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Estimation of genetic potential for growth traits in Anatolian buffaloes

Yusuf Kaplan[1]*, **Samet Çinkaya**[2], **Mustafa Demirtaş**[2], **Mustafa Tekerli**[2]

[1] Republic of Türkiye Ministry of Agriculture and Forestry, General Directorate of Livestock, Ankara, Türkiye.
[2] Afyon Kocatepe University, Faculty of Veterinary Medicine, Department of Animal Science, Afyonkarahisar, Türkiye.

***Corresponding author:**
yusufkaplan66@gmail.com

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ABSTRACT - To conduct an optimal breeding and selection program, it is necessary to understand the genetic underpinnings of the desired traits. Early growth is an indicator of future success in the production and reproduction of buffaloes. This study aimed to estimate the (co)variance components for growth traits of Anatolian buffalo calves in Yozgat by employing six animal models with the different combinations of additive genetic, maternal genetic, maternal permanent effects, and covariance between offspring and dam. Birth weight (BW), six-month weight (SMW), twelve-month weight (TMW), and average daily gain (ADG) were analyzed with the data collected from 2726 Anatolian buffalo calves born between 2016 and 2023. Estimation of variance components and genetic parameters for growth traits of Anatolian buffaloes was performed with WOMBAT software. For each trait, Akaike's information criterion was used to detect the most appropriate model. The results showed that the best-fitted models explaining the variation in weights at birth (BW), six (SMW), and twelve (TMW) months of age and average daily gain (ADG) were models 3, 4, 1, and 1, respectively. Direct heritabilities for BW, SMW, TMW, and ADG were estimated in the range of 0.04±0.09-0.14±0.06, 0.23±0.09-0.49±0.15, 0.36±0.18-0.68±0.31, and 0.41±0.19-0.86±0.33, respectively. Maternal heritabilities for same traits were ranged between 0.02±0.09-0.04±0.03, 0.02±0.09-0.36±0.15, 0.05±0.14-0.22±0.24, and 0.00±0.15-0.20±0.25, respectively. This study unveiled genetic variability for growth traits in Anatolian buffaloes, suggesting that focusing selection efforts on these traits holds considerable promise for enhancing overall performance.

Keywords: Anatolian buffalo, (co)variance components, growth traits, maternal effect

1. Introduction

The Anatolian buffalo, a riverine type, has deep roots and significant connections with the social life of the population from the past to the present, notably spreading across the regions of the Black Sea, Marmara, Aegean, Central Anatolia, and Southeast Anatolia in Türkiye (Tekerli, 2016; Soysal et al., 2018). The buffalo is known as a robust and thrifty animal, providing various benefits to people through meat and milk products (Çinkaya and Tekerli, 2023; Jaglan et al., 2023). Anatolian buffaloes are characterized by crescent-shaped horns that extend by curving from front to back. Some of them have white spots on their heads, feet, and tails. The skin color of Anatolian buffaloes is typically gray-toned or black. The breed is also considered a significant animal genetic resource in Türkiye (Kaplan and Tekerli, 2023). Body weight at different stages is an important indicator of growth in livestock. The growth of calves not only reflects their adaptability to the environment but also implies an earlier onset of their reproductive and productive cycle. Early development and growth establish critical physiological foundations that significantly influence health, performance, and longevity in later life stages of animals (Joshi et al., 2022; George et al., 2023). The birth, six, and twelve-month weights (BW, SMW, and TMW) and average daily gains (ADG) are affected by both genetic and environmental factors (Erdoğan et al., 2021; Kaplan and Tekerli, 2024). Estimating (co)variance components and breeding values of interested traits is essential to breeding programs for genetic improvement (Koçak et al., 2024). According to the literature, some researchers have estimated the genetic parameters of growth traits using the paternal half-sib and animal model in buffaloes (Shahin et al., 2010; Gupta et al., 2015; Kaplan et al., 2024). Meyer (1992), Malhado et al. (2007), Thiruvenkadan et al. (2009) and Joshi et al. (2022) have suggested statistical models incorporating direct and maternal effects jointly. There is a scarcity of studies investigating the genetic determinants of growth through various animal models in buffalo breeds. The present study aimed to estimate the (co)variance components for growth traits of Anatolian buffaloes utilizing six different statistical models for each trait, accounting for direct, maternal, and permanent environmental effects.

