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Bayesian censored models for genetic analysis of age at first kidding in Murciano-Granadina goats

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Abstract The purpose of the present study was to investigate the effect of censoring in the genetic analysis of age at first kidding (AFK) in the Murciano-Granadina goat breed. The dataset included information on first-kidding records collected from 2016 to 2024 from a private dairy farm of the Murciano-Granadina goat breed, in Ghale-Ganj city, located in the southern area of Kerman province, Iran. Five animal models, including linear model (LM), penalty model (PM), modified penalty model (MPM), linear-threshold model (LTM), and modified linear-threshold model (MLTM), were applied for genetic analysis of AFK. The predictive ability of the models was assessed by cross-validation via mean square error of prediction (MSE) and Pearson's correlation coefficient between observed and predicted values ($r(y, \hat{y})$). The lowest MSE and highest $r(y, \hat{y})$ were obtained under MLTM, indicating the adequacy of MLTM for genetic analysis of AFK, including censored records. The Spearman's rank correlations between predicted breeding values of animals under LM and other censorship handling investigated models for all and 1% top-ranked animals were low and statistically non-significant ($p > 0.05$). By considering the models that contained censoring scenarios, all Spearman's rank correlations among the models were positive and statistically significant ($p < 0.01$), ranging from 0.56 (LTM-MPM) to 0.96 (LTM-MLTM) when all animals were considered and from 0.75 (LTM-MPM) to 0.96 (LTM-MLTM and PM-MLTM) when 1% top-ranked animals were considered. The averages for accuracy of the predicted breeding values of animals were 0.43, 0.49, 0.47, 0.47, and 0.49 under LM, PM, MPM, LTM, and MLTM, respectively, implying that the accuracy of the model under uncensored data is partly lower than the model accuracies under censoring scenarios. Posterior means for heritability estimates of AFK were 0.20 ± 0.03 , 0.23 ± 0.02 , 0.19 ± 0.02 , 0.18 ± 0.03 , and 0.18 ± 0.02 under LM, PM, MPM, LTM, and MLTM, respectively. Due to the superiority of MLTM over LM, according to the predictive ability measures, it may be concluded that ignoring censored records under LM results in re-ranking of animals based on the predicted breeding values. Therefore, including censored records by applying MLTM is of crucial importance for genetic evaluation of AFK in the Murciano-Granadina goat breed.

Keywords: age at first kidding, Bayesian approach, censored data, model comparison

Introduction

Goats are well adapted to endure harsh climatic conditions that may be unfavorable for other animals (Oliveira et al., 2016). The Murciano-Granadina goat

breed is a famous dairy breed in Spain that has been exported to several countries to improve the production efficiency of the native breed (Martinez et al., 2010). In 2015, the private sector introduced the Murciano-

Granadina goat breed from Spain to the southern area of Iran, which has a tropical climate. This initiative aimed to enhance production efficiency in the region's native and nomadic goat flocks by introducing Murciano-Granadina does and bucks and distributing them into local flocks as purebred animals, or through crossbreeding with native goat breeds (Mokhtari et al., 2024).

Optimal reproductive performance in livestock is an important factor to enhance production efficiency across diverse environments and production systems (Mia et al., 2013) and is considered a key determinant of productivity and the economic sustainability of commercial goat farming practices (Mellado et al., 2006).

Age at first parturition is one of the selection criteria for promoting reproductive efficiency in livestock through genetic improvement (Lazaro et al., 2019). Although recording this trait is relatively easy, unusual values can arise from several reasons, such as wrong or delays in data entry. Furthermore, censored records may exist when a goat has not yet kidded by the end of the kidding period or is removed from the herd due to factors such as culling, death, and sale. Censoring ensures that incomplete data does not bias survival analyses. Consequently, it is commonly classified as a censored trait (Tarres et al., 2006). The conventional method to overcome this issue is to exclude these observations (Lazaro et al., 2019). Guo et al. (2001) pointed out that this method would result in a loss of information for genetic analysis and may influence the real variation of the trait by masking the genetic differences between individuals.

An alternative for handling censored data is to use appropriate statistical models to cover censored records in genetic evaluation (Lazaro et al., 2019). Integrating censored records into genetic evaluation programs increases the accuracy of the estimated genetic parameters and consequently estimated breeding values of individuals (Ramos et al., 2018; Costa et al., 2019).

