Breeding value for stayability and productive traits of Saanen does obtained by survival analysis versus traditional genetic evaluation

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ABSTRACT

Our objectives were (1) to evaluate how production traits (lactation length, milk production, and protein, lactose, fat and total dry extract yields) affect the permanence of Saanen goats in the herd for longer than 28 months; (2) to estimate genetic parameters for stayability (STAY28) using an Weibull proportional risk model; and (3) to evaluate the genetic associations between both stayability and production through genetic correlations and regression analysis. Two methodologies were utilized in the evaluation: (1) survival analysis using the Weibull animal model; and (2) threshold-linear model through Bayesian approach using Gibbs sampler in two-trait analysis. The data set had 3344 information. Animal effect was included as random in both methodologies. In analyses with Weibull distribution, the contemporary group effect was considered random and in the threshold-linear model was systematic. In the Weibull risk model, production traits were divided in five classes (class 0, class 1, class 2, class 3, and class 4) and the effect of parturition age was significant ($P < 0.05$) for all production variables. For milk production, the highest class (class 4) presented significant effect on STAY28, with reduced culling risk of does from this class in comparison with the other ones. Heritability values for STAY28 were low in both methodologies (between 0.05 and 0.09 across classes for the Weibull model and 0.07 for the threshold-linear model). Genetic correlation estimates between STAY28 and production traits were null in the threshold-linear model. Regression of breeding values of production traits as a function of STAY28 demonstrated a significant relationship between these traits. Even with slower favorable changes, the use of STAY28 for selecting animals with higher breeding values is a viable option to increase the productive lifespan of dairy goats, resulting in animals that are more productive. Therefore, the improvement of productive traits of does brings positive effects in the stay in the herd for longer than 28 months.

1. Introduction

Body performs three main functions: growth, survival, and reproduction (Gadgil and Bossert, 1970; Stearns, 1992). These functions are valorized in distinct ways in production animals. In general, dairy production systems exploit the capacity of producing milk from females and artificially select the most productive ones. However, the intensive search for more producing animals, which is well reported in dairy cows, can negatively affect other important traits related with reproduction, health, and the length that animals stay in herds stayability (Wall et al., 2005; Pérez-Cabal et al., 2006).

Stayability can be expressed by the length of an animal's life until slaughter, death, or culling, in addition to the number of parturitions or production until a certain age (Imbayarwo-Chikosi et al., 2015). Despite being a little discussed trait in the genetic evaluation of dairy goats, stayability has economic merit for reducing the costs of rearing replacement animals (Castañeda-Busto et al., 2014). These costs are high in dairy goat production systems (Borges, 2003), thus the inclusion

of stayability as a selection criterion in dairy goat breeding programs can positively affect the profitability of production systems. Besides, the joint evaluation of this trait with others frequently used in breeding programs of dairy goats can help in the most appropriate selection of animals that must remain productive in the herd. Among the traits of greatest interest in dairy goats are those related to milk production, such as the volume of produced milk, lactation length, and production of fat, protein, lactose and total dry extract in milk.

Survival analysis can contribute to the genetic selection of animals that have increased stayability because it models the non-linear and time-dependent factors that influence productive life and describes a risk function throughout the animal's life (Ducrocq, 2005).

In addition, the evaluation of stayability through genetic evaluations using threshold-linear models has been already applied in dairy cows (Rocha et al., 2018). However, there are limited studies reporting evaluation of Saanen does though survival analysis. These models have as an advantage over survival analysis the possibility of a joint evaluation of two or more traits, making possible the estimation of genetic correlations between traits that require concomitant improvements in the herd.

Our objectives were (1) to evaluate how production traits (lactation length, milk production, and protein, lactose, fat and total dry extract yields) affect the permanence of Saanen goats in the herd for longer than 28 months; (2) to estimate genetic parameters for stayability (STAY28) using an Weibull proportional risk model; and (3) to evaluate the genetic associations between both stayability and production through genetic correlations and regression analysis.

2. Materials and methods

2.1. Data

The dataset had records of 3344 Saanen does from 34 different herds, born between 1995 and early 2015. The official milking control started in 2006 with the first results of genetic evaluations obtained in 2011 (Facó et al., 2011). All evaluated animals had the same chances to be observed and the opportunity to kid at least twice within 28 months of age. Does were kept in the herd at least for two years, in feedlot facilities, and weaned at approximately two months of age. These does were subjected to artificial insemination or controlled natural mating. Institutional animal care and use committee approval was not requested for the present study because data were provided by the Brazilian Agricultural Research Corporation Goats and Sheep (*EMBRAPA Caprinos e Ovinos*, Sobral, CE, Brazil), from an existing database.

Lactation length (LL), milk production until 305 days (MP305), and protein (PROT305), lactose (LAC305), fat (FAT305), and total dry extract (TDE305) yields until 305 days of the first controlled lactation were evaluated. In addition, the ability of a doe not being culled before 28 months of age (STAY28) and to stay in the herd was evaluated. This last trait was considered as stayability trait (Ferreira et al., 2020). The beginning (starting point) was the date of birth and the end was at least two parturitions and at least 28 months of age in the herd of origin (Gonçalves et al., 1997). This period (28 months) was determined based on the lactation curve of dairy goats. Until 28 months of age, the does will be at the maximum starting their third lactation, since the age at first kidding ranges between 12 and 15 months and the kidding interval is 8 months (Sarmento et al., 2003; Gonçalves et al., 2008). Until the third lactation, milk production of the goats remains high, decreasing sharply from the fourth lactation onwards (Cabrita, 2013; Arnal et al., 2018). Censored information was considered in different ways for both Weibull and threshold models. For Weibull models, the risk of a production trait was estimated in relation to two different response variables: fail or censure. For threshold models, censure was considered as a categorical trait, with two factors (0 if censored or 1 if non-censored). This trait was analyzed in two-trait models, with the first trait being the censure, and the second trait, a productive phenotype. Censorship

was considered when does were not successful and were culled from the herd. If this variable was greater than 28 months, we considered that the doe was successful and its registry was not censored (C = 1). On the other hand, does that stayed for less than 28 months in the herd had their registry censored (C = 0), that is, they did not have their observation completed in the study since it was considered the doe would kid in the future. Does sold to other producers were also considered censored; when the exact slaughtering date was missing, the last registered kidding date was utilized as the slaughtering date. Does presenting more than 85 months of age were also censored. The descriptive statistic of the database is presented in Table 1.

