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GENETIC AND ENVIRONMENTAL SOURCES OF VARIATION FOR LACTATION MILK YIELD IN KILIS GOATS

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Abstract: The Kilis goat is one of the most important indigenous dairy goat breeds in Türkiye and plays a significant role in milk production systems of the southeastern region. Despite its economic importance, information regarding genetic parameters for milk production traits remains limited. Therefore, the present study aimed to estimate variance components and genetic parameters for lactation milk yield in Kilis goats using a repeatability animal model. A total of 3,655 lactation milk yield records collected from 1,698 does and a pedigree comprising 1,815 animals were analyzed using the restricted maximum likelihood (REML) method implemented in WOMBAT software. Herd-year subclasses were included as fixed effects, while additive genetic and permanent environmental effects were fitted as random effects. The mean lactation milk yield was 402.23±84.02 kg. The estimated additive genetic, permanent environmental, residual, and phenotypic variances were 733.09±250.29, 0.01±264.20, 6298.76±187.39, and 7031.86±167.08 kg^2, respectively. Heritability for lactation milk yield was estimated as 0.10±0.03, indicating that additive genetic effects accounted for approximately 10.4% of the total phenotypic variation. The permanent environmental ratio was estimated to be negligible (0.00±0.00), resulting in a repeatability estimate equal to the heritability estimate (r=0.10). The results revealed that environmental and management factors constituted the major sources of variation in lactation milk yield, while a measurable but relatively low additive genetic component was present. These findings suggest that genetic improvement of milk yield in Kilis goats is possible through selection, although substantial gains will also require improvements in management practices and recording systems. The study provides baseline genetic parameters that may support the development of sustainable dairy-oriented breeding programs for the Kilis goat breed.

Keywords: Kilis goat, Lactation milk yield, Heritability, Genetic parameters, Animal model

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1. Introduction

Goat production has an important place in Türkiye's livestock sector because goats are well adapted to marginal environments, low-input production systems, mountainous areas, and semi-arid regions where cattle production is often limited (Gül et al., 2023). According to recent official statistics, Türkiye's goat population reached approximately 11.19 million head in 2025, representing a 3.4% increase compared with the previous year (TUIK, 2025). This population size indicates that goats continue to contribute substantially to rural livelihoods, household income, meat and milk production, and the sustainable use of natural grazing resources in Türkiye. In addition to their economic value, local goat breeds represent an important component of Türkiye's animal genetic resources and provide adaptive traits that are valuable under changing environmental and climatic conditions.

Among Turkish goat breeds, the Kilis goat is one of the most important dairy-oriented local genetic resources. The breed is mainly raised in the southeastern provinces of Türkiye, particularly Kilis, Gaziantep, Şanlıurfa, and Hatay, and is well adapted to the hot and dry conditions of the Fertile Crescent region (Gul et al., 2023). Kilis goats are generally considered to have originated from crossbreeding between the native Hair goat and the Damascus goat, combining the adaptability and hardiness of the Hair goat with the higher milk production potential of the Damascus goat (Karaköse and Gündüz, 2025; Korkmaz Ağaoğlu and Ertuğrul, 2012). Due to its developed udder structure, dairy type conformation, relatively long lactation period, and good reproductive performance, the Kilis goat has been recognized as an important breed for dairy goat production in Türkiye

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(Tatar et al., 2019). Reported lactation milk yields for Kilis goats vary widely depending on herd management, feeding conditions, age, year, and production system, with values commonly ranging from approximately 200 to 300 kg under ordinary conditions and reaching 400–500 kg under improved management (Gül et al., 2024). Previous studies have also shown that year, age, and environmental conditions significantly influence milk yield and reproductive traits in Kilis goats (Gul et al., 2023; Gül et al., 2024).

Genetic parameter estimation is essential for designing effective and sustainable breeding programs. Heritability, repeatability, and variance component estimates provide information on the proportion of phenotypic variation attributable to additive genetic, permanent environmental, and residual sources (Falconer and Mackay, 1996; Lynch and Walsh, 1998). These parameters are required to predict breeding values, determine expected genetic response to selection, and optimize selection strategies (Mrode, 2014). In dairy goats, milk yield is affected by both genetic and non-genetic factors, including herd, year, age at kidding, parity, litter size, lactation length, nutrition, and management (Mucha et al., 2018). Therefore, accurate estimation of genetic parameters under field conditions is particularly important for local breeds, where recording systems, pedigree depth, and management uniformity may be limited. Without population-specific genetic parameters, breeding programs may rely only on phenotypic performance, which can reduce selection accuracy and slow genetic improvement (Falconer and Mackay, 1996; Mrode, 2014).