2. Material and methods

The research was carried out using body weight records and pedigree information from 2,726 Anatolian buffalo calves of the Mediterranean type. The study was conducted on all recorded calves that required a comprehensive statistical analysis in the region between 2016 and 2023. Animals were raised in 21 villages with almost the same environmental conditions in Yozgat province where community-based Anatolian buffalo improvement program (TAGEM/66MANDA2015-01) conducted by the Ministry of Agriculture and Forestry of Türkiye. Yozgat is settled between the 38°40'–40°18' north parallel and the 34°05'–36°10' east meridians in the Central Anatolia Region and the prevailing climate is warm-summer Mediterranean. The primary economic sectors in the province are agriculture and livestock. Approximately 42% of farms produce all or part of their own feed requirements. Buffaloes are supplemented with concentrate at varying rates depending on pasture conditions, consuming approximately 9 kg of forage and 4 kg of concentrate per day. Buffalo calves are housed in barns for half of the year and spend the remainder grazing on pastures throughout the day (Kaplan et al., 2018). In a previous study, a smaller amount of data from the aforementioned project was analyzed using a simpler genetic model (Kaplan and Tekerli, 2023). The records of birth weight (BW), six-month weight (SMW), twelve-month weight (TMW), and average daily gain (ADG) were used as growth traits. The traits were measured by technical staff periodically. Over the years, the amount of collected data increased and the scope of the project expanded. The data were retrieved from a database managed using computer software known as Manda Yıldızı (Tekerli et al., 2025). This software processes the raw data through interpolation to determine weights for specific dates.

The ADG was calculated based on the weights at birth and twelve months of age. Initially, given tangible environmental conditions in the region, the least squares analysis was performed in Minitab 18 (Minitab, State College, PA, USA), including village, season, year of birth, sex, and dam age as fixed effects in the model. In all models, the village was considered as a fixed effect due to similar housing, feeding, and management practices provided. Only spring and summer born calves were used in this study. Given that the calves were suckled by their dams, dam age was included as a fixed effect with three categories: <5, 5–10, and >10 years. Furthermore, the outlier records ($\mu \pm 3$ standard deviations) were excluded from the analyses. (Co)variance components for growth traits were estimated by WOMBAT software (Meyer, 2007) using the average information-restricted maximum likelihood algorithm. The following six univariate models were fitted for each trait, considering direct, maternal, and the environmental fixed effects.

$$Y = X\beta + Z_a a + e \qquad \text{Model [1]}$$

$$Y = X\beta + Z_a a + Z_c c + e \qquad \text{Model [2]}$$

$$Y = X\beta + Z_a a + Z_m m + e \quad Cov(a, m) = 0 \qquad \text{Model [3]}$$

$$Y = X\beta + Z_a a + Z_m m + e \quad Cov(a, m) = A\sigma_{am} \qquad \text{Model [4]}$$

$$Y = X\beta + Z_a a + Z_m m + Z_c c + e \quad Cov(a, m) = 0 \qquad \text{Model [5]}$$

$$Y = X\beta + Z_a a + Z_m m + Z_c c + e \quad Cov(a, m) = A\sigma_{am} \qquad \text{Model [6]}$$