Individual records for each productive trait in which the range exceeded 3.5 standard deviations were excluded. Contemporary groups were constituted based on birth year and herd of the does. Those groups with less than three animals and composed of daughters of only one sire were excluded, totaling 161 contemporary groups. The pedigree matrix contained 4738 animals. Data consistency checking and the determination of significant systematic effects in the statistical model for genetic evaluation were performed using the R statistical software (R Development Core Team, 2015).

2.2. Survival analysis

The capability of each of the evaluated productive traits in increasing or reducing the risk of early culling of does with less than 28 months of age was estimated through the Weibull proportional hazard model. Culling risk of a doe in the moment t $[\lambda(t)]$, since the animal was alive before t, was modeled using a Weibull hazard function. The impact of each production variable on STAY28 was evaluated separately, one analysis for each variable, thus six distinct models were adjusted.

The complete model utilized that describes the relation between productive traits and stayability of Saanen does reared in tropical environment can be written as:

$$\lambda(t) = \lambda_0(t)exp\{pr_i + h_j + afl_k + lw_l\}$$

in which $\lambda(t)$ represents the basal hazard function of the doe in time t, defined as a Weibull hazard function by the equation $\lambda(t) = \lambda_\rho(\lambda t)^{\rho-1}$ with scale parameter λ and shape parameter ρ which define the increase or reduction in the risk of culling does from the herd. Thus, values of $\rho > 1$ indicate that culling risk or the hazard function increases along time, ρ

Table 1

Descriptive statistics of data analysis of the ability of Saanen does reared in tropical environments to not being culled from the herd before 28 months of age (STAY28) and their productive traits.

Item	n	$\overline{X}$	SD	CV (%)	Minimum	Maximum
STAY28	3344	–	–	–	0	1
Lactation length (day)	2527	331.57	123.97	37.38	150.00	745.00
Milk production until 305 days (kg)	2545	816.82	312.35	38.24	84.30	1761.17
Protein yield until 305 days (kg)	1836	22.28	8.54	38.33	2.58	50.00
Lactose yield until 305 days (kg)	1680	32.93	12.70	38.57	5.36	72.34
Fat yield until 305 days (kg)	1923	27.00	10.82	40.07	3.19	59.55
Total dry extract yield until 305 days (kg)	1723	89.38	33.89	37.92	9.95	192.96

n = number of observations; $\overline{X}$ = average; SD = standard deviation; CV = coefficient of variation.

< 1 indicate that culling rate decreases with time, and $\rho = 1$ indicate that culling risk is independent of the lifetime in the herd (Percontini et al., 2013). pr_i is the random effect of contemporary group i in which the animal belongs to; h is the fixed effect of the productive trait which the impact on the STAY28 is under evaluation (h = LL, MP305, PROT305, LAC305, FAT305, and TDE305), that is included in the model in $j = 5$ classes. The classes were determined according to the production in 1 (regular), 2 (good), 3 (great), or 4 (excellent), with limits of classes defined by the quartiles individually observed for each trait (Table 2). The class 0 (absent) was included in each trait to refer to does without production. afl_k is the fixed effect of age of the doe at the moment of kidding k and lw_l represents the additive genetic effect for STAY28 of animal l. A priori log-gama distributions were assumed for the random effect of contemporary group and the multivariate normal distribution for the additive genetic effect.

The significance of the fixed effects of age and production covariates was verified using the chi-square test. The effect of classes on the risk rate was estimated through the ratio between the culling risk estimated for each class of this effect and the estimated risk for the reference class. For all productive traits, class 3 (great) was considered intermediary and the reference class for contraposition.

Variances were obtained by the Weibull animal model and heritability of doe survival was estimated considering the equation

$$h^2_{STAY28} = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_c^2 + 1}$$

in which h^2 represents the heritability for the doe STAY28; σ_a^2 is the additive genetic variance; σ_c^2 is the variance of the effect of contemporary group and 1 is the standard environment variance (Jenko et al., 2013).

The global influence of each production trait on STAY28 was evaluated by using likelihood ratio tests, comparing complete model including each productive trait with a reduced model without the inclusion of the trait. All analyses were performed using the Survival Kit software (version 6.12; Mészáros et al., 2013).

The percentage contribution of each productive trait on survival was performed using the adjustment of each studied model, using the -2logL statistic. As the only factor that differentiated the models was the productive trait used as a covariate, we assumed that the changes in -2logL values are due to the contribution of each trait to the overall adjustment of the model. The -2logL values of the models that considered the other traits as covariate were evaluated as proportion of the -2logL value of the best-adjusted model as a way to infer on the contribution of these other traits to the culling risk in relation to the one of greatest contribution to the risk.

2.3. Traditional genetic evaluation

Genetic analysis between production traits and STAY28 were performed using the linear-threshold animal model in two-trait analysis. The general statistical model utilized in the analysis can be described as

$$Y_{ij} = \mu + b_1 AGE_i + CG_j + a_i + e_{ij}$$

in which Y represents the phenotype of animal i, μ is the general constant in all observations; b_1 is the regression coefficient associated with age at the moment of kidding; AGE_i represents the age of the doe at the moment of kidding, included as covariate for productive traits; CG_j is the contemporary group j; a_i is the additive genetic effect of animal i; and e_{ij} is the error associated the each observation, which adjusts for the differences found between the observed and the estimated phenotypes by the model for each animal.

In matrix notation, the general model utilized in the analyses was

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & \varnothing \\ \varnothing & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & \varnothing \\ \varnothing & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Table 2
Description of production traits of Saanen does reared in tropical environments analyzed according to their classification by class.

Covariate	Class 1					Class 2					Class 3					Class 4				
	n	$\overline{X}$	SD	Min	Max	n	$\overline{X}$	SD	Min	Max	n	$\overline{X}$	SD	Min	Max	n	$\overline{X}$	SD	Min	Max
Lactation length (day)	623	203.1	28.22	150.0	240.0	646	278.1	15.82	250.0	304.0	603	335.9	21.85	305.0	379.0	655	502.5	100.51	380.0	745.0
Milk production until 305 days (kg)	623	430.2	95.12	84.3	568.5	643	688.0	64.57	569.5	797.0	643	908.0	65.61	799.5	1029.2	636	1233.6	165.99	1029.9	1761.2
Protein yield until 305 days (kg)	424	11.8	2.63	2.6	15.5	500	18.7	1.75	15.5	21.5	451	24.4	1.75	21.5	27.5	461	33.7	5.22	27.5	50.0
Lactose yield until 305 days (kg)	424	17.7	4.13	5.4	23.5	454	28.2	2.57	24.6	32.5	390	36.8	2.61	32.6	41.5	412	50.2	7.15	41.5	72.3
Fat yield until 305 days (kg)	464	13.9	3.09	3.2	18.5	469	22.1	2.04	18.5	25.5	477	29.4	2.27	25.5	33.5	513	41.2	6.12	35.5	59.6
Total dry extract yield until 305 days (kg)	421	48.1	11.27	10.1	63.4	439	75.4	6.54	63.5	86.5	427	98.6	7.10	87.9	111.3	436	134.3	19.34	111.5	193.0

n = number of observations; $\overline{X}$ = average; SD = standard deviation; Min = minimum value; Max = maximum value.

