for milk yield.

The negative genetic correlations between milk yield and fat and protein contents revealed unfavorable associations, which could negatively affect the cheese industry. Those genetic correlations also indicate the need for selecting dairy goats using selection indices that properly weigh these three traits in order to maximize the economic response for the local markets.

The methodology for projecting incomplete records to 305-day records for MILK, FAT and PROT implemented in this study was reliable, with high correlation values between projected and total lactation records (≥0.97) and small biases (≤0.03%) for records with 150 or more DIM.

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