In Türkiye, studies on goat milk production have mostly focused on phenotypic performance, environmental factors, reproductive traits, growth traits, milk composition, or crossbreeding comparisons. For example, studies on Kilis goats have reported variation in lactation milk yield and lactation length and emphasized the influence of environmental factors on performance traits (Tatar et al., 2019; Şen et al., 2021; Gül et al., 2024). However, genetic parameter studies for lactation milk yield in Turkish local goat breeds remain limited. This gap is important because local breeds such as Kilis, Hair, Honamlı, Angora, and Norduz goats are not only production animals but also reservoirs of adaptive genetic diversity. Estimating breed-specific genetic parameters would help determine whether improvement in milk yield can be achieved through selection and to what extent environmental management should be prioritized.

International literature shows that heritability estimates for milk yield in dairy goats vary considerably according to breed, trait definition, lactation stage, recording system, statistical model, and population structure. In mixed-breed dairy goats involving Alpine, Saanen, and Toggenburg ancestry, (Mucha et al., 2014) estimated genetic parameters for milk yield across lactations and reported that heritability varied across days in milk and lactation number. A broader meta-analysis including 963 heritability estimates from 162 studies reported pooled heritability estimates for milk production traits in dairy goats ranging from 0.27±0.03 to 0.48±0.13 (Mucha et al., 2022). Studies in Murciano-Granadina goats, Saanen goats, Jamunapari goats, and other dairy breeds have also demonstrated that milk yield and milk composition traits usually show sufficient genetic variation for selection, although estimates differ among populations and production environments (Analla et al., 1996; Rout et al., 2018; Ehsaninia et al., 2025). These findings suggest that genetic improvement of dairy traits in goats is possible, but reliable population-specific estimates are needed before implementing selection programs.

Despite the known dairy potential of Kilis goats, there is still a lack of detailed quantitative genetic information on lactation milk yield under field conditions. Such information is particularly important for community-based breeding programs and commercial herds aiming to improve milk yield while maintaining adaptation to regional environmental conditions. Therefore, the objective of the present study was to estimate variance components, heritability, permanent environmental ratio, and repeatability for lactation milk yield in Kilis goats using a repeatability animal model based on pedigree and repeated lactation records. The results are expected to provide baseline genetic parameters for future selection strategies and contribute to the development of sustainable dairy-oriented breeding programs for the Kilis goat population in Türkiye.

2. Materials and Methods

2.1. Animals and Data

The study was conducted using lactation milk yield records collected from Kilis goats reared under field conditions within the National Community-based Small Ruminant Breeding Programmein Türkiye. A total of 3655 lactation milk yield records obtained from 1698 does were used for the genetic analyses. Records were collected from three herds over a period of ten consecutive years.

Milk recording was performed at approximately 28-day intervals according to the International Committee for Animal Recording (ICAR) Alternate Test-Day (AT) method (Keskin et al., 2017; ICAR, 2021). Lactation milk yield (LMY) was estimated as the cumulative milk production over the lactation using the standard ICAR test-interval procedure based on successive test-day records.

The pedigree file comprised 1815 animals, of which 1814 remained after pedigree pruning procedures implemented by the analytical software. The pedigree included 44 sires and 214 dams, whereas 1,251 animals had unknown sires, 1537 had unknown dams, and 1180 animals had both parents unknown, reflecting the characteristics of a field-recording breeding population. The dataset contained repeated lactation records, with 54.8% of does contributing more than one observation.

Among the recorded animals, 45.2% had a single lactation record, while the remaining animals had between two and ten lactation records. Lactation milk yield (LMY, kg) was defined as the total milk produced during a lactation period. The average lactation milk yield was 402.23±84.02 kg, ranging from 155.90 to 699.30 kg.

Prior to the genetic analyses, the dataset was subjected to routine quality control procedures. Records with missing animal identification, inconsistent pedigree information, duplicate observations, or biologically implausible production records were excluded from the analyses. Pedigree integrity was verified before analysis, and pedigree pruning was automatically performed by WOMBAT to remove animals that did not contribute information to the relationship matrix.