The Bayesian approach is a statistical inference method that utilizes Bayes' theorem to update our knowledge about a model and its parameters, represented as a probability distribution, based on the outcome of an experiment (Casadei et al., 2018). Under the Bayesian approach, a variety of statistical models have been proposed to cover censored records in genetic evaluation programs. One such model is the penalty model, which substitutes censored data by adding a constant value to the actual records (Johnston and Bunter, 1996). An alternative approach is fitting a linear-threshold model, which combines a continuous fertility trait with a binary variable representing censorship status (Garcia et al., 2016).

Some studies have explored the implementation of censoring scenarios in the genetic analysis of reproductive traits across livestock species, mainly in cows (Ramos et al., 2018; Costa et al., 2019; Lazaro et al., 2019; Atapour et al., 2022). No study has examined

the incorporation of censored records for genetic analysis of age at first kidding (AFK) in dairy goats. Therefore, the purpose of the current study was to perform genetic analysis of the AFK in the Murciano-Granadina goat breed under different Bayesian left- and right-censoring censoring scenarios.

Materials and methods

Flock management

Animals in the flock were generally kept under an intensive management system on a single farm. They were kept in separate enclosures based on their age, sex, physiological condition, and health status (Ehsaninia et al., 2025). At birth, the newborn kids were weighed and ear-tagged, while information regarding their sex, birth type, and also the identities of their dams and sires was recorded. The matings were controlled. Considering a mating ratio of 1 buck per 15 does, maiden does were mated to fertile bucks at about 11 months of age and with a live body weight of 25 kg (Mokhtari et al., 2024). Dairy goats are fed commercial concentrates (1350 g/day/goat), alfalfa hay (250 g/day/goat), wheat straw (25 g/day/goat), forage corn silage (1000 g/day/goat), and sugar beet pulp (1000 g/day/goat). The concentrate mixture contained the following ingredients: 210 g/kg of barley; 400 g/kg of corn; 225 g/kg of soybean and rapeseed meals; 85 g/kg of meat and fat powder; 77 g/kg of vitamin and mineral mixture; and 3 g/kg of common salt. The amounts of concentrate and hay were calculated based on the animals' age and production status. Water was freely available to all animals. Animals receive veterinary care and antiparasitic drugs, as well as vaccinations against diseases like enterotoxaemia, foot-and-mouth disease, goat pox, and brucellosis (Ehsaninia et al., 2025).

Pedigree and data

In the present study, the pedigree information included 35,121 individuals from 937 sires and 11,328 dams collected from 2016 to 2024 in a private dairy farm of the Murciano-Granadina goat breed, in Ghale-Ganj city, located in the southern area of Kerman province, Iran. The pedigree structure is shown in Table 1. Kidding information on the first parity of 5,018 does was used for the calculation of AFK in days as the difference between the birth date and the first-kidding date of the does.

Table 1. Pedigree structure of the population of the Murciano-Granadina goats

Item	Numbers
Individuals in total	35121
Inbreds in total	2484
Sires in total	937
Dams in total	11328
Individuals with both parents known	31543
Individuals with both parents unknown	3358
Individuals with one parent unknown	220

Data from does with AFK out of the range of 480 to 960 days were considered as censored, and data in the

range of 480-960 days for AFK were considered as uncensored records. In other words, AFK lower than 480 days were left-censored, and AFK higher than 960 days were right-censored. Descriptive statistics for the censored and uncensored records are presented in Table 2.

Table 2. Descriptive statistics for the censored and uncensored records of age at first kidding in Murciano-Granadina goats

Item	Censored records	Uncensored records
No. of records (% of total records)	973 (19.39%)	4045(80.61%)
Average (days)	1058.00	794.49
Standard deviation (days)	94.89	84.01
Coefficient of variation (%)	8.97	10.57
Range (days)	<480, >960	480-960

Statistical models

Five models, including the linear model (LM), penalty model (PM), modified penalty model (MPM), linear-threshold model (LTM), and modified linear-threshold model (MLTM), were used for genetic analysis of AFK. The LM is the conventional model routinely used for estimating genetic parameters of AFK, which contains uncensored records for genetic analysis. The remaining four models handle alternative scenarios for handling censored data.

