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ESTIMATION OF HERITABILITY AND GENETIC CORRELATION USING CROSS-CORRELATION METHOD IN ANATOLIAN BUFFALOES RAISED IN İSTANBUL PROVINCE

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Abstract: In animal breeding, increasing yields fundamentally requires the improvement of environmental factors and the selection of genetically superior animals. If the environmental conditions deteriorate, the yield increase will not be sustainable due to management and nutrition only. Sustainable improvement of yields depends on selecting animals with high genetic breeding values and allowing them to reproduce. However, an accurate estimation of breeding values needs to know some genetic parameters such as heritability and genetic correlation for the trait of interest. Methods used for estimating these parameters include parent-offspring correlation and regression, half-sib correlation, maximum likelihood, REML, GWAS, among others. The methods are necessary for pedigree information except for parent-offspring correlation and regression. Obtaining pedigree information, however, is not always possible in extensive farming conditions, whereas data on parents and offspring are more accessible. The aim of this study is to introduce the cross-correlation method based on parent-offspring correlation and demonstrate how genetic correlation coefficient and heritability are calculated using this method. Heritabilities were found 0.39 for birth weight, 0.12 for six-month weight, and 0.08 for yearling weight. The genetic correlations between birth and sixth-month, birth and yearling, sixth-month and yeraling weights were positive 0.07, 0.25, and 0.67 respectively. To increase success in breeding programs, preferring the most appropriate model and calculations may be useful for estimating the genetic parameters of traits, for revealing the relationships among traits, and calculating the breeding values of individuals through these results.

Keywords: Anatolian buffalo, growth traits, cross-correlation, genetic parameters

INTRODUCTION

Estimation of genetic parameters such as the heritability of traits of interest and genetic correlations between them in breeding programs applied in farm animals is an important condition for genetic progress in the increase in yield traits. This requires detailed knowledge about the inheritance of phenotypic traits. Until recently, genetic parameter estimates were primarily obtained using parent-offspring correlations and regressions. However, it has been stated by Akesson et al. (2008) that animal models perform better than parent-offspring regressions due to their use of the numerated relationship matrix and their ability to explicitly model shared environmental effects among individuals. In recent years, there has been an increase in the use of generalized linear mixed animal models based on pedigree information to estimate genetic variance components for economic traits in buffalo breeding (Çinkaya and Tekerli 2023, Güllüce 2023, Kaplan and Tekerli 2023, Kaplan et al. 2023). In some cases, insufficient pedigree may occur in breeder conditions, and genetic parameters that are needed to determine breeding value can be estimated using data on parents and offspring. Akesson et al. (2008) and Villemereuil et al. (2013) have calculated genetic parameters using animal models and methods based on parent-offspring relationships for some traits and reported their results comparatively. Similarly, Düzgüneş et al. (2003) and Xu (2022) reported that the cross-correlation method can be used to calculate the heritability and genetic correlation coefficients of two traits across two generations. Cross-correlation is defined as the relationship between a trait X belonging to a parent and a trait Y belonging to its offspring, or between a trait Y belonging to a parent and a trait X belonging to its offspring. In extensive breeding conditions where accessing pedigree information is not always possible, dams are commonly used as parents. When the relationship between parents and offspring is known, the cross-correlation method can be utilized to calculate the heritability for each trait and the genetic correlation between two traits (Xu 2022, Düzgüneş et al. 2003). This study aims to estimate genetic parameters using the cross-correlation method for birth, six-month, and one-year weights observed in dams and their offspring within the Anatolian buffalo breeding project conducted by community based buffalo improvement program in İstanbul province.

MATERIALS AND METHODS

The material for this study consisted of Anatolian buffaloes in the sub-project implemented in İstanbul province under the "*community-based animal improvement program*" managed by the General Directorate of Agricultural Research and Policies (Project No: TAGEM/34/MANDA2011-01). A total of 1597 buffalo cows born between 2012 and 2022, obtained from the "Buffalo Star" data registration program (Tekerli 2019), and the birth, six-month, and one-year weights of their calves were used in the study. Variance analysis with the factors of village, year, season, and gender was performed using Model 1 to measure the effects of these factors on the data using the general linear model option of the Minitab software (Minitab 18). The effects of factors significantly influencing the interested traits were standardized using the breeding assistant (Tekerli 2017).

$$Y_{ijklm} = \mu + v_i + y_j + s_k + g_l + e_{ijklm}$$ Model [1]

where

Y_{ijklm} = birth, six-month, and one-year weights, μ = expected mean for all calves, v_i = effect of the i_{th} village, i = 1(Baklalı), 2(Binkılıç), ..., 21(Yolçatı), y_j = effect of the j_{th} year, j = 1(2012), 2(2013), ..., 11(2022), m_k = effect of the k_{th} season, k = 1(Winter), 2(Spring), 3(Summer), 4(Autumn), c_l = effect of the l_{th} gender, l = 1(Female), 2(Male), e_{ijklm} = random Error, N (0, σ²).

