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Different Statistical Models for Genetic Evaluation of some Milk and Prolificacy Traits in Zaraibi Goats in Egypt

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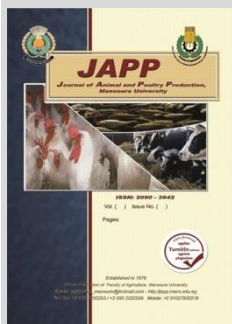
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ABSTRACT

The aim of this study is to identify the most suitable model for fitting data related to some milk traits, including total milk yield (TMY) and lactation period (LP) and prolificacy traits, including the number of kids born (NKB) and the number of kids weaned (NKW). The models under consideration varied based on the absence or presence of additive and maternal genetic effects, permanent environmental effect, and the direct-maternal genetic covariance (σ_{am}). The dataset comprised 1638 kidding records from 411 does and 79 bucks. Statistical analyses were performed using the MTDFREML software, with model selection guided by the Akaike information criterion (AIC). Across all examined models, direct heritabilities ranged from 0.258 to 0.375 for TMY, 0.172 to 0.252 for LP, 0.220 to 0.265 for NKB, and 0.074 to 0.133 for NKW. Corresponding maternal heritabilities estimates varied from 0.094 to 0.144, 0.089 to 0.112, 0.078 to 0.097, and 0.043 to 0.080, respectively. Direct-maternal genetic correlations were positive for milk traits (0.123 for TMY and 0.093 for LP) and negative for prolificacy traits (-0.261 for NKB and -0.082 for NKW). Genetic, maternal, and phenotypic correlation were positive between studied traits. Additionally, a wide range of breeding values was noted among sires for TMY, LP, and NKB. In conclusion, it is advised to incorporate both direct and maternal effects, and their covariance in statistical models for optimal genetic improvement of Zaraibi goats in Egypt.

Keywords: Milk yield, Litter size, Models comparisons, Zaraibi goats



INTRODUCTION

The Egyptian Nubian goats, also known as the Zaraibi goat, stand out as a crucial and famous indigenous breed recognized for its exceptional reproductive and productivity prowess. This breed widely distributed in the North Delta region of Egypt, is often hailed as the ancestor of the Anglo-Nubian breed. Consequently, there is a pressing need for genetic evaluations focusing on the most economically traits in this breed (Aboul-Naga et al., 2012). In recent times, Egyptian animal breeders have shown a keen interest in improving goat breeding practices for both meat and milk production. This heightened interest is a response to growing need for dairy products and a rising beef prices. To meet these demands, it is essential to implement well-designed breeding schemes that incorporate genetic evaluations covering a spectrum of productive and reproductive traits in goats. This strategic approach seeks to position native goat breeds as reliable sources of meat and milk (Moawed and Shalaby, 2018). Animal breeding objectives extend beyond the creation of outstanding individual animals; they also focus on enhancing the entire herd by choosing genetically superior sires and dams to serve as ancestors for succeeding generations (Bourdon, 1997).

The fundamental objective of animal breeding is to identify parents capable of producing offspring with improved phenotypes (Al-Samarai et al., 2015). To develop successful breeding programs, a thorough comprehension of genetic inheritance of particular traits is indispensable (Bugeac et al., 2013). The capacity to improve a trait genetically heavily relies

on the genetic diversity existing within the population of focus. Goshu et al. (2014) noted that the genetic variation of a trait within a herd is evaluated by measuring the heritability of that trait in particular environmental circumstance. Additionally, using the appropriate method for the genetic assessment of sires and dams is crucial for genetic improvements (Kheirabadi et al., 2013).

Improving goat performance involves implementing selection programs on the basis of multiple traits, individual records, and ancestral lineage. The productivity of dairy goats is not solely depending on milk production efficiency but also on their mothering ability, translated by the reproductive status of does and their longevity in performance. The maternal effect of a healthy dam significantly affects the early-life performance of their offspring, particularly in prolificacy -related traits such as litter size at birth and weaning. Ghafouri-Kesbi and Eskandarianasab (2008) showcased that neglecting maternal effects in animal models led to exaggerated estimates of direct heritability. Therefore, employing a precise and concise statistical model is crucial for obtaining accurate genetic parameters estimates. Additionally, any enhancements in the reproduction rate of goats will have a direct effect on selection strategies and the genetic enhancement of production traits (El-Awady et al., 2019). This study focused on genetically evaluates some milk and prolificacy traits of Zaraibi goats using different statistical models to explore whether more intricate models generate estimates comparable to those yielded by simpler alternatives.