Linear model

Under LM, which is a conventional linear animal model, only uncensored records (does with AFK from 480 to 960 days) were considered for genetic analysis. The LM in matrix notation is as follows:

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

where, $\mathbf{y}$ is the vector of uncensored records, $\mathbf{b}$, $\mathbf{a}$, and $\mathbf{e}$ are the vectors of the fixed (birth year of does and the kidding season), additive genetic, and residual effects, respectively. $\mathbf{X}$ and $\mathbf{Z}$ are the incidence matrices associated with the fixed and the additive effects, respectively.

Censoring models

Under censoring models, including PM, MPM, LTM, and MLTM, for both censored and uncensored records, a contemporary group (CG) was considered in the data set. In the present study, CG was defined by the birth year of the does.

Penalty model

The matrix notation of this model is similar to LM (Donoghue et al., 2004b). The difference is that here, there are both uncensored and censored records for AFK, and censored records were replaced by a set of augmented data, which is obtained by adding a constant value of 21 days to the highest AFK value within each CG. In other words, for censored records, a new AFK record would be the highest AFK value in the corresponding CG, plus 21 days. The value of 21 was

considered equal to the length of the estrus cycle in goats.

Modified penalty model

The matrix notation of MPM is equivalent to PM; however, in MPM, censored records are substituted by adding a constant value of 21 days to the average of the AFK value within each CG (Costa et al., 2019). In other words, for censored records, a new AFK record would be the average AFK value in the corresponding CG, plus 21 days.

Linear-threshold model

The LTM is a bivariate model that consists of a linear model for AFK, in which both censored and uncensored records were considered, and a threshold model for a dummy binary trait related to censorship status, where 0 represents uncensored records and 1 represents censored records (Lazaro et al., 2019). Hou et al. (2009) demonstrated that incorporating a vector containing censoring status as a correlated trait enhances the accuracy of genetic parameter estimates and predicted breeding values. Under the LTM, for censored records, a new AFK record would be the highest AFK value in the corresponding CG, plus 21 days. The LTM in matrix notation is as follows (Lazaro et al., 2019):

$$\begin{bmatrix} \mathbf{y} \\ \mathbf{l} \end{bmatrix} = \begin{bmatrix} \mathbf{X}_y & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_l \end{bmatrix} \begin{bmatrix} \mathbf{b}_y \\ \mathbf{b}_l \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_y & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_l \end{bmatrix} \begin{bmatrix} \mathbf{a}_y \\ \mathbf{a}_l \end{bmatrix} + \begin{bmatrix} \mathbf{e}_y \\ \mathbf{e}_l \end{bmatrix}$$

where, $\mathbf{y}$ is the vector of censored and uncensored records for AFK, and $\mathbf{l}$ is the vector of underlying liability for censoring status, which has two values, including 0 for uncensored records and 1 for censored records; $\mathbf{b}$, $\mathbf{a}$, and $\mathbf{e}$ are the vectors of the fixed, additive genetic, and residual effects; and $\mathbf{X}$ and $\mathbf{Z}$ are incidence matrices associated with $\mathbf{b}$ and $\mathbf{a}$, respectively. It should be noted that the same fixed and random effects were fitted for the dummy correlated binary trait.

Modified linear threshold model

MLTM is equivalent to LTM. For censored records, a new AFK record would be the average AFK value in the corresponding CG, plus 21 days. The matrix notation and statistical assumptions for MLTM are similar to LTM.

Genetic analysis

Bayesian Markov Chain Monte Carlo (MCMC) was performed using the GIBBS2F90 program for running LM, PM, and MPM, and the THRGIBBSF90 program (Mizstal et al., 2002) for running LTM and MLTM. To conduct genetic analyses under any investigated model, 200,000 iterations were run, of which the first 20,000 iterations were excluded as burn-in, and posterior samples from each chain were thinned, considering thinning intervals of 100 iterations. The values of priors for the variance components were determined based on the literature and preliminary evaluations by running the

models with the THRGIBBSF90 program. For calculating features of means and posterior standard deviations (PSD) of variance components and heritability estimates, the POSTGIBBSF90 program (Mizstal et al., 2002) was used. Convergence for the MCMC chains was evaluated by visual inspection of trace plots for the posterior samples of parameters. Furthermore, the effective sample size was also considered as a diagnostic measure of convergence for MCMC samples (Burkner, 2017).