2.2. Statistical Analysis

Variance components and genetic parameters for lactation milk yield were estimated using the restricted maximum likelihood (REML) methodology implemented in the software WOMBAT (Meyer, 2007).

Because repeated lactation records were available for individual animals, a repeatability animal model was fitted. This model accounts for the correlation among repeated records obtained from the same doe by partitioning the phenotypic variance into additive genetic, permanent environmental, and residual components, thereby providing unbiased estimates of genetic parameters.

The statistical model can be expressed as given in equation 1:

$$y = Xb + Za + Wpe + e \quad (1)$$

where:

(y) is the vector of lactation milk yield observations,

(b) is the vector of fixed effects,

(a) is the vector of additive genetic effects,

(pe) is the vector of permanent environmental effects associated with repeated records of the same animal,

(e) is the vector of random residual effects,

(X), (Z), and (W) are the corresponding incidence matrices relating observations to fixed and random effects.

The additive genetic effects were assumed to follow as in equation 2:

$$Var(a) = A\sigma_a^2 \quad (2)$$

where (A) is the numerator relationship matrix derived from pedigree information and (σ_a^2) is the additive genetic variance.

Permanent environmental effects were assumed to be as in equation 3:

$$Var(p) = I\sigma_{pe}^2 \quad (3)$$

and residual effects were assumed to be as in equation 4:

$$Var(e) = I\sigma_e^2 \quad (4)$$

where (I) is an identity matrix.

Herd-year subclasses were fitted as fixed effects to account for systematic environmental variation among herds and production years, including differences in management practices, feeding strategies, climatic conditions, and other non-genetic factors known to influence milk production. The herd-year effect consisted of 30 subclasses (3 herds × 10 production years), each representing a unique combination of herd and year. Animal additive genetic effects and permanent environmental effects were included as random effects.

Phenotypic variance was calculated as given in equation 5:

$$\sigma_p^2 = \sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2 \quad (5)$$

Heritability (h^2) was estimated as given in equation 6:

$$h^2 = \sigma_a^2/\sigma_p^2 \quad (6)$$

The proportion of permanent environmental variance was calculated as given in equation 7:

$$pe^2 = \sigma_{pe}^2/\sigma_p^2 \quad (7)$$

Repeatability ((r)) was estimated as given in equation 8:

$$r = \left(\sigma_a^2 + \sigma_{pe}^2\right)/\sigma_p^2 \quad (7)$$

where σ_a^2, σ_{pe}^2 and σ_e^2 denote additive genetic, permanent environmental, residual, and phenotypic variances, respectively.

3. Results

The structure and descriptive statistics of the dataset are presented in Table 1. A total of 3,655 lactation milk yield records obtained from 1,698 Kilis goats were included in the analysis. The pedigree file consisted of 1,815 animals, of which 1,814 remained after pedigree pruning. Mean lactation milk yield was 402.23 ± 84.02 kg, ranging from 155.90 to 699.30 kg.

The distribution of records across herds and years is shown in Table 2. Herd 3 contributed the largest proportion of observations (40.0%), followed by Herd 1 (35.7%) and Herd 2 (24.3%). The number of records increased over time, with the first four years accounting for only 27.5% of observations, whereas years 5–10 contributed approximately 72.5% of all records.

The repeated-record structure of the dataset is summarized in Table 3. Of the 1,698 does with records, 768 animals (45.2%) had a single lactation record, while 930 animals (54.8%) contributed repeated observations. Among these, 366 (21.6%), 271 (16.0%), 157 (9.2%), and 108 (6.4%) does had two, three, four, and five lactation records, respectively.

Variance component estimates and genetic parameters for lactation milk yield are presented in Table 4. The additive genetic variance (σ_a^2) was estimated as 733.09±250.29 , whereas the residual variance (σ_e^2) was estimated as 6298.76±187.39. Permanent environmental variance was estimated to be close to zero (σ_{pe}^2= 0.01±264.20). The estimated phenotypic variance was

7031.86±167.08. The heritability estimate for lactation milk yield was 0.104±0.035. The proportion of variance attributed to permanent environmental effects was negligible (0.000±0.00). Consequently, repeatability was estimated as 0.104, identical to the heritability estimate due to the near-zero permanent environmental variance component.