in which Y, β, a, m, c, and e represent the vectors of observations, fixed effects, direct additive genetic effects, maternal additive genetic effects, maternal permanent environmental effects, and residuals, respectively. The incidence matrices X, Z_a, Z_m, and Z_c correspond to the fixed effects, direct additive genetic effects, maternal additive genetic effects, and maternal permanent environmental effects, respectively. The direct additive, maternal additive, maternal permanent environmental, and residual effects are assumed to be normally and independently distributed with mean 0 and variances $A\sigma_a^2$, $A\sigma_m^2$, $I_d\sigma_{pe}^2$, and $I_n\sigma_e^2$, respectively. Here, A represents the numerator relationship matrix between animals, σ_a^2 denotes the direct additive genetic variance, σ_m^2 denotes the variance of maternal additive variance, σ_{am} is the covariance between additive and maternal genetic variance. σ_{pe}^2 and σ_e^2 expresses the variances of the maternal permanent environment and residual, respectively. I_d and I_n represent identity matrices, with their dimensions corresponding to the number of dams and calves, respectively (Hızlı et al., 2022).

Raw variances for each trait were used as the starting values in the estimation of genetic variances (Kaplan and Tekerli, 2020). The default value of 10^{-4} was used as a convergence criterion for the analyses according to Meyer (2007). By taking the Akaike information criterion (AIC) into account, the log-likelihood ratio test was made a decide which model was best suited for traits. The following is the AIC formula (Akaike, 1973).

$$AIC = -2logL_i + 2p_i \qquad \text{Formula [1]}$$

in which $log\ L_i$ represents the maximized log likelihood of model i at convergence, and p_i denotes the number of random (co) variance parameters of model i. The model minimum AIC value was selected as the most suitable model for each trait. The total heritability was computed for each model using the following formula described by Willham (1972).

$$h_T^2 = (\sigma_a^2 + 0.5\sigma_m^2 + 1.5\sigma_{am}) / \sigma_p^2 \qquad \text{Formula [2]}$$

3. Results

The structure of the data and the significance of fixed effects were presented in Table 1. The high variation in traits contributes to the understanding and explanation of random and fixed effects such as animal, sex, and year. According to Table 1, the coefficient of variations for BW, SMW, TMW, and ADG are 13.26, 18.25, 17.46, and 21.13%, respectively. The average number of offspring per dam of the BW, SMW, TMW, and ADG were found to be 2.75, 2.36, 3.14, and 2.99, respectively. The average inbreeding coefficient was determined as 2% of the population. All fixed effects were detected to be significant for the examined traits, except for dam age. Dam age did not have a significant effect on SMW and TMW, indicating that the physiological maturity of cows influences the fetal development of buffalo calves. (Co)variance components and genetic parameters were estimated by the six models in the univariate analyses for growth traits (Table 2). The model with a minimum AIC value was selected as the most appropriate model. According to AIC, the most suitable models for BW and SMW were model 3 and model 4, respectively. Model 1 was also the most suitable for TMW and ADG. Model 1 have the highest total heritabilities, with values more than twice their standard errors for all traits except ADG. The ADG has the highest total heritability in Model 6 accompanied by the highest AIC. Model 4 was identified as the most suitable for SMW and resulted the highest direct heritability (0.49±0.15) of SMW compared with the others. The direct genetic and maternal effects were found to have highly negative correlations in SMW. The total heritability estimate for SMW was 0.17±0.10. Model 1 was found to be superior for the TMW among all animal models based on AIC. Model 1 was found to be the best equation for the ADG. Our results showed that the average daily gain has a large genetic variation.

Table 1 - Characteristic of the data structure for body weights of Anatolian buffalo

Item	Traits			
	BW	SMW	TMW	ADG
Village	***	***	***	***
Birth year	***	***	***	***
Birth season	**	***	***	***
Sex	**	***	***	***
Age of dam	***	ns	ns	*
Number of records	2726	2461	1724	1703
Number of dams	992	1045	572	569
Average number of offspring per cow	2.75	2.36	3.14	2.99
Mean	31.14	106.68	157.61	345.46
Standard deviation	4.14	19.47	27.51	73.01
Minimum	18.00	49.85	71.61	133.97
Maximum	44.00	169.71	245.55	570.85
CV%	13.26	18.25	17.46	21.13
Average inbreeding coefficient (%)	0.02			

BW - birth weight; SMW - six months weight; TMW - twelve-month weight; ADG - average daily gain between birth and twelve weight.
ns - non-significant (P>0.05); *P<0.05; **: P<0.01; ***: P<0.001.
The unit of all traits is kg, except for ADG (g).