in which y_h represents the vector with the observations of the trait h ($h = 1$ for STAY28 or $h = 2$ for LL, MP305, PROT305, LAC305, FAT305, and TDE305); X_h is the incidence matrix of the systematic effects of trait h; b_h is the vector with the solution of the systematic effects; Z_h is the incidence matrix of the direct additive genetic random effects for the trait h; a_h is the vector with the solution of the direct additive genetic effect for the trait h; and e_h is the vector of the errors associated with each observation h.

The assumed assumptions for random effects were

$$\begin{bmatrix} a_1 \\ a_2 \\ e_3 \\ e_4 \end{bmatrix} \sim \left\{ \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} A\sigma_{a_1}^2 & A\sigma_{a_1,a_2} & 0 & 0 \\ & A\sigma_{a_2}^2 & 0 & 0 \\ & & I_1\sigma_{e_1}^2 & I_V\sigma_{e_1,e_2} \\ sym & & & I_2\sigma_{e_2}^2 \end{bmatrix} \right\}$$

in which A represents the relationship matrix (4738 animals); $\sigma_{a_h}^2$ is the direct additive genetic variance for the trait h (in which h1 is stay28, and h2 (lactation length, milk production, and protein, lactose, fat and total dry extract yields); $\sigma_{e_h}^2$ is the residual variance for trait h; $\sigma_{ah,ah'}$ is the covariance between the effects h and h'; and I_1 and I_2 are identity matrices of equal orders to the numbers of observations of the trait h.

In the threshold model, we consider that the subjacent scale presents continuous normal distribution, represented as $U|\theta \sim N(W\theta, \ I\sigma_e^2)$, in which U is the vector of the base order scale r; $\theta' = (\beta', a')$ is the vector of the location parameters of order s, with β' defined as systematic effects and order s, and a' as direct additive genetic random effects; W is the known incidence matrix of order r by s; I is the identity matrix of order r; and σ_e^2 is the residual variance. When it is considered that the variable in the subjacent distribution is not observable, the $\sigma_e^2 = 1$ parameterization is adopted to identify in the likelihood function (Sorensen and Gianola, 2002). Such assumption is standard in analysis for categorical data in the threshold model. We considered, a priori, that β has uniform distribution that reflects vague prior knowledge about this vector. This kind of likelihood distribution indicates the same likelihood of occurrence in each of the possible values of the variable. It is considered that the remaining components have inverted Wishart distribution, a standard adopted in the THRGIBBS1F90 software (Misztal et al., 2002).

Samples of conditional distributions were obtained by Gibbs sampler using the THRGIBBS1F90 software (Misztal et al., 2002). We considered Gibbs chains of 1,100,000 samples with initial discard of 100,000 samples, with a sampling of component values of covariance at each 100 cycles. The size of the chain was defined in preliminary analyses, according to the methods described by Raftery and Lewis (1992), available in the Bayesian Output Analysis statistical package (Smith, 2005) of the R software (R Development Core Team, 2015). Convergence of chains was verified by the criterion proposed by Geweke (1992) and through visual graphic inspection of samples sampled at each iteration. From each analysis, 10,000 samples were obtained for each trait. The samples of each trait were grouped, totalizing 110,000 samples, and the a posteriori means and high posterior density intervals with 90 % of samples (HPD90) were estimated.

Genetic trends of the direct effects for all evaluated traits were calculated through linear regression of the estimated breeding values (EBV) as functions of birth year of the animals, utilizing the R software (R Development Core Team, 2015). The trends were realized to animals that had phenotypical information. Regression coefficients of the genetic trends were tested using the F statistics.

2.3.1. Regression of estimated breeding values

Estimated breeding values of direct additive effects for STAY28 was regressed as a function of EBV from the direct effects of animal for the evaluated productive traits. The regression of all breeding values of animals that had phenotypic information for both traits (STAY28 and

productive ones) were considered. The EBV in the traditional genetic evaluation were obtained considering the productive traits as continuous. To highlight the relationship between EBV of productive traits and culling risk estimated for does (while categorical measures) in the survival analysis, the different classes were sorted using different colors in the visual demonstration of the EBV regressed as a function of STAY28. Breeding values regressed as a function of the breeding value for the other trait allow observing the influence that each trait has on the other.

3. Results

3.1. Weibull genetic evaluation

When considering STAY28 as indicative of survival, 1344 does had censored registry, which represents 40.2 % of the dataset. There was an effect ($P \le 0.05$) of MP305 and moment of kidding inserted in the model for STAY28. The trait FAT305 was the second greatest covariate contributing to the culling risk followed by PROT305, TDE305, LL, and LAC305 which presented the same contribution on the culling risk for STAY28.

A significant difference between class of missing data (animals without milk production information) and reference class (class 3) for individual LL and MP305 was confirmed, as well as a difference between class 4 and the reference class for all variables, except LL which demonstrated having the same culling risks independently of the class (Table 3). For MP305, PROT305, LAC305, FAT305, and TDE305, we observed that lower production classes (classes 1 and 2) did not differ from the reference class to increase or decrease the culling risk (Table 3). For class 4, does had less culling risk compared to the reference class for the analyzed production covariates.

Variances and heritabilities for STAY28 were low and similar when evaluated as function of the different productive traits for STAY28 (Table 4).

3.2. Traditional genetic evaluation

The *a posteriori* averages limits of the highest posterior density intervals (HPD) with 90 % of the samples (between parenthesis) of the variances for each evaluated trait by the linear-threshold model (Table 1S) demonstrated low value [0.08 (0.00; 0.20)] for additive genetic variance of STAY28. Heritabilities obtained through this methodology for MP305, PROT305, LAC305, FAT305, and TDE305 had values ranging from 0.23 and 0.29. For LL, we observed low heritability of 0.06 (0.01; 0.11). The genetic, phenotypic, and environmental correlations between STAY28 and the evaluated productive traits did not differ from zero, as the HPD90 passed through the zero (Table 5).