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MATERIALS AND METHODS

Data:

This study utilized data was gathered over a continuous span of 10 years (2005-2014) from the Zaraibi herd at the El-Serw Experimental Station Damietta, Egypt. This farm is managed by the Animal Production Research Institute (APRI). The dataset comprises 1638 lactation records; detailing information about 411 does mated with 79 bucks. The study concentrated on the first five lactations of these does

Management of flock:

At the experimental farm, a system of one mating per year was adhered to by dividing the herd into two groups, with one group mated in June and the other in October. A strict protocol was followed, ensuring that does were not bred before attaining a body weight of 30 kg or reaching approximately 18 months of age. During mating season, female goats were randomly splitting into groups of 30-35 does, each group being assigned randomly to a fertile buck. Special care was taken to avoid inbreeding among full siblings, and the bucks were rotated every three mating seasons. After birth, kids were kept alongside their mothers during the suckling period until weaning at 3 months old. The kids were identified with ear tags and weighed within 24 hours of birth and then monthly until they reached 18 months of age. Post-weaning, kids were fed a diet consisting of a concentrate feed mixture and green clover (*Trifolium Alexandrinum*) during winter, while in the summer; they were fed a combination of concentrate feed mixture and crop stubbles or rice straw, along with green fodder when available. The animals were provided with diets tailored to meet their nutritional needs based on the feeding system practiced at the farm and recommended by the Animals Production Research Institute (NRC, 1981). All animals were kept in semi-open barns and were fed twice daily, after evening grazing and before morning grazing. Water access was provided three times a day after meals, and mineral blocks were consistently available. Two weeks before the start of the mating season, a supplementary concentrate feed mixture was introduced at a rate of around 0.25 kg per doe per day. This supplementary feed was continued during the final 2-4 weeks of pregnancy and the first week of lactation whenever it was accessible. Throughout the suckling period, milk production within this flock was recorded biweekly, transitioning to weekly milking until the end of lactation. Post-weaning of the kids, milk yield was assessed through hand milking sessions conducted twice daily.

Statistical models:

The variance, covariance components, and genetic parameters related to different milk and prolificacy traits were calculated using the Derivative-free restricted maximum likelihood (REML) method via the MTDFREML software developed by Boldman et al. (1995). All studied models included random effects and consistent fixed effects, with fluctuations in the random effects. With regard to milk traits, the fixed effects considered in the analyzed models included kidding season (spring and autumn), kidding year (from 2005 to 2014) and their interaction, parity order, number of kids born, number of kids weaned, and age at first kidding as a covariate (*linear and quadratic*). The same fixed effects were applied in the model for the prolificacy traits. Additionally, the exclusion or inclusion of

covariance terms was carefully deliberated when fitting models that accounted for both the animal's additive and maternal genetic effects. Four distinct animal models were utilized and fitted for the analysis. The first model was the most basic, featuring only the direct additive genetic effect as the random effect alongside the residual term. The second model incorporated both the direct additive genetic effects and maternal additive genetic effects. The third model encompassed permanent environmental effects, direct additive genetic effects, and maternal additive genetic effects, without considering covariance between direct and maternal genetic effects. The fourth model mirrored the third one but permitted the presence of direct-maternal genetic covariance. These four models were succinctly described as follows:

$$\text{Model I: } Y = Xb + Z_1a + e$$

$$\text{Model II: } Y = Xb + Z_1a + Z_2m + e, \quad \text{Cov}(a, m) = 0A \sigma_{am}$$

$$\text{Model III: } Y = Xb + Z_1a + Z_2m + Z_3c + e, \quad \text{Cov}(a, m) = 0A \sigma_{am}$$

$$\text{Model IV: } Y = Xb + Z_1a + Z_2m + Z_3c + e, \quad \text{Cov}(a, m) = A \sigma_{am}$$

Where Y represents the observations vector, with b , a , m , c , and e symbolizing the vectors of fixed effects, direct genetic affects, maternal genetic effects, permanent environmental effect, and the residual effect, respectively. Furthermore, X , Z_a , Z_m , and Z_c are matrices that represent the fixed effects, direct additive effects, maternal effects, and permanent environmental effects. A stands for the numerator additive genetic relationship matrix among animals, and $\text{Cov}(a, m) = A\sigma_{am}$ where σ_{am} signifies the covariance between direct additive and maternal genetic effects.