4. Discussion

Growth traits are influenced by both genetic and environmental factors (Erdoğan et al., 2021). Accurately estimating (co)variance components of traits of interest is essential for animal breeding programs (Koçak et al., 2024). A few studies have reported the genetic parameters of growth traits using different animal models in various buffalo breeds. Some of them (Malhado et al., 2007; Thiruvenkadan et al., 2009; Joshi et al., 2022) have suggested statistical models incorporating direct and maternal effects jointly.

Model 1 showed a relatively higher estimate of heritability for birth weight, but Model 3 provided the best fit compared with the others. In the absence of AIC results to determine the best-fitting model, those with higher heritability estimates should be considered when evaluating the animals. In this study, the estimated direct (0.05±0.07) and maternal (0.04±0.03) heritabilities for birth weight (BW) in Model 3 were low for Anatolian buffaloes, whereas Joshi et al. (2022) reported higher estimates for direct (0.19±0.03) and maternal (0.13±0.04) heritabilities. Additionally, heritabilities for BW have been reported in the range of 0.18 to 0.66 for Swamp, Murrah, Egyptian, Nili-Ravi, Surti and Anatolian buffalo breeds (Thevamanoharan et al., 2001; Yadav et al., 2001; Thiruvenkadan et al., 2009; Shahin et al., 2010; Akhtar et al., 2012; Gupta et al., 2015; Pandya et al., 2015; Kaplan et al., 2024). Across all models, heritability estimates for BW were low, likely due to environmental influences, data characteristics, and breed variation. Therefore, only slight improvements in BW could be achieved through selection based on the current findings.

Model 4 was identified as the most suitable for SMW and provided the highest direct heritability (0.49±0.15) of SMW compared with the others. Joshi et al. (2022) reported Model 3 as the best fitted for SMW in Murrah buffaloes, and almost the same direct heritability was reported by those researchers.

Table 2 - (Co)Variance components and genetic parameters for BW, SMW, TMW, and ADG of Anatolian buffalo calves obtained by different six models