For productive traits, the coefficients of genetic traits of EBV along

Table 3
Relative risk of culling considering different production traits (reference: Class 3) of Saanen does reared in tropical environments.

Class	Productive trait					
	Lactation length	Milk production until 305 days	Protein yield until 305 days	Lactose yield until 305 days	Fat yield until 305 days	Total dry extract yield until 305 days
1	0.92	1.04	0.86	0.88	1.06	0.93
2	1.05	0.97	0.86	0.80	0.85	0.86
3	1.00	1.00	1.00	1.00	1.00	1.00
4	0.82	0.70*	0.68*	0.72*	0.70*	0.70*
Missing data	1.87*	1.82*	1.03	1.10	1.20	1.01

Values with an asterisk (*) are different (P < 0.05) by qui-square test. Only classes with a minimum of 50 non-censored failures are presented.

Table 4
Genetic parameters for the ability of not being culled from the herd before 28 months of age (STAY28) of Saanen does reared in tropical environments, evaluated in two-trait analysis with productive traits obtained by the Weibull model.

Parameter	Trait					
	Lactation length	Milk production until 305 days	Protein yield until 305 days	Lactose yield until 305 days	Fat yield until 305 days	Total dry extract yield until 305 days
σ_a^2	0.18 (0.01)	0.16 (0.02)	0.14 (0.04)	0.10 (0.02)	0.17 (0.01)	0.12 (0.05)
σ_c^2	1,18 (0.07)	0.69 (0.07)	0.96 (0.06)	0.75 (0.08)	0.86 (0.08)	0.75 (0.07)
h^2	0.08	0.09	0.07	0.05	0.08	0.06

σ_a^2 = genetic variance of the animal; σ_c^2 = variance of the contemporary group effect; h^2 = heritability.

Table 5
A posteriori means (lower and upper limits of the highest posterior density interval with 90 % of samples) of heritabilities (h^2) and genetic (r_g), phenotypic (r_p), and residual (r_e) correlations between the ability of Saanen does reared in tropical environments not being culled from the herd before 28 months of age (STAY28) and their productive traits.

Trait	Genetic parameter			
	h^2	$r_{g_{1n}}$	$r_{p_{1n}}$	$r_{e_{1n}}$
STAY28	0.07 (0.00; 0.17)			
Lactation length	0.06 (0.01; 0.11)	−0.11 (-1.00; 0.91)	−0.06 (-0.15; 0.03)	−0.06 (-0.19; 0.05)
Milk production until 305 days (kg)	0.23 (0.16; 0.30)	0.26 (-0.55; 1.00)	0.07 (-0.02; 0.16)	0.04 (-0.11; 0.17)
Protein yield until 305 days (kg)	0.29 (0.19; 0.38)	0.11 (-0.76; 1.00)	0.00 (-0.10; 0.11)	−0.02 (-0.20; 0.17)
Lactose yield until 305 days (kg)	0.29 (0.19; 0.40)	0.11 (-0.76; 1.00)	0.03 (-0.08; 0.15)	0.03 (-0.15; 0.22)
Fat yield until 305 days (kg)	0.26 (0.17; 0.35)	0,01 (-1,00; 0,78)	0,06 (-0,05; 0,15)	0.06 (-0.10; 0.22)
Total dry extract yield until 305 days (kg)	0.29 (0.19; 0.40)	0,17 (-0,71; 1,00)	0,01 (-0,09; 0,13)	−0.01 (-0.19; 0.18)

the years were significant ($P < 0.0001$) and indicated positive changes of 2.59 kg/year, 0.07 kg/year, 0.008 kg/year, and 0.22 kg/year for MP305, PROT305, LAC305, FAT305, and TDE305, respectively. However, for LL, the change was low (0.06 days/year) and significant (Fig. 1S).

Dividing the slope coefficients of the regression equations (Fig. 1S) by the genetic standard deviations of each trait, changes of less than 1.00 % were observed in the traits. The changes were of 0.02 % in MP305, PROT305, and LAC305 and 0.01 % in TDE305 throughout the evaluated years. Discrete modifications of LL ad FAT305 occurred in the evaluated period, both with 0.002 % of change per year. Genetic trends of EBV of the direct effects along birth years for STAY28 were positive and significant ($P < 0.0001$; Fig. 2S).

Although the genetic correlations between STAY28 and productive traits were not different than zero, when regressing the EBV of STAY28 in function of the EBV of the productive traits, we observed that the regressions are significant ($P < 0.0001$). Modifications in the STAY28 according to the productive traits were detected. For all productive traits, except LL, the increases of these traits implied in increase of STAY28 (Fig. 1). The average change in the EBV of STAY28 lead to an additional change on the direct EBV of production traits. The increase of 1 kg on the EBV of LAC305 increased the STAY in 0.004 units (Fig. 1); similar interpretations could be performed for PROT305, FAT305, and TDE305. The representation of the classes in the graph demonstrated separation among them, that is, the does are grouped in different classes. When the EBV approximate the value zero, initiates a mixture between

class 1 with 2 and 3 with 4, but with the advance of the breeding value of the does in the graph, the separation of classes is resumed.

4. Discussion

4.1. Weibull genetic evaluation

Productive traits influence the extension of the female's life in the herd (Roxström et al., 2003; Melendez and Pinedo, 2007; Pritchard et al., 2013; Castañeda-Busto et al., 2014; Kern et al., 2016). It is noteworthy that the phenotypic averages of traits evaluated in this study are within the ones reported in the literature (Castañeda-Busto et al., 2014; Lôbo et al., 2017).

After the beginning of the official milking control (occurred in 2006) and with the first results of genetic evaluations in 2011 (Facó et al., 2011), identification and selection of animals in a precise manner were possible based on their breeding values for milk production and quality. In Brazil, producers are still paid only based on quantity and not by quality, thus the goal of selection is focused on milk production and days in lactation, in addition to age at first kidding. However, this situation tends to change as the market starts paying for total solids and low somatic cell counts (Facó et al., 2011).

The MP305 was the covariate that most affected the STAY28 of does, which is explained by the intensive selection that has been practiced directly for higher volume of milk produced, since it is the most economically important trait (Facó et al., 2014). The results of the official milking control demonstrate that there was also an increase in protein and fat contents in milk over the years from 2002 to 2014, with the highest values for milk components tending to be observed in the first lactation (Lôbo et al., 2017).