Table 1. Structure of the dataset used for genetic analyses

Item	Value
Lactation milk yield records	3655
Does with records	1698
Animals in pedigree	1815
Animals included in analysis	1814
Herds	3
Years	10
Repeated records (%)	54.8
Mean LMY (kg)	402.23
Standard deviation (kg)	84.02
Minimum LMY (kg)	155.90
Maximum LMY (kg)	699.30

Table 2. Distribution of lactation milk yield records across herds and years

Factor	Level	Records (n)	Percentage (%)
Herd	1	1304	35.7
	2	888	24.3
	3	1463	40.0
Year	2015	101	2.8
	2016	265	7.3
	2017	306	8.4
	2018	328	9.0
	2019	438	12.0
	2020	439	12.0
	2021	438	12.0
	2022	450	12.3
	2023	445	12.2
	2024	445	12.2

Table 3. Distribution of lactation records per doe in the Kilis goat population

Number of lactation records per doe	Number of does	Percentage (%)
1	768	45.2
2	366	21.6
3	271	16.0
4	157	9.2
5	108	6.4
6	23	1.4
7–10	5	0.3
Total	1698	100.0

Table 4. Variance components and genetic parameters for lactation milk yield in Kilis goats estimated using a repeatability animal model

Parameter	Estimate	Standard Error (SE)
Additive genetic variance (σ_a^2)	733.09	250.29
Permanent environmental variance (σ_{pe}^2)	0.01	264.20
Residual variance (σ_e^2)	6298.76	187.39
Phenotypic variance (σ_p^2)	7031.86	167.08
Heritability (h^2)	0.10	0.035
Permanent environmental ratio (pe^2)	0.00	0.00
Repeatability (r)	0.10	NR*

* NR = Not reported by WOMBAT. The standard error of repeatability was not directly estimated. Because the permanent environmental variance approached zero, the repeatability estimate was effectively equal to the heritability estimate.

4. Discussion

The present study provides one of the few quantitative genetic evaluations of lactation milk yield in the Kilis goat breed. The estimated heritability for lactation milk yield was 0.104±0.035, indicating that approximately 10.4% of the observed phenotypic variation was attributable to additive genetic differences among animals. This result suggests that genetic improvement through selection is possible, although a substantial proportion of the phenotypic variation remained unexplained by the fitted model and was captured by the residual variance. This residual component may include temporary environmental influences, measurement error, and other unaccounted biological or environmental sources of variation.

The heritability estimate obtained in this study was lower than estimates reported for several specialized dairy goat breeds. Analla et al. (1996) reported heritability estimates of approximately 0.17–0.18 for milk yield in Murciano-Granadina goats, while repeatability estimates ranged between 0.36 and 0.39. Similarly, Rout et al. (2018) reported heritability estimates of 0.15–0.26 for milk yield traits in Jamunapari goats. In a large-scale study involving Alpine-, Saanen-, and Toggenburg-derived dairy goats, Mucha et al. (2014) reported heritability estimates varying between 0.25 and 0.45 depending on lactation stage and parity. Compared with these studies, the estimate obtained in the present Kilis goat population can be considered relatively low.

Several factors may explain this difference. First, the present data originated from field conditions within the National Community-based Small Ruminant Breeding Programme, where environmental heterogeneity is

generally greater than in nucleus breeding herds or research stations. Variability in feeding practices, health management, housing conditions, reproductive performance, and climatic conditions can substantially increase residual variance and consequently reduce heritability estimates. This interpretation is consistent with the relatively large residual variance observed in the present study. However, the residual component likely represents a combination of temporary environmental effects, measurement error, and other unaccounted sources of variation rather than environmental and management factors alone.

Second, pedigree completeness was limited. A large proportion of animals had one or both parents unknown, reducing genetic connectedness within the population. In animal model analyses, incomplete pedigree information generally reduces the accuracy of additive genetic variance estimation and may lead to lower heritability estimates. Improved pedigree recording would likely increase the precision of future genetic evaluations.