Direct heritability (h^2d) and maternal heritability (h^2m) were calculated using the following equations:

$$h^2d = \frac{\sigma^2d}{\sigma^2p} \quad h^2m = \frac{\sigma^2m}{\sigma^2p}$$

Repeatability (r) was calculated according to Willham (1972):

$$r = \frac{\sigma^2d + 0.5\sigma^2m + 1.5\sigma dm + \sigma^2c}{\sigma^2p}$$

$\sigma^2p = \sigma^2a + \sigma^2e$ in model 1, $\sigma^2a + \sigma^2m + \sigma^2e$ in model 2, $\sigma^2a + \sigma^2m + \sigma^2c + \sigma^2e$ in model 3 and $\sigma^2a + \sigma^2m + \sigma_{am} + \sigma^2c + \sigma^2e$ in model 4. The residual sums of squares were used directly to estimate the error variance.

Here, σ^2d , σ^2m , σ^2c , σ^2e , and σ^2p represent the variances for direct genetic effects, maternal genetic effects, permanent environmental effects, residual effects, and phenotypic outcomes, respectively.

Akaike information criterion was performed for comparing models, calculated as: $AIC(\theta) = (-2) * \log(L) + 2k$, k is the parameters number in each statistical model while $\log L$ represents the maximum Log Likelihood. The most optimal model was detected as the one with the smallest AIC (Akaike, 1974).

RESULTS AND DISCUSSION

Descriptive statistics of studied traits are illustrated in Table 1. The overall average along with their standard deviations of TMY, LP, NKB, and NKW were 256.26 ± 72.67 kg, 249.33 ± 44.80 days, 2.069 ± 0.68 kids, and 1.978 ± 0.63 kids, respectively. The mean TMY in this study closely matched the results of Hamed et al. (2009) and Aboul-Naga et al. (2012) for Zaraibi goats (253.14 kg and 253 kg, respectively). In the same herd, Aboul-Naga et al. (2012) reported LP, NKB, and NKW of 251.3 days, 2.1 kids, and 1.6 kids, respectively. Additionally, Moawed and Shalaby (2018) reported LP, NKB, and NKW of 256.56 days, 1.81 kids, and 1.65 kids, respectively, which were in proximity to the estimates in this study. The computed value of coefficient of variation for NKB (32.87 %), closely resembling the estimate for NKW (31.85 %). Notably, LP exhibits the lowest

coefficient of variation at 17.97%. Meanwhile, the coefficient of variation was 28.36% for TMY, indicating a discernible environmental impact on these traits.

Table 1. Descriptive statistics for milk and prolificacy traits in Zaraibi goats

| Items | Traits | | | |
|-----------------------------|---------|---------|----------|----------|
| | TMY, kg | LP, day | NKB, kid | NKW, kid |
| Minimum | 60 | 72 | 1 | 1 |
| Maximum | 372 | 465 | 4 | 4 |
| Mean | 256.26 | 249.33 | 2.069 | 1.978 |
| Standard deviation | 72.67 | 44.80 | 0.68 | 0.63 |
| Coefficient of variation, % | 28.36 | 17.97 | 32.87 | 31.85 |
| Numbers of records | 1638 | | | |
| Numbers of sires | 79 | | | |
| Numbers of dams | 411 | | | |

TMY, total milk yield; LP, lactation length, NKB, numbers of kids born; NKW, numbers of kids weaned

Genetic parameters:

The variances, covariances, and genetic parameters for TMY, LP, NKB, and NKW obtained from the four tested models are illustrated in Table 2. The heritability estimates in our study exhibited a wide range and notable variation across most all studied traits. It was observed that direct heritability estimates surpassed maternal heritability values in models incorporating maternal effects. For milk traits, direct heritability estimates fell within the range of 0.258–0.375 and 0.172–0.252 for TMY and LP, respectively. Meanwhile, direct heritability for NKB and NKW ranged from 0.220 to 0.265 and 0.074 to 0.133, respectively. The heritability estimate for TMY in the present study agreed closely with the findings of Farrag et al. (2007), Hamada et al. (2016) concerning Zaraibi goats (27.4% and 28%, respectively), and Kamal El-den et al. (2020) regarding Damascus goats (29%). However, it exceeded the values reported by Delfino et al. (2011) for Maltese goats (21%). Additionally, Muhammed et al. (2007) reported higher heritability estimates for TMY in Sudanese Nubian goats (44%). The discrepancies in heritability estimates between different studies could be attributed to the inclusion of different effects in animal models, breed variations, and the sample sizes of the analyzed data. The moderate heritability estimates for TMY in the current study imply that the yield assessment method used is sufficiently precise. Early measurements conducted with suckling kids also provide satisfactory results in this regard, indicating their viability as a criterion in an effective selection program (Shaat et al., 2007). The estimated heritability for LP in this study aligns with the 0.20 reported by Pimenta Filho et al. (2004). In contrast, a notably low heritability value for LP (0.04) was reported by Valencia et al. (2007) in a Saanen goat flock in Mexico. The heritability estimates for NKB and NKW in this study are on line with the range reported by Moawed and Shalaby (2018), being between 0.09–0.21 and 0.05–0.22 for NKB and NKW, respectively. Lower estimates for NKB (11%) were noted by Menéndez-Buxadera et al. (2016) in Creole goats Also, Bagnicka et al. (2007) found heritability values of 13% for Norwegian goat and 11% for Polish goat. The low heritability of NKW in this study is probably due to the predominant impact of environmental factors and limited genetic variability in litter size survivability (Bangar et al., 2023). The direct heritability findings for milk and prolificacy traits in the current study are consistent with Weppert and Hayes (2004), who noted that direct heritability values increased for all production traits when statistical models without maternal effects were employed.

Furthermore, Mostafa et al. (2017) illustrated that models excluding maternal additive genetic effects led to elevated estimates of direct additive genetic variances and consequently, inflating estimates of direct heritability. In essence, the absence of a genuine maternal genetic effect in the statistical model could result in a biased heritability estimate (Sanad and Gharib, 2018). The negative correlations observed between direct and maternal genetic effects for prolificacy traits, as presented in Table 2, could potentially be attributed to the restricted number of offspring per dam, as outlined by Gerstmayer and Horts (1995). Additionally, Heydarpour et al. (2008) emphasized the necessity of enhanced relationships between dam and their offspring performance, along with an increased number of progeny per dam, to ensure accurate estimation of maternal genetic parameters across single and multiple traits. Conversely, the correlations between direct and maternal genetic effects were positive for LP and TMY, suggesting that genetic advancement of these traits could be achievable on the long term plans within the current flock. In same context, to maximize genetic improvement in breeding programs, consideration should be given to both direct and maternal additive genetic effects, especially in situations where there exists a negative correlation between these effects (Supakorn and Pralomkam, 2012). In this study, the Akaike information criteria (AIC) values were calculated to rank the different animal models assessed (Table 2). Model 4 had the lowest AIC value (6183.64), emerged as the most suitable model for genetic assessment and improvement of the current Zaraibi herd. It is widely acknowledged that models with an increased number of parameters offer substantial insights for animal breeders (Osman, 2013). Therefore, the inclusion of both the animal's additive genetic and maternal genetic effects, along with their covariances, within Model 4 shows potential for constructing a breeding program aimed at improving milk and prolificacy traits in Zaraibi goats. Although the correlations between direct and maternal genetic effects were generally found to be modest across all traits in this study, the existence of covariances between direct and maternal genetic effects influences the estimation of heritability levels, especially concerning direct heritabilities. This result underscores the importance of considering the covariance term within the statistical models. The repeatability estimates ranged from moderate to higher values for TMY (0.460-0.464), LP (0.328-0.349), and NKB (0.282-0.377), while they were lower for NKW, ranging from 0.159 to 0.175. These results align with genetic principles indicating that repeatability serves as an upper limit for heritability estimates (Odubote, 1996). The outcomes of this study imply that the most crucial management practice to improve TMY, LP, and NKB might involve culling unproductive animals in their first parities (Hamed et al., 2009).