Measures for comparison of models

Predictive ability

The predictive ability of models was assessed via a two-fold cross-validation study in which the whole dataset, including pedigree information, fixed, and random effects, was randomly partitioned into two sets containing training (50% of the dataset) and testing (the remaining 50% of the dataset). This partitioning process was replicated five times. Consequently, five training and five associated testing datasets were generated. Then, solutions for all effects, including fixed and random, of each training set were estimated and applied to predict records in the associated testing set. The PREDICTF90 program (Mizstal et al., 2002) was used to evaluate the predictive ability of the investigated models by applying two measures, the mean square of error (MSE) and Pearson's correlation coefficient between observed and predicted values ($r(y, \hat{y})$) in the testing set. MSE was computed as follows:

$$MSE = \frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2}{n}$$

where, y_i and $\hat{y}_i$ denote i^{th} observed and predicted record for AFK in the testing set, and n is the number of records in the testing set. The MSE and $r(y, \hat{y})$ values were calculated five times and averaged. The lower the average MSE and the higher the average $r(y, \hat{y})$ value implies the superiority of the model.

Accuracy of models and ranking of animals

The accuracy of predicted breeding value for each animal i (Accuracy _{i}) was calculated by the following formula (Lazaro et al., 2019):

$$Accuracy_i = \sqrt{1 - \left(\frac{SD_i^2}{\sigma_a^2}\right)}$$

In which SD_i is the posterior standard deviation of the predicted breeding value of the i^{th} animal, and σ_a^2 is the posterior mean for direct genetic variance. Models were also compared in terms of the average of predicted breeding values of animals under the investigated models.

Furthermore, by considering all and the 1% top-ranked individuals (51 does), the coefficients of Spearman's rank correlations between predicted breeding values under the investigated models were applied to evaluate the effect of the model on the ranking of animals based on the predicted breeding values.

Results and discussion

General considerations

As shown in Table 1, animals with both known parents, one known parent, and both unknown parents were 89.81%, 9.56%, and 0.63 % of the total animals, respectively, implying an appropriate quality of the pedigree used for genetic analysis. As shown in Table 2, The proportion of censored records was 19.39% (973 records out of 5,018 records). The means of AFK were 1,058 days for censored records and 794 days for uncensored records. It was also observed that uncensored records tended to have greater variability than censored records (C.V. of 10.57% in uncensored records vs. C.V. of 8.97% in censored records). The means for AFK in US dairy goats (Castaneda-Bustos et al., 2014), Alpine, LaMancha, Nubian, Oberhasli, Saanen, and Toggenburg dairy goat breeds (Garcia-Peniche et al., 2012) were reported as 507.97, 517, 495, 537, 470, 472, and 494 days, respectively. Higher phenotypic mean for AFK in the present study than those reported in other breeds, denoting that low selection pressure for precocity has been imposed (Costa et al., 2019).

Model comparisons

The predictive ability of different models used for genetic analysis of AFK in Murciano-Granadina goat breed is shown in Table 3. The MLTM had the lowest MSE and highest $r(y, \hat{y})$ among the investigated models, indicating that MLTM is the best model for genetic analysis of AFK with censored records in the Murciano-Granadina goat breed. There are no published documents on incorporating censored records into the estimation of genetic parameters for reproductive traits like AFK in goats. Therefore, comparing the conventional LM, which does not consider censored records, with models that are capable of handling censored records in other livestock, such as cows, may be interesting. For example, Lazaro et al. (2019) compared some Bayesian models to cover censored data, including PM and LTM, with LM for genetic analysis of age at calving in Brazilian Brahman cattle. They reported that LM was the best model for genetic analysis of age at first calving in Brazilian Brahman cattle based on the evaluation of predictive ability of models, which is not in agreement with that obtained in the present study.

Table 3. The predictive ability of different models used for genetic analysis of AFK in Murciano-Granadina goats

Model ¹	MSE ²	$r(y, \hat{y})$
LM	4269.28	0.71
PM	6292.36	0.73
MPM	6591.93	0.68
LTM	3833.83	0.63
MLTM	3663.54	0.87

¹LM: Linear model; PM: Penalty model; LTM: Linear-threshold model; MPM: Modified penalty model; MLTM: Modified linear-threshold model.

²MSE: mean square error, $r(y, \hat{y})$ = Pearson correlation between observed and predicted values.