The phenotypic correlation coefficients between birth, six-month, and one-year weights determined in dams and their offspring with data adjusted for environmental factors were determined using the Pearson correlation option of the Minitab software (Minitab 18). The obtained coefficients were substituted in the following main formulas reported by Xu (2022), and the heritabilities and genetic correlation coefficients for the traits were estimated.

$$h_X^2 = 2r_{X_0X_1}$$ Main Formula [1]

$$r_A = r_{X_0Y_1} + r_{Y_0X_1}/2 * \sqrt{r_{X_0X_1} \times r_{Y_0Y_1}}$$ Main Formula [2]

Where;.

h_X^2: heritability for each trait, $r_{X_0X_1}$: the phenotypic correlation coefficient between parent and offspring for each trait, r_A: the genetic correlation coefficient between traits, X_0: the first trait in the parent, X_1: the first trait in the offspring, Y_0: the second trait in the parent, Y_1: the second trait in the offspring.

Additionally, the application of symbols in the above two main formulas to each of the birth, six-month, and one-year weights, which are the subject of research, is shown in the following sub-formulas.

$$h_{DA}^2 = 2 * r_{DA_aDA_y}$$ Sub-Formula [1]

$$h_{AA}^2 = 2 * r_{AA_aAA_y}$$ Sub-Formula [2]

$$h_{BY}^2 = 2 * r_{BY_aBY_y}$$ Sub-Formula [3]

$$r_{(DA),(AA)} = r_{DA_aAA_y} + r_{DA_yAA_a}/2 * \sqrt{r_{DA_aDA_y} \times r_{AA_aAA_y}}$$ Sub-Formula [4]

$$r_{(DA),(BY)} = r_{DA_aBY_y} + r_{DA_yBY_a}/2 * \sqrt{r_{DA_aDA_y} \times r_{BY_aBY_y}}$$ Sub-Formula [5]

$$r_{(AA),(BY)} = r_{AA_aBY_y} + r_{AA_yBY_a}/2 * \sqrt{r_{AA_aAA_y} \times r_{BY_aBY_y}}$$ Sub-Formula [6]

Where

$h^2_{DA}, h^2_{AA}, h^2_{BY}$: the heritabilities for birth, six-month, and one-year weight, $r_{(DA),(AA)}, r_{(DA),(BY)}$: the genetic correlation coefficients between birth, six-month, and one-year weight $r_{AA_aAA_y}, r_{BY_aBY_y}, r_{DA_aAA_y}, r_{DA_yAA_a}, r_{DA_aBY_y}, r_{DA_yBY_a}, r_{AA_aBY_y}, r_{AA_yBY_a}$: the correlation coefficients between parent and offspring for birth, six-month, and one-year weight.