Table 3 shows the direct additive and maternal additive genetic correlations, as well as phenotypic correlations across the four traits based on the best fitted model (Model 4). The results from the direct additive genetic correlation exhibit positive estimates between all studied traits, particularly notable correlations between NKB and NKW (0.842), TMY and LP (0.942), and TMY and NKB (0.548). These findings align with former studies. Shaat et al. (2007) noted a positive and highly genetic correlation between TMY and LP (0.80). Also, several former studies reported positive and high genetic correlation between NKB and NKW in different breeds (Rashidi et al., 2011; Mokhtari et al., 2019; Bangar et al., 2021). The positive genetic and

phenotypic correlations identified between TMY and both of litter size at birth and weaning corresponded with the findings of Bolacali et al. (2019) in Hair Goats. The present positive correlation between these traits may be attributed to the stimulating effect of suckling, which can enhance milk

production. According to the current results, breeders could enhance milk production by opting for animals giving high litter size at birth. Additionally, focusing on selecting for NKB could substantially boost the genetic potential for improving kids' numbers at weaning.

Table 2. Variance components and genetic parameters for milk and prolificacy traits in Zaraibi goats

| Traits* | $\sigma^2 a$ | $\sigma^2 m$ | σ_{am} | $\sigma^2 c$ | $\sigma^2 e$ | $\sigma^2 p$ | $h^2 a$ | $h^2 m$ | r_{am} | c^2 | r | AIC |
|-----------|--------------|--------------|---------------|--------------|--------------|--------------|------------|------------|-------------|------------|-------|---------|
| Model-I | | | | | | | | | | | | |
| TMY, kg | 1970.254 | | | | 3290.436 | 5260.690 | 0.375±0.13 | | | | | |
| LP, day | 509.452 | | | | 1508.318 | 2017.770 | 0.252±0.10 | | | | | 6205.26 |
| LSB, kid | 0.138 | | | | 0.382 | 0.520 | 0.265±0.11 | | | | | |
| LSW, kid | 0.059 | | | | 0.384 | 0.442 | 0.133±0.04 | | | | | |
| Model-II | | | | | | | | | | | | |
| TMY, kg | 1707.426 | 764.122 | | | 2828.912 | 5300.460 | 0.322±0.11 | 0.144±0.06 | | | | |
| LP, day | 455.136 | 226.045 | | | 1331.229 | 2012.410 | 0.226±0.10 | 0.112±0.04 | | | | 6193.88 |
| LSB, kid | 0.119 | 0.048 | | | 0.329 | 0.497 | 0.240±0.07 | 0.097±0.04 | | | | |
| LSW, kid | 0.050 | 0.034 | | | 0.345 | 0.430 | 0.117±0.06 | 0.080±0.03 | | | | |
| Model-III | | | | | | | | | | | | |
| TMY, kg | 1499.654 | 539.249 | | 687.004 | 2557.044 | 5282.950 | 0.284±0.12 | 0.102±0.04 | | 0.130±0.10 | 0.464 | |
| LP, day | 389.059 | 236.248 | | 198.035 | 1195.327 | 2018.670 | 0.193±0.07 | 0.117±0.05 | | 0.098±0.06 | 0.349 | 6186.83 |
| LSB, kid | 0.117 | 0.049 | | 0.054 | 0.299 | 0.518 | 0.225±0.10 | 0.094±0.04 | | 0.104±0.06 | 0.377 | |
| LSW, kid | 0.034 | 0.018 | | 0.030 | 0.333 | 0.416 | 0.082±0.06 | 0.043±0.02 | | 0.072±0.03 | 0.175 | |
| Model-IV | | | | | | | | | | | | |
| TMY, kg | 1363.275 | 497.697 | 101.392 | 672.069 | 2651.578 | 5286.010 | 0.258±0.13 | 0.094±0.05 | 0.123±0.06 | 0.127±0.08 | 0.460 | |
| LP, day | 347.244 | 178.636 | 23.225 | 189.680 | 1276.445 | 2015.230 | 0.172±0.07 | 0.089±0.03 | 0.093±0.04 | 0.094±0.04 | 0.328 | 6183.64 |
| LSB, kid | 0.109 | 0.039 | -0.017 | 0.037 | 0.327 | 0.496 | 0.220±0.10 | 0.078±0.02 | -0.261±0.11 | 0.075±0.03 | 0.282 | |
| LSW, kid | 0.031 | 0.019 | -0.002 | 0.029 | 0.340 | 0.417 | 0.074±0.04 | 0.045±0.06 | -0.082±0.04 | 0.070±0.03 | 0.159 | |