Another noteworthy result was the near-zero estimate of permanent environmental variance. Permanent environmental effects represent non-genetic influences that consistently affect repeated records of the same animal across lactations. In dairy species, these effects are often associated with long-term management conditions, physiological characteristics, udder development, and lifetime health status. Therefore, repeatability estimates are usually higher than heritability estimates. For example, Analla et al. (1996) reported repeatability values around 0.39 for milk yield, whereas Rout et al. (2018) reported repeatability estimates between 0.68 and 0.73. In contrast, the present study produced a permanent environmental ratio close to zero, resulting in a repeatability estimate identical to the heritability estimate.

The near-zero estimate of permanent environmental variance should be interpreted with caution because its relatively large standard error indicates considerable uncertainty in estimating this variance component. Therefore, this result should not be regarded as evidence that permanent environmental effects are biologically absent in Kilis goats. Instead, it may reflect characteristics of the available data structure, including the distribution of repeated records, pedigree depth, and the limited ability of the model to separate permanent environmental effects from residual variation. Although 54.8% of animals contributed repeated records, nearly half of the does had only a single lactation record, and approximately two-thirds had no more than two records. Such a distribution may reduce the ability of the model to separate permanent environmental effects from residual variation. In the present dataset, although 54.8% of animals contributed repeated records, nearly half of the does had only a single lactation record, and approximately two-thirds had no more than two records. Such a distribution may reduce the ability of the repeatability model to distinguish permanent environmental effects from residual variation. (Arzik et al., 2024). Phenotypic investigations conducted under different production systems reported significant effects of year, management, and physiological factors on milk yield and reproductive performance (Arzik et al., 2025). The current findings are consistent with those observations and indicate that management interventions may produce faster short-term improvements than genetic selection alone.

Despite the relatively low heritability estimate, the existence of a measurable additive genetic component indicates that selection for increased milk yield remains feasible. However, substantial genetic progress will require improved pedigree recording, systematic performance recording, and greater connectedness among herds. The establishment of structured breeding programs combining accurate genetic evaluation with improved management practices may therefore enhance the dairy potential of the Kilis goat while preserving its adaptation to the environmental conditions of southeastern Türkiye.

5. Conclusion

This study estimated variance components and genetic parameters for lactation milk yield in Kilis goats using a repeatability animal model based on 3655 lactation records from 1698 does. The estimated heritability for lactation milk yield was low (h^2=0.104±0.035), indicating that additive genetic effects explained approximately 10% of the total phenotypic variation. In contrast, residual variance accounted for the largest proportion of the observed variation, highlighting the substantial influence of environmental and management factors on milk production performance. Although the heritability estimate was lower than those commonly reported for specialized dairy goat breeds, the presence of a measurable additive genetic component suggests that genetic improvement through selection is achievable in the Kilis goat population.

The permanent environmental variance was estimated to be negligible, resulting in a repeatability estimate equal to the heritability estimate. This finding likely reflects limitations in the structure of the available data, including incomplete pedigree information and the relatively low number of repeated records for many animals. Therefore, future studies should focus on improving pedigree completeness and expanding long-term performance recording systems. Overall, the results provide baseline genetic parameters for lactation milk yield in Kilis goats and indicate that sustainable improvement of milk production will require a combination of genetic selection and enhanced management practices. These findings may contribute to the design of future breeding programs aimed at improving dairy performance while maintaining the adaptation and resilience characteristics of this important indigenous Turkish goat breed.

Author Contributions

The percentages of the authors' contributions are presented below. All authors reviewed and approved the final version of the manuscript.

	Y.A.	S.G.	S.B.	M.K.	R.K.
C	25	20	20	20	15
D	25	20	20	20	15
S	15	25	25	25	10
DCP	25	20	20	20	15
DAI	25	20	20	20	15
L	25	20	20	20	15
W	25	20	20	20	15
CR	25	20	20	20	15
SR	25	20	20	20	15
PM	25	20	20	20	15
FA	10	30	10	30	20

C= concept, D= design, S= supervision, DCP= data collection and/or processing, DAI= data analysis and/or interpretation, L= literature search, W= writing, CR= critical review, SR= submission and revision, PM= project management, FA= funding acquisition.

Conflict of Interest

The authors declared that there is no conflict of interest.

Ethical Consideration

According the Regulation on the Working Procedures and Principles of Animal Experiments Ethics Committees of the Ministry of Forestry and Water Affairs (approval date: February 15, 2014, protocol code: 28914).

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