	Model	σ^2_a	σ^2_{pe}	σ^2_m	σ_{am}	σ^2_e	σ^2_p	h^2_a	pe^2	h^2_m	r_{am}	h^2_T	LogL	AIC
BW	1	1.90±0.80				12.11±0.84	14.01±0.38	0.14±0.06				0.14±0.06	-4979.271	9962,542
	2	1.14±0.98	0.45±0.33			12.42±0.87	14.02±0.38	0.08±0.07	0.03±0.02			0.08±0.07	-4978.301	9962,602
	3	**0.72±1.01**		**0.61±0.35**		**12.70±0.88**	**14.02±0.38**	**0.05±0.07**		**0.04±0.03**		**0.07±0.06**	**-4977.671**	**9961,342**
	4	0.55±1.24		0.29±0.70	0.40±0.83	12.82±1.06	14.06±0.39	0.04±0.09		0.02±0.05	1.00±failed	0.09±0.07	-4977.041	9962,082
	5	0.71±1.04	0.00±0.93	0.61±0.98		12.70±0.92	14.02±0.38	0.05±0.07	0.00±0.07	0.04±0.07		0.07±0.07	-4977.672	9963,344
	6	0.51±1.23	0.00±0.96	0.31±1.30	0.40±0.85	12.85±1.06	14.07±0.39	0.04±0.09	0.00±0.07	0.02±0.09	1.00±failed	0.09±0.07	-4977.042	9964,084
SMW	1	127.19±23.21				198.10±21.93	325.29±9.49	0.39±0.07				0.39±0.07	-8303.49	16610,980
	2	82.32±27.52	29.96±10.05			214.51±22.61	326.79±9.65	0.25±0.08	0.09±0.03			0.25±0.08	-8298.309	16602,618
	3	74.87±28.21		30.49±10.44		221.58±22.80	326.94±9.66	0.23±0.09		0.09±0.03		0.28±0.08	-8298.691	16603,382
	4	**158.01±50.11**		**116.62±28.61**	**-107.68±34.74**	**155.87±37.98**	**322.82±9.53**	**0.49±0.15**		**0.36±0.09**	**-0.79±0.10**	**0.17±0.10**	**-8292.1**	**16592,200**
	5	80.12±30.05	24.21±28.15	6.36±29.95		216.16±24.35	326.85±9.65	0.25±0.09	0.07±0.09	0.02±0.09		0.25±0.08	-8298.286	16604,572
	6	158.12±50.13	0.00±30.16	116.63±47.35	-107.71±35.97	155.78±38.02	322.82±9.53	0.49±0.15	0.00±0.09	0.36±0.15	-0.79±0.12	0.17±0.10	-8292.1	16594,200
TMW	**1**	**356.36±58.99**				**249.41±52.96**	**605.77±21.49**	**0.59±0.09**				**0.59±0.09**	**-6319.782**	**12643,564**
	2	263.96±90.76	38.48±28.53			302.97±68.31	605.41±21.54	0.44±0.15	0.06±0.05			0.44±0.15	-6318.877	12643,754
	3	218.74±108.89		49.90±34.11		336.51±80.14	605.15±21.53	0.36±0.18		0.08±0.06		0.40±0.16	-6318.836	12643,672
	4	413.16±189.55		130.48±86.14	-129.44±116.18	192.64±138.64	606.84±21.67	0.68±0.31		0.22±0.14	-0.56±0.24	0.47±0.16	-6318.35	12644,700
	5	230.57±118.83	14.70±70.95	32.74±86.87		327.20±88.44	605.21±21.53	0.38±0.20	0.02±0.12	0.05±0.14		0.41±0.16	-6318.816	12645,632
	6	412.52±189.83	0.02±76.56	130.33±144.10	-129.14±124.26	193.10±138.74	606.83±21.68	0.68±0.31	0.00±0.13	0.22±0.24	-0.56±0.24	0.47±0.16	-6318.35	12646,700
ADG	**1**	**2197.85±428.51**				**2088.85±393.02**	**4286.70±152.30**	**0.51±0.09**				**0.51±0.09**	**-7885.385**	**15774,770**
	2	1839.19±646.51	143.82±198.58			2301.15±491.31	4284.16±152.31	0.43±0.15	0.03±0.05			0.43±0.15	-7885.13	15776,260
	3	1755.40±801.59		153.66±246.52		2374.12±587.81	4283.18±152.23	0.41±0.19		0.04±0.06		0.43±0.16	-7885.222	15776,444
	4	3719.21±1431.47		853.15±626.56	-1192.13±861.50	925.34±1042.77	4305.57±154.26	0.86±0.33		0.20±0.15	-0.67±0.16	0.55±0.17	-7884.565	15777,130
	5	1838.28±907.52	144.07±517.98	0.02±650.80		2301.77±674.70	4284.14±152.32	0.43±0.21	0.03±0.12	0.00±0.15		0.43±0.16	-7885.13	15778,260
	6	3711.21±1433.85	6.11±563.00	840.78±1094.92	-1183.62±938.24	931.02±1043.78	4305.51±154.27	0.86±0.33	0.00±0.13	0.20±0.25	-0.67±0.23	0.55±0.17	-7884.565	15779,130

σ^2_a - direct additive genetic variance; σ^2_{pe} - maternal permanent environmental variance; σ^2_m - maternal additive genetic variance; σ_{am} - genetic covariance of direct-maternal effect; σ^2_e - residual variance; σ^2_p - phenotypic variance; h^2_a - direct heritability; pe^2 - ratio of maternal permanent environmental effect; h^2_m - maternal heritability; r_{am} - genetic correlation between additive and maternal effect; h^2_T - total heritability; BW - birth weight; SMW - six months weight; TMW - twelve month weight; ADG - average daily gain between birth and twelve weight.
Bold text indicates the best model with the lowest value of AIC.