*See abbreviation in Table 1; $\sigma^2 a$ =direct additive genetic variance; $\sigma^2 m$ =maternal additive genetic variance; σ_{am} =covariance between direct and maternal effects; $\sigma^2 c$ =permanent environmental variance; $\sigma^2 e$ = residual variance; $\sigma^2 p$ = phenotypic variance; $h^2 a$ = direct heritability; $h^2 m$ = maternal heritability; r_{am} =genetic correlation between direct and maternal effects; r =repeatability.

Table 3. Genetic correlation (above diagonal), maternal correlation (between brackets), and phenotypic correlation (below diagonal) for milk and prolificacy traits in Zaraibi goats

| Traits* | TMY | LP | NKB | NKW |
|---------|-------|------------------------------|------------------------------|------------------------------|
| TMY | -- | 0.942±0.082 (0.446±0.065) | 0.548±0.073 (0.350±0.043) | 0.235±0.081 (0.228±0.069) |
| LP | 0.566 | -- | 0.109±0.052 (0.045±0.014) | 0.112±0.055 (0.035±0.002) |
| NKB | 0.130 | 0.102 | -- | 0.842±0.001 (0.775±0.088) |
| NKW | 0.182 | 0.070 | 0.679 | -- |

*See abbreviation in Table 1

Herein, the maternal genetic correlation values mirrored the patterns seen in corresponding direct genetic correlations. This suggests the potential for genetic enhancements in these traits, even in the presence of an antagonistic and low correlation between direct and maternal genetic effects of certain traits (Supakorn and Pralomkarn, 2012). The current results align with Moawad and Shalaby (2018), working with another dataset from the same herd, highlighted positive maternal genetic correlations between litter size born and weaned, first lactation milk yield, and both litter size born and weaned. However, they observed negative and weak maternal genetic correlations between TMY and both of LSB and LSW.

Table 4 displays the breeding value estimates for studied traits. The sire ranges for TMY, LP, NKB, and NKW were 32.45 kg, 15.64 days, 0.06 kids, and 0.03 kids, respectively. Sires play a crucial role in shaping the inheritance of forthcoming generations. This is potentially attributed to the practice of random mating involving available Zaraibi bucks and does, which maintains ample genetic diversity for milk production and litter size within this

herd. Correspondingly, dam ranges were 25.64 kg, 10.50 days, 0.05 kids, and 0.02 kids for the same traits. Interestingly, the breeding value ranges for goats surpassed those of sires and dams for TMY and LP, indicating that selecting for these traits will lead to their improvement in subsequent generations. Stamer et al. (2004) noted great differences in breeding values between sires, accompanied by high reliabilities for economic traits. The different sire rankings based on breeding values allow the selection of sires with varied levels of TMY, LP, NKB, and NKW. These observations underscore the influential role of sire effects on these traits, potentially influenced by the higher number of daughters per sire.

Table 4. Minimum and maximum expected breeding values along with their corresponding accuracies for milk and prolificacy traits in Zaraibi goats