Spearman's rank correlations between predicted breeding values of all, 1% top-ranked animals, and averages for prediction accuracy of models are shown in Table 4. The averages for accuracy of the predicted breeding values of animals were 0.43, 0.49, 0.47, 0.47, and 0.49 under LM, PM, MPM, LTM, and MLTM, respectively, implying that the accuracy of the model under censored data (LM) is partly lower than the model accuracies under censoring scenarios. In the present study, the highest model accuracy was obtained under PM and MLTM. Higher accuracies based on the uncensored data than the censored ones were also documented (Donoghue et al., 2004a; Lazaro et al., 2019). The Spearman's rank correlations between the LM and investigated censored models for all and 1% top-ranked animals were low and statistically non-significant ($p>0.05$). It implied that ignoring censored records under LM results in the re-ranking of animals based on the predicted breeding values. By considering the models that contained censoring scenarios, all Spearman's rank correlations among the models were positive and statistically significant ($p<0.05$), ranging from 0.56 (LTM-MPM) to 0.96 (MPM-MLTM) when all animals were considered and from 0.75 (LTM-MPM) to 0.96 (MPM-MLTM and PM-MLTM) when 1% top-ranked animals were considered. Lazaro et al. (2019) remembered that Spearman's rank correlation between LM and censored data handling models was lower than that among models with censored data because the censored data handling

models showed higher variation due to the process of data generation. In contrast, the LM is most consistent since only uncensored observations have been used for the analysis. Contrary to us, Costa et al. (2019) and Atapour et al. (2022) compared Bayesian linear-threshold censored models with LM and concluded that LM is recommended for genetic analysis of age at first calving in Nellore and Iranian Holstein cows, respectively. But, Malhado et al. (2013) reported that the censorship approach is the most influential alternative for the analysis of age at calving in cattle, which is in agreement with our finding.

The percentage of animals in common for 1% and 10% top-ranked breeding values for AFK from the investigated models is shown in Table 5. For both 1% top-ranked and 10% top-ranked breeding values, the LM has the least commonality with other investigated models. When comparing the 10% top-selected animals with the 1% top-selected ones, the commonality of individuals decreased due to the smaller sample size and stricter selection criteria. A similar pattern was also observed by Atapour et al. (2022) in the genetic analysis of age at first calving of Iranian Holstein cows under LM and censored-data handling models. The low overlap for common animals between the two models denotes that they rank animals differently, while the high overlap shows their agreement in identifying top-ranked animals (Lazaro et al., 2019). Therefore, choosing the appropriate model plays a key role in determining the best selection candidates.

Table 4. Spearman's rank correlation between predicted breeding values of all (above diagonal), 1% top-ranked (below the diagonal) animals, and averages for prediction accuracy of models (on diagonal)

Model ¹	LM	PM	MPM	LTM	MLTM
LM	0.43	0.05 ^{ns}	0.05 ^{ns}	0.12 ^{ns}	0.03 ^{ns}
PM	0.08 ^{ns}	0.49	0.85 ^{**}	0.76 ^{**}	0.95 ^{**}
MPM	0.02 ^{ns}	0.87 ^{**}	0.47	0.56	0.96 ^{**}
LTM	0.10 ^{ns}	0.86 ^{**}	0.75 ^{**}	0.47	0.69 ^{**}
MLTM	0.05 ^{ns}	0.96 ^{**}	0.96 ^{**}	0.84 ^{**}	0.49

¹ LM: Linear model; PM: Penalty model; LTM: Linear-threshold model; MPM: Modified penalty model; MLTM: Modified linear-threshold model.

^{**}: Statistically significant at $P<0.01$, ^{ns}: Not statistically significant at $P>0.05$.

Table 5. Percentage of common animals for 1% top-ranked (above the diagonal) and 10% top-ranked predicted breeding values (below the diagonal)

Model ¹	LM	PM	MPM	LTM	MLTM
LM	-	4.41	6.85	7.82	5.16
PM	10.42	-	28.20	31.83	37.75
MPM	13.24	43.80	-	17.47	20.56
LTM	10.85	65.07	40.23	-	37.32
MLTM	11.97	63.10	78.03	40.84	-

¹ LM: Linear model; PM: Penalty model; LTM: Linear-threshold model; MPM: Modified penalty model; MLTM: Modified linear-threshold model.