The relative risk of culling was higher for the class of animals without MP305 information. Does belonging to the class 4, that is, the ones that had higher milk production (1200 l in the lactation), had the lower culling risk from herds. Sewalem et al. (2005) and Ducrocq (2005), evaluating Holstein cows in Canada and France, respectively, reported opposite results in dairy cattle since selection for high milk production is the major factor that affects longevity of cows in the herd (Ducrocq, 2005; Jenko et al., 2013; Pritchard et al., 2013; Kern et al., 2016).

Animals with lower productive performance classified in the lower classes (1 and 2) had the same culling risk compared to the animals with intermediate performance (class 3). The decisions that each producer makes regarding selection may or may not cause more or less culling of less productive animals. In some situations such as when quality replacing does is not available or when genetic material for maintaining the herd is lacking (due to the restriction of importing live animals) could lead to retaining healthy does for longer, regardless of milk production. In dairy goat herds, there is always a search for high milk producing animals; thus, considering the relationship between production traits with stayability is important to obtain profitability.

The Weibull parameter ρ describes the shape of the baseline hazard function: when it is greater than 1, the hazard function increases with time and the higher the parameter, the more pronounced the increase. Class 3 was utilized as reference because it is an intermediate value for
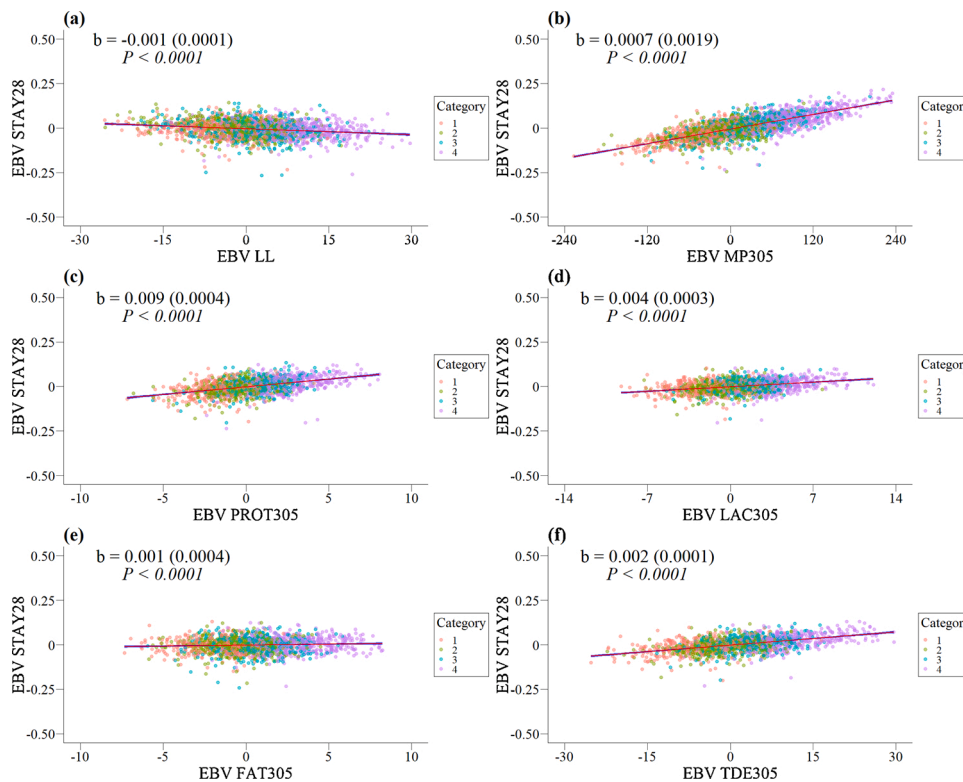
Fig. 1. Variation of estimated breeding values (EBV) of the direct effect of stayability at 28 months of age (STAY28) as function of EBV of the direct effect of production traits. (a) LL = length of lactation; (b) MP305 = milk production until 305 days, (c) PROT305 = protein yield until 305 days; (d) LAC305 = lactose yield until 305 days; (e) FAT305 = fat yield until 305 days; (f) TDE305 = total dry extract yield until 305 days. Linear regression (red line) and confidence intervals (blue line); b = angular coefficient (standard error) and level of significance are presented in the respective figures. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

production, allowing a comparison between this class with the others. Differences between class 3 and class 4 were demonstrated in the evaluated traits. Does with no milk production information were classified as 0 or having missing data; these animals were the ones with higher relative risks of being culled from the herd. The extreme classes (0 and 4) were the ones that showed expressive results, even though no differences were found compared with intermediate classes, demonstrating that there is a diversity of environments that herds are subjected, in addition to a variation in the genetic potential. It is noteworthy to mention that the data set utilized herein is an official dairy goat milking control with more than 10 years of data collection in Brazil.

Heritability values were low for STAY28 when there was an influence of production traits on the Weibull animal model. Nevertheless, reports in the literature indicate that the selection response can be achieved if there is selection pressure for this trait (Yazdi et al., 2002). Thus, it is observed that productive traits affects heritability of STAY28 and its evaluation becomes important to obtain more animals with a longer productive life, suggesting that the phenotypic value for the production traits is a good indicator of the animal's breeding value. Consequently, daughters of these animals will be able to stay longer in the herd.

4.2. Traditional genetic evaluation

The genetic evaluation of dairy goats established in 2009 has demonstrated economic relevance, as the animals are selected according to their genetic merits, excluding the influences, for instance, of preferential treatment with better feeding for high milk producing animals (Facó et al., 2011). Heritability obtained for STAY28 in the present study (0.07) was similar to that obtained in the United States for dairy goats at 24 (0.08) and 36 (0.09) months of age (Valencia-Posadas et al., 2017).

Low and similar heritability for different species and length of stay are reported in the literature (Kern et al., 2015; Rocha et al., 2018). With that, we can conclude that stayability is a trait that has different environmental factors and, or non-genetic ones that influence it. Possibly, traits genetically associated with stayability and presenting higher

heritability values should respond better to genetic selection.

Stayability of goats is a trait that is not commonly evaluated, limiting the available information on the productive life of animals (Torrero, 2010). High and positive correlations were reported between stayability and milk production in dairy goats in the USA (Valencia-Posadas et al., 2017). Castañeda-Busto et al. (2014), evaluating the productive life of goats until 72 months of age, reported moderate genetic and phenotypic correlations. Considering this observation, when selecting animal for other productive trait, improvements in the length of productive life will occur. If the doe have higher milk and fat production, it will stay longer in the herd (Castañeda-Busto et al., 2014). In dairy cows, Sewalem et al. (2004) proved that the greater the milk and protein productions, the greater the stayability of the cow in the herd. However, in the present study, the genetic and phenotypical correlations between STAY28 and productive traits were not different from zero, indicating that these traits are not correlated.