| Traits* | Min. | Acc. | Max. | Acc. | Range |
|----------|----------|--------|---------|--------|---------|
| TMY, kg | | | | | |
| Sires | -14.3771 | 0.8621 | 18.0821 | 0.7523 | 32.4592 |
| Dams | -11.3814 | 0.4752 | 14.2661 | 0.5132 | 25.6475 |
| Goats | -12.5214 | 0.5526 | 17.6251 | 0.4717 | 30.1465 |
| LP, day | | | | | |
| Sires | -9.1863 | 0.8132 | 6.4920 | 0.4932 | 15.6783 |
| Dams | -4.1605 | 0.5934 | 6.3487 | 0.6228 | 10.5092 |
| Goat | -12.6242 | 0.6021 | 8.1634 | 0.6002 | 20.7876 |
| NKB, kid | | | | | |
| Sires | -0.01881 | 0.6553 | 0.04855 | 0.7112 | 0.0673 |
| Dams | -0.02413 | 0.7103 | 0.03416 | 0.8231 | 0.0582 |
| Goats | -0.02946 | 0.5142 | 0.03163 | 0.7514 | 0.0610 |
| NKW, kid | | | | | |
| Sires | -0.01381 | 0.4938 | 0.01815 | 0.5102 | 0.0319 |
| Dams | -0.01425 | 0.4429 | 0.01325 | 0.4412 | 0.0275 |
| Goats | -0.02414 | 0.5321 | 0.01136 | 0.4221 | 0.0355 |

*See abbreviation in Table 1; Min, minimum; Max, maximum; Acc., accuracy

CONCLUSION

Moderate heritability estimates for milk traits and litter size at birth hint at the potential for genetic improvement within this breed. For optimal genetic progress, it is crucial to incorporate both direct and maternal genetic effects into the analytical model. Genetic correlation assessments illustrate the advantages of selection programs targeting these traits in the current herd, potentially benefiting various other traits as well. The negative correlation between the direct additive and maternal genetic effects underscores the importance of considering their co-variances in the statistical models. Enhancing the survival rates of growing kids during the pre-weaning period primarily depends on alleviating the influence of stressful environmental conditions. Essential measures include optimizing the animals' microclimate, redesigning the physical environment, and improving managerial practices to maximize outcomes.

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نماذج احصائية مختلفة للتقييم الوراثي لبعض صفات الحليب والتكاثر في الماعز الزرايبي في مصر

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المخلص

تهدف هذه الدراسة إلى تحديد النموذج الإحصائي الأمثل للبيانات المتعلقة ببعض صفات الحليب (إنتاج اللبن الكلي وطول موسم الحليب) إلى جانب بعض صفات التكاثر (عدد الجداء المولودة والمفطومة). اختلفت النماذج الإحصائية المستخدمة من حيث وجود أو غياب التأثيرات الوراثية الأمومية والتجمعية والتباين البيئي الدائم والتغاير الوراثي الأمومي التجمعي. استخدم في هذه الدراسة 1638 سجل ولادة نتاج لعدد 411 أم و 79 أب. تم إجراء التحليل الإحصائي ببرنامج MTDFREML وتم اختيار النموذج الأمثل بناء على معيار AIC. تراوحت قيم المكافئ الوراثي التجمعي في جميع النماذج المدروسة في المدى ما بين 0.258 إلى 0.375 لإنتاج اللبن الكلي ومن 0.172 إلى 0.252 لطول موسم الحليب ومن 0.220 إلى 0.265 لعدد الجداء المولودة ومن 0.074 إلى 0.133 لعدد الجداء المفطومة. بينما كانت المكافئات الوراثية الأمومية في المدى من 0.094 إلى 0.144 لإنتاج اللبن الكلي ومن 0.089 إلى 0.112 لطول موسم الحليب ومن 0.078 إلى 0.097 لعدد الجداء المولودة ومن 0.043 إلى 0.080 لعدد الجداء المفطومة. كان الارتباط الوراثي التجمعي الأمومي موجب لصفات الحليب (0.123) لإنتاج اللبن الكلي و 0.093 لطول موسم الحليب) وسالب لصفات التكاثر (-0.261 لعدد الجداء المولودة و -0.082 لعدد الجداء المفطومة). كان الارتباط الوراثي التجمعي والأمومي والارتباط المطهري موجب بين جميع الصفات المدروسة. أيضا كان هناك مدى واسع للقيم التربوية للأبواء بالنسبة لإنتاج اللبن الكلي وطول موسم الحليب وعد الجداء المولودة. وتوصي الدراسة بدمج التأثير الوراثي الأمومي والتأثير الوراثي التجمعي مع التغاير الوراثي بينهم في النموذج الإحصائي لتحسين الوراثي الأمثل للماعز الزرايبي في مصر.

الكلمات المفتاحية: إنتاج اللبن، عدد البطن، الماعز الزرايبي، نماذج مقارنة.