The direct genetic and maternal effects were found to have highly negative correlations in SMW. The probable reason for the negative correlation could be nontangible environmental factors, collinearity and the structure of data including pedigree (Lee, 2002; Illa et al., 2024). The total heritability estimate for SMW was 0.17±0.10. The negative covariance between direct and maternal genetic effects considered to estimate total heritability may result in decreased total heritability and this aligns with Joshi et al. (2022). Pandya et al. (2015) found a similar heritability by the paternal half-sib method in Surti buffaloes (0.22±0.12). However, a higher estimate (0.44) was also found in the Murrah buffalo (Shahin et al., 2010). Our result showed that the maternal inheritance lost its effect on growth after six months of age. This was in consonance with the findings Khattab et al. (2009) and Singh et al. (2010).

Model 1 was found to be superior for the TMW among all animal models based on AIC. As calves get older, the maternal effect may decrease and lose its impact on their growth. Similarly, Joshi et al. (2022) reported Model 1 as the best equation for this trait. In our study, the total and direct heritabilities were estimated as 0.47±0.16 and 0.68±0.31, respectively. The estimates were higher than the range of 0.10-0.39 reported by Akhtar et al. (2012), Pandya et al. (2015), Joshi et al. (2022), and Kaplan et al. (2024) for different buffalo breeds. Furthermore, our result for TMW is consistent with the value of 0.66 reported for Anatolian buffalo (Çinkaya and Tekerli, 2023). This finding further confirms the potential for genetic improvement of this trait in buffalo populations.

Model 1 was also identified as the best fit for the ADG. Our results showed that the average daily gain was largely influenced by genetics. The additive heritability estimate (0.51±0.09) for this trait was high and consistent with the result (0.69±0.17) of Kaplan and Tekerli (2023). These findings highlight the strong genetic component of ADG, suggesting that genetic selection could be an effective strategy for improving growth rate in buffalo populations.

5. Conclusions

The maternal and direct additive effects contribute significantly to the phenotypic variation in the growth of Anatolian buffalo calves. The best models were 1 for TMW and ADG, 3 for BW, 4 for SMW while heritability estimates ranged from low to high. The results showed that Anatolian buffaloes have substantial genetic variation that can be exploited to enhance growth traits through a selective breeding program. When evaluating the animals in their early life, it is essential to consider the influence of both direct and maternal effects. The TMW could be considered as significant selection criteria due to higher direct heritabilities and computational ease. Comprehensive studies would be beneficial for obtaining more precise estimates of genetic parameters using advanced statistical models.

Data availability

The growth data used in this study belong to the General Directorate of Agricultural Research and Policies in Türkiye. The records from the study will be made available upon reasonable request, subject to approval from the Ministry of Agriculture and Forestry.

Author contributions

Conceptualization: Kaplan, Y.; Çinkaya, S.; Demirtaş, M. and Tekerli, M. **Formal analysis:** Kaplan, Y.; Çinkaya, S. and Demirtaş, M. **Investigation:** Kaplan, Y. and Tekerli, M. **Methodology:** Kaplan, Y. and Tekerli, M. **Resources:** Kaplan, Y. and Tekerli, M. **Software:** Kaplan, Y. and Tekerli, M. **Writing – original draft:** Kaplan, Y. **Writing – review & editing:** Çinkaya, S. and Demirtaş, M.

Conflict of interest

The authors declare no conflict of interest.

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