When regressing the EBV of STAY28 as a function of EBV of productive traits, it is possible to prove the existing relationship between those traits that are not detected by genetic correlation. The use of productive information from does is an option that permits an indirect improvement in the survival of milk-producing goats and, therefore, are effective predictors of stayability. The regression coefficients of direct genetic effects were significant for all productive traits, signaling the presence of genetic compensations between survival and production. The selection to increase the genetic effects of STAY28 is beneficial to enhance production traits. It was highlighted that selection to extend LL affects the animal's permanence in the herd, due to the decreasing pattern of breeding value of animals when the lactation days are extended. Thus, identifying the causes that compromise reproductive efficiency will help the animal stay in the herd and control the effects such as the prolongation of LL, which impairs the increase of the average of does stayability over the years.

The phenotypic production information presented in this study are from commercial properties that, in partnership with Embrapa and the Association of Goats and Sheep Breeders of Minas Gerais (ACCOMIG/Caprileite), participate in the official dairy control of goats in Brazil.

Selection during these years has been based on increasing milk production per doe in the herd. In this scenario, the improvement in MP305 followed by TDE305, LAC305, PROT305, and FAT305 showed a greater increase in the genetic trend in relation to other production traits, because of direct selection. The variability observed for milk components was important and should be considered for the development of the dairy goat industry in Brazil, since currently producers, cooperatives and industries have been looking for alternatives, such as the development of dairy products from goat milk.

A slight increase in the trend of breeding values for STAY28 was confirmed, even though there was no direct selection. Thus, it is feasible to select for stayability because we can have in the same animal the best STAY28 without impairing or ignoring other production traits. In addition, when an animal stays longer in the herd is because it reached superior performance both in production and in the ability to leave progenies on the production system. If a doe stayed more than 28 months in the herd it was because she reached at least two births and generated about 3.2 kids on the farm.

4.3. Traditional genetic evaluation vs. Weibull genetic evaluation

The implication of different models to give a bigger picture of the impact of productive phenotypes on survival of goats will be scrutinized in this topic. The use of animal model permits precisely estimate the genetic and non-genetic effects that affect multiple traits (Henderson, 1973). To obtain adequate estimates that allow to conclude the results, the animal model of this study was based on the direct genetic and non-genetic (age and contemporary groups) effects of the animal.

The use of two-trait analysis in linear-threshold model enables to evaluate the genetic factors that affect continuous and categorical traits and their associations. This provides a more consistent assessment of the effects that affect the results, suggesting that through selection programs expressive benefits are evidenced for genetic improvement of herds.

Culling of animals has to be a balance between milk production, births and genetic progress. The genetic effects were responsible for the differences when the animals were divided into classes, making the separation clear, in which the animals that have the highest values for production traits are in the highest classes and also have the highest breeding values.

The opposite effect occurred for LL, as the greater the extent of lactation and also the categorical classification of the animal, the lower its breeding value for stayability, which demonstrates that long lactation durations are not advantageous for female survival. Animals classified in the intermediate classes (2 and 3) were together in the graph and close to does belonging to class 1, noting that genetic improvements for LL occur in animals that are moderately selected. This statement was possible because of the performance of genetic evaluation, which allowed the detection of traits that can also increase STAY28 when used as a selection criterion.

It is common the increase of LL in order to alleviate reproductive problems that impair pregnancy in does, even though their milk production is low and a negative pregnancy diagnosis; therefore, this management reflects in an increase of kidding interval and reduces the number of goats that will be lactating in the next season (López-Gatius et al., 2002). Other issues may indirectly lead to an extension of lactation, such as increased blood concentrations of ketone bodies and non-esterified fatty acids after parturition, associated with metabolic problems of ketosis (Rodrigues et al., 2007), in addition to management problems in the farm such as low detection of estrus (Morais et al., 2008). Moreover, body condition score is another factor that affects the potential of a doe to cycle again after kidding, thus influencing the LL, as hormonal changes interfere with follicular maturation and ovulation, compromising fertility and embryo quality (Rodrigues et al., 2007).

Keeping animals with very prolonged LL impairs STAY28. The increase of LL is a costly investment, as an increase in energy requirements for milk production is observed, affecting reproduction and decreasing the number of kids per doe. Thus, a small increase in production can be compensated by combining the selection adjustment with an adjustment of the proportion of the LL (Douhard et al., 2014).

Some animals that were classified in classes 2 and 3 for milk production presented a similar breeding value to animals belonging to class 4. Selection of animals with best values or classified in higher classes for these traits could be efficient in the indirect improvement of their productive life. However, it is necessary the animal be raised in a favorable environment to allow the expression of its production potential so that it is not undersized. This fact validates that the use of phenotypic information is effective for improving the stayability of females in the herd. However, wrong choices of sires may occur, indicating the selection of animals should be based on their breeding value.

Survival analysis permitted to know the culling risk of a doe. However, differences only between animals belonging to class 4 and those without production information were detected and significant in the model. The traditional genetic evaluation through two-trait analysis enabled to understand the structure of variance and covariance that influence stayability and productive traits. In addition, this approach favored the estimation of genetic trend and proved that the animal selection process has been effective. Besides, the most relevant point of the traditional genetic evaluation is that permitted to know, through regression analysis, how the breeding values of two traits behave and to adequately quantify the influence of the production traits in STAY28. The effects possibly masked by the correlation analysis can be checked by the regression analysis, which also verifies the relationship between two variables. It can be inferred from this regression that animals with the highest genetic values for STAY28 also have the highest genetic values for the direct effect of production characteristics.

Improving the productive life of dairy goats also improves production efficiency, decreasing replacement costs, exploring the greatest milk production potential from mature does, while also allowing producers to choose which animals should be retained and raised in the system. The concern with animal health and welfare also plays an important role in longevity goals; as shown in the results, high-production animals remain longer in the herd and more attention should be given, so that the selection only for high volumes of milk produced do not affect animal health.