Heritability estimates

Posterior means of additive genetic variance, residual variance, and the heritability estimates for AFK under the investigated models, by 95% highest posterior density (HPD) intervals, are shown in Table 6. Although the posterior means for heritability of AFK under different models were not statistically different (95% of HPD intervals overlap), the large differences in posterior

means of additive genetic variance and also residual variance across models were observed. These differences may be, to a large extent, related to considering different censoring scenarios and data structures. The lowest and highest posterior means for additive genetic variances were obtained under LTM (274.95) and PM (2300.15), respectively. The same trend was also observed for the posterior means of the residual variances. The posterior means for additive

genetic and residual variances for AFK under MPM and LTM were generally similar. Heritability estimates were statistically significant (95% of HPD intervals did not include zero) values of 0.20 ± 0.03 , 0.23 ± 0.02 , 0.19 ± 0.02 , 0.18 ± 0.03 , and 0.18 ± 0.02 under LM, PM, MPM, LTM, and MLTM, respectively. The estimated heritability for

AFK under MLTM (0.18) implies a low contribution of direct genetic effects for this trait. It may be concluded that direct genetic selection for genetically improving the AFK in the studied population of the Murciano-Granadina goat breed is not so effective and considering non-additive genetic and environmental effects into account is more important for improving this trait.

Table 6. Posterior means of genetic variance, residual variance, and the heritability (h^2) with 95% highest posterior density (HPD) intervals under different models

Model ¹	σ_a^2	σ_e^2	$h^2 \pm \text{PSD}$	95% HPD interval
LM	1294.48	5157.96	0.20 ± 0.03	0.12-0.28
PM	2300.15	7784.73	0.23 ± 0.02	0.18-0.28
MPM	982.60	4273.19	0.19 ± 0.02	0.14-0.24
LTM	274.95	1279.37	0.18 ± 0.03	0.10-0.26
MLTM	942.20	4301.85	0.18 ± 0.02	0.13-0.23

¹LM: Linear model; PM: Penalty model; LTM: Linear-threshold model; MPM: Modified penalty model; MLTM: Modified linear-threshold model.

σ_a^2 : direct variance, σ_e^2 : residual variance, h^2 : heritability, PSD: Posterior standard deviation

The differences between heritability estimates of AFK under different investigated models were not statistically significant (95% of HPD intervals overlap), indicating the inclusion of censored records in the genetic analysis models did not substantially influence the heritability estimate of AFK in the Murciano-Granadina goat breed. Bagnicka et al. (2007) reported a heritability value of 0.13 for AFK in Polish dairy goats. Garcia-Peniche et al. (2012) reported heritability estimates for AFK in Alpine, LaMancha, Nubian, Oberhasli, Saanen, and Toggenburg dairy goat breeds as 0.22, 0.28, 0.32, 0.61, 0.16, and 0.23, respectively. By considering all six breeds, they also reported an estimate of 0.23 for the heritability of AFK in US dairy goat breeds, which is close to the heritability estimates obtained for AFK in the present study. Castaneda-Bustos et al. (2014) estimated the heritability of 0.16 for AFK in US dairy goats, which is close to that obtained in our study under MLTM. Banger et al. (2022) reported an estimate of 0.06 for the heritability of AFK in Beetal goat, which is lower than the corresponding estimate in the present study. The application of censored models for estimating the heritability of reproductive traits, such as age at first calving, is more prevalent. Garcia et al. (2016) obtained heritability estimates of age at first calving in Nellore cattle breed under linear, penalty, and linear-threshold models as 0.18, 0.12, and 0.17, respectively. Lazaro et al. (2019) reported that the heritability estimates for age at first calving in Brazilian Brahman cattle ranged from 0.09 (under LTM) to 0.20 (LM). It should be noted that differences in species, environments, data structure, and modeling approaches may limit direct comparability.

Conclusions

The influences of handling censored records by including them in the genetic analysis of AFK in the Murciano-Granadina goat breed under several scenarios were investigated. The plausibility of handling censored records under MLTM was confirmed in terms of the better predictive ability of the model, higher accuracy of the model for predicting the breeding values, and also a more accurate ranking of animals based on the predicted

breeding values over LM. Due to the superiority of MLTM over LM, it may be concluded that ignoring censored records under LM results in re-ranking of animals based on predicted breeding values. Therefore, including censored records by applying MLTM is of crucial importance for genetic evaluation of AFK in the Murciano-Granadina goat breed.

Conflicts of Interest

The authors declare no conflicts of interest.

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