5. Conclusions

Stayability for longer than 28 months of age is efficient to early select for stay in the herd of dairy goats even with slower favorable changes because of lower heritability values. It is a valuable trait when culling decision-making is necessary instead of using traits that are expressed late in does; even with low heritability values, selection could have its benefit increased. Thus, producers can use STAY28 as a criterion to select more efficient producing females and thus keeping these animals in the herd. Milk production traits affect STAY28 in Saanen does reared in tropical environments, thereby producers can select does with high production of milk and its constituents since these does stay longer in the herd, or at least for 28 months of age, kidding twice, since selection is efficient to increase jointly the averages of production traits. However, selection considering only the volume of milk produced deserves attention because it is favoring animals more and more productive with larger body structures for the production system. Therefore, the balance between production, genetics and animal health must be prioritized.

Declaration of Competing Interest

The authors report no declarations of interest.

utilized in the present study and the Association of Goats and Sheep Breeders of Minas Gerais ('Associação dos Criadores de Caprinos e Ovinos de Minas Gerais'; ACCOMIG/Caprileite). The authors also declare that this research did not receive any specific funding.

Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.smallrumres.2021.10 6573.

References

Arnal, M., Robert-Granié, C., Larroque, H., 2018. Diversity of dairy goat lactation curves in France. J. Dairy Sci. 101, 11040–11051. https://doi.org/10.3168/jds.2018-14980.

Borges, C.H.P., 2003. Goat milk production costs in the southeastern region of Brazil. In: II Simpósio Internacional sobre Caprinos e Ovinos de Corte, I Simpósio Internacional sobre o Agronegócio da Caprinocultura Leiteira. João Pessoa, Brazil.

Cabrita, A.M.F.L., 2013. Curvas de lactação em cabras Saanen, Alpinas e cruzadas. Master's Dissertation. Universidade Técnica de Lisboa, Lisboa, Portugal. https://www.repository.utl.pt/bitstream/10400.5/6399/1/Tese_curvasdelactacao_AnaMartaCabrita.pdf.

Castañeda-Busto, V.J., Montaldo, H.H., Torres-Hernandez, G., Pérez-Elizalde, S., Valencia-Posadas, M., Hernández-Mendo, O., Shepard, L., 2014. Estimation of genetic parameters for productive life, reproduction, and milk-production traits in US dairy goats. J. Dairy Sci. 97, 2462–2473. https://doi.org/10.3168/jds.2013-7503.

Douhard, F., Tichit, M., Amer, P.R., Friggens, N.C., 2014. Synergy between selection for production and longevity and the use of extended lactation: insights from a resource allocation model in a dairy goat herd. J. Anim. Sci. 92, 5251–5266. https://doi.org/10.2527/jas.2014-7852.

Ducrocq, V., 2005. An improved model for the French genetic evaluation of dairy bulls on length of productive life of their daughters. Anim. Sci. 80, 249–256. https://doi.org/10.1079/ASC41720249.

Facó, O., Lôbo, R.N.B., Gouveia, A.M.G., M.P.S.L.M.P. Guimarães, Fonseca, J.F., Santos, T.N.M., Silva, M.A.A., Villela, L.C.V., 2011. Breeding plan for commercial dairy goat production systems in southern Brazil. Small Rumin. Res. 98, 164–169. https://doi.org/10.1016/j.smallrumres.2011.03.034.

Facó, O., Lôbo, R.N.B., Fonseca, J.F., Lôbo, A.M.B.O., Verneque, R.S., Pimentel, C.M.M., Paiva, S.R., 2014. Programa de Melhoramento Genético de Caprinos Leiteiros – Capragene®; sumário de avaliação genética – Ano 2014 – raça Saanen. Embrapa Caprinos e Ovinos, Sobral, Brazil, 30 pp. https://ainfo.cnptia.embrapa.br/digital/bitstream/item/147201/1/CNPC-2014-Sumario.pdf (Accessed 21 September 2018).

Ferreira, T.A., Martins, P.G.M.A., Gouveia, G.C., Abreu, L.R.A., Gouveia, A.M.G., Facó, O., Colosimo, E.A., Furusho-Garcia, I.F., Pereira, I.G., 2020. Proportional hazard models associated with the survival of dairy goats reared in a tropical environment. Small Rumin. Res. 184, 106063. https://doi.org/10.1016/j.smallrumres.2020.106063.

Gadgil, M., Bossert, W.H., 1970. Life historical consequences of natural selection. Am. Nat. 104, 1–24.

Geweke, J., 1992. Evaluating the accuracy of sampling-based approaches to the calculation of posterior moments. In: Bernardo, J.M., Berger, J.O., Dawid, A.P., Smith, A.F.M. (Eds.), Bayesian Statistics 4. Clarendon Press, Oxford, pp. 169–193.

Gonçalves, H.C., Silva, M.A., Ramos, A.A., Espeschit, C.J.B., Wechsler, F.S., 1997. Fatores genéticos e de meio no intervalo de partos de caprinos leiteiros. R. Bras. Zootec. 26, 905–913.

Gonçalves, A.L., Lana, R.P., Vieira, R.A.M., Henrique, D.S., Mancio, A.B., Pereira, J.C., 2008. Avaliação de sistemas de produção de caprinos leiteiros na região sudeste do Brasil. R. Bras. Zootec. 37, 366–376. https://doi.org/10.1590/S1516-35982008000200025.

Henderson, C.R., 1973. Sire evaluation and genetic trends. J. Anim. Sci. 10–41. https://doi.org/10.1093/ansci/1973.Symposium.10.

Imbayarwo-Chikosi, V.E., Dzama, K., Halimani, T.E., van Wyk, J.B., Maiwashe, A., Banga, C.B., 2015. Genetic prediction models and heritability estimates for functional longevity in dairy cattle. S. Afr. J. Anim. Sci. 45, 106–121. https://doi.org/10.4314/sajas.v45i2.1.

Jenko, J., Ducrocq, V., Kovač, M., 2013. Comparison of piecewise Weibull baseline survival models for estimation of true and functional longevity in Brown cattle raised in small herds. Animal 7, 1583–1591. https://doi.org/10.1017/s1751731113001055.

Kern, E.L., Cobuci, J.A., Costa, C.N., McManus, C.M., Braccini Neto, J., 2015. Genetic association between longevity and linear type traits of Holstein cows. Sci. Agric. 72, 203–209. https://doi.org/10.1590/0103-9016-2014-0007.

Kern, E.L., Cobuci, J.A., Costa, C.N., Ducrocq, V., 2016. Survival analysis of productive life in Brazilian Holstein using a piece wise Weibull proportional hazard model. Livest. Sci. 185, 89–96. https://doi.org/10.1016/j.livsci.2016.01.019.

Lôbo, A.M.B.O., Lôbo, R.N.B., Facó, O., Souza, V., Alves, A.A.C., Costa, A.C., Albuquerque, M.A.M., 2017. Characterization of milk production and composition of four exotic goat breeds in Brazil. Small Rumin. Res. 153, 9–16. https://doi.org/10.1016/j.smallrumres.2017.05.005.

López-Gatius, F., Santolaria, P., Yániz, J., Rutllant, J., López-Béjar, M., 2002. Factors affecting pregnancy loss from gestation day 38 to 90 in lactating dairy cows from a single herd. Theriogenology 57, 1251–1261. https://doi.org/10.1016/S0093-691X(01)00715-4.

Melendez, P., Pinedo, P., 2007. The Association between reproductive performance and milk yield in Chilean Holstein cattle. J. Dairy Sci. 90, 184–192. https://doi.org/10.3168/jds.S0022-0302(07)72619-X.

Mészáros, G., Sölkner, J., Ducrocq, V., 2013. The Survival Kit: software to analyze survival data including possibly correlated random effects. Comput. Meth. Prog. Bio. 110, 503–510. https://doi.org/10.1016/j.cmpb.2013.01.010.

Misztal, I., Tsuruta, S., Strabel, T., Auvray, B., Druet, T., Lee, D.H., 2002. BLUPF90 and related programs (BGF90). In: Proceedings of the 7th World Congress on Genetics Applied to Livestock Production. Montpellier, France.

Morais, D.A.E.F., Lima, F.R.G., Vasconcelos, A.M., Lima, P.O., Morais, J.H.G., 2008. Manifestação de estro, fertilidade e desempenho reprodutivo de cabras leiteiras de diferentes raças em ambiente quente. Caatinga 21, 62–67.

Percontini, A., Blas, B., Cordeiro, G.M., 2013. The beta Weibull Poisson distribution. Chil. J. Stat. 4, 3–26.

Pérez-Cabal, M.A., García, C., González-Recio, O., Alenda, R., 2006. Genetic and phenotypic relationships among locomotion type traits, profit, production, longevity, and fertility in Spanish dairy cows. J. Dairy Sci. 89, 1776–1783. https://doi.org/10.3168/jds.s0022-0302(06)72246-9.

Pritchard, T., Coffey, M., Mrode, R., Wall, E., 2013. Understanding the genetics of survival in dairy cows. J. Dairy Sci. 96, 3296–3309. https://doi.org/10.3168/jds.2012-6219.

R Development Core Team, 2015. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria.

Raftery, A.E., Lewis, S.M., 1992. One long run with diagnostics: Implementation strategies for Markov chain Monte Carlo. Stat. Sci. 7, 493–497. https://doi.org/10.1214/ss/1177011143.

Rocha, G.M.F., Cobuci, J.A., Costa, C.N., Abreu, L.R.A., Mota, L.F.M., Pires, A.V., Villela, S.D.J., Martins, P.G.M.A., 2018. Genetic association between stayability, and productive and reproductive traits in Holstein cows. Anim. Prod. Sci. 58, 1788–1793. https://doi.org/10.1071/AN16563.

Rodrigues, C.A.F., Rodrigues, M.T., Branco, R.H., Carvalho, G.R., Torres, R.A., Torres Filho, R.A., 2007. Avaliação do consumo e de metabólitos plasmáticos de cabras gestantes com duas condições corporais alimentadas com dietas formuladas com diferentes níveis de energia. R. Bras. Zootec. 36, 945–952. https://doi.org/10.1590/S1516-35982007000400026.

Roxström, A., Ducrocq, V., Strandberg, E., 2003. Survival analysis of longevity in dairy cattle on a lactation basis. Genet. Sel. Evol. 35, 305–318. https://doi.org/10.1186/1297-9686-35-3-305.

Sarmento, J.L.R., Pimenta Filho, E.C., Ribeiro, M.N., Araújo, C.V., Breda, F.C., Pires, A.V., Torres Filho, R.A., Torres, R.A., 2003. Fatores genéticos e de ambiente sobre o intervalo de partos de cabras leiteiras no semi-árido nordestino. R. Bras. Zootec. 32, 875–879. https://doi.org/10.1590/S1516-35982003000400012.

Sewalem, A., Kistemaker, G.J., Miglior, F., Van Doormaal, B.J., 2004. Analysis of the relationship between type traits and functional survival in Canadian Holsteins using a Weibull proportional hazards model. J. Dairy Sci. 87, 3938–3946. https://doi.org/10.3168/jds.s0022-0302(04)73533-x.

Sewalem, A., Kistemaker, G.J., Ducrocq, V., Van Doormaal, B.J., 2005. Genetic analysis of herd life in Canadian dairy cattle on a lactation basis using a Weibull proportional hazards model. J. Dairy Sci. 88, 368–375. https://doi.org/10.3168/jds.S0022-0302(05)72696-5.

Smith, B.J., 2005. Bayesian Output Analysis Program (BOA) Version 1.1 User`s Manual. University of Iowa, Iowa City.

Sorensen, D., Gianola, D., 2002. Likelihood, Bayesian, and MCMC Methods in Quantitative Genetics, 2nd ed. Springer, New York.

Stearns, S.C., 1992. The Evolution of Life Histories. Oxford Univ. Press, Oxford.

Torrero, G.Y., 2010. Estimación de covarianzas para características de longevidad y producción en cabras. Master's Thesis. Universidad de Guanajuato, Irapuato, Mexico.

Valencia-Posadas, M., Torrero-Garza, Y., Torres-Vázquez, J.A., Ángel-Sahagún, C.A., Gutiérrez-Chávez, A.J., Shepard, L., Montaldo, H.H., 2017. Genetic parameters for functional stayability to 24 and 36 months of age and first lactation milk yield in dairy goats. Small Rumin. Res. 149, 209–213. https://doi.org/10.1016/j.smallrumres.2017.02.010.

Wall, E., White, I.M.S., Coffey, M.P., Brotherstone, S., 2005. The relationship between fertility, rump angle, and selected type information in Holstein-Friesian cows. J. Dairy Sci. 88, 1521–1528. https://doi.org/10.3168/jds.s0022-0302(05)72821-6.

Yazdi, M.H., Visscher, P.M., Ducrocq, V., Thompson, R., 2002. Heritability, reliability of genetic evaluations and response to selection in proportional hazard models. J. Dairy Sci. 85, 1563–1577. https://doi.org/10.3168/jds.s0022-0302(02)74226-4.