RESULTS AND DISCUSSION

Descriptive statistics regarding growth traits, heritabilities, and findings related to phenotypic and genetic correlations are presented in Tables 1, 2, 3, and 4. In Table 1, the descriptive statistics indicate variations in the number of animals for birth weight, birth to sixth-month weight, and birth to one-year weight. This variation shows that couldn't all calves for which birth weight was recorded weights at six months and one year. Therefore, when calculating heritabilities for traits, the highest number of observations (n) was considered. Similarly, when calculating correlation coefficients, the highest number of observations where both traits could be measured simultaneously was taken into account. The mean birth weight ranges from 33.26 to 34.02 kg in dams and from 33.40 to 34.88 kg in calves. These birth weight values are lower than those reported for Egyptian and Nili Ravi buffaloes (Ahmad et al., 2002; Akhtar et al., 2012; Iam, 2019; Kuthu & Hussain, 2020) and higher than those reported for Anatolian buffaloes by Çelikeloğlu et al. (2015), Uğurlu et al. (2016), and Kul et al. (2015). Barbosa et al. (2006) and Thiruvenkadan et al. (2009) reported birth weights of 34.20 ± 5.02 kg and 32.40 ± 0.30 kg, respectively, for Murrah buffaloes. The differences observed may be attributed to breed, methodology, climate, management, feeding, and other similar conditions. The average sixth-month weight ranges from 109.07 to 116.13 kg in dams and from 109.26 to 112.48 kg in calves. This weight reported by Shahin et al. (2010) as 113.95 kg for Egyptian buffaloes is similar to the values found in this study. However, it is slightly higher than the 87.9 ± 0.95 kg reported for Murrah buffaloes by Thiruvenkadan et al. (2009). The authors attributed the lower sixth-month weight to the influence of a hot and humid climate on the genotype. Additionally, the values are slightly lower than the 121.701 ± 5.071 kg reported for Anatolian buffaloes by Çelikeloğlu et al. (2015). These differences may be due to the management and feeding conditions of buffaloes in university farms in Afyon and under breeder conditions in Istanbul. Moreover, while the values are higher than the 73.42 ± 1.65 kg reported for Surti buffaloes by Pandya et al. (2015), they are lower than those reported for Mediterranean crossbred buffaloes in Bangladesh (144.14 ± 4.10 kg) by Shahjahan et al. (2017). This may be due to differences in breed, geographical and breeding conditions. The average yearling weight was found to be 188.68 kg in dams and 193.12 kg in calvess. This finding is consistent with the value reported for Anatolian buffaloes by Çelikeloğlu et al. (2015). The one-year weight is slightly higher than the values reported for Egyptian, Murrah, and Nili Ravi buffaloes by different researchers (Akhtar et al., 2012; Thiruvenkadan et al., 2009; Shahin et al., 2010). These differences could be attributed to breed, rearing practices, geographical conditions, management and feeding practices. Overall, there was an increase in buffalo weights. It could be due to the selection in the breeding project implemented over the past decade. As seen in Table 2, It was found that phenotypic correlation coefficients between some weights were significant like birth weights dam and calves. It can be said that the selection to be made for one of these traits will be positively affected by the other traits. The heritability

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estimates for birth, six-month, and one-year weights are 0.39, 0.12, and 0.08, respectively. A decreasing trend in heritability estimates for growth traits from birth to one year of age has been observed. This decline may be due to the decrease in the number of observations used for heritability estimation from birth to one year. For birth weight, heritability estimates have been reported between 0.12 and 0.66 by different researchers (Akhtar et al., 2012; Thiruvenkadan et al., 2009; Thevamanoharan et al., 2001; Barbosa et al., 2006; Shahin et al., 2010; Iam, 2019; Kaplan & Tekerli, 2023; Kaplan et al., 2023). This variability may stem from the studies being conducted on different breeds and the statistical models used. Additionally, since heritability is a trait that can vary between populations, breeds, and even herds, this variability is considered natural (Düzgüneş, 2003). Contrary to our findings for sixth-month weight, moderate heritability estimates have been reported for Egyptian, Murrah, and Surti buffaloes by different researchers (Thiruvenkadan et al., 2009; Shahin et al., 2010; Pandya et al., 2015). The heritability estimate for one-year weight is consistent with the results obtained by Thiruvenkadan et al. (2009), Akhtar et al. (2012), and Pandya et al. (2015) for Murrah, Nili Ravi, and Surti buffalo breeds. The genetic correlations between birth and sixth-month, birth and one-year, and sixth-month and one-year live weights are positively 0.07, 0.25, and 0.67, respectively. Some researchers (Thiruvenkadan et al., 2009; Shahin et al., 2010; Kaplan et al., 2023; Kaplan & Tekerli, 2023) have reported similar results for different buffalo breeds. Moderate to high genetic correlations in the desired direction between traits indicate that selection for these traits will increase growth rates in future generations.

RESULTS AND DISCUSSION

In this study, the cross-correlation method was demonstrated for growth traits, which are important quantitative characters in animal breeding. Heritabilities, phenotypic and genetic correlation coefficients were determined. It has been shown that genetic parameters can be estimated using cross-correlation even in breeding studies where pedigree information is difficult to obtain under extanxive breeding conditions. Consequently, estimating genetic parameters using the most appropriate model and the most accurate calculations for the traits to be selected, revealing the relationships between these traits, and estimating the breeding values of individuals based on these results are major factors that increase success in breeding programs. In summary, when breeding buffaloes selected with a high degree of accuracy based on scientific methods are allowed to reproduce calves under similar environmental conditions, genetic progress can be achieved.

CONFLICT OF INTEREST

No conflict of interest is declared by the authors.

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Number of traits and generations	Trait name	n	Mean.	SE	SD	Min.	Max.
One traits, two generations	DA_a	1597	33,95	0,13	5,36	16,81	49,76
	DA_y	1597	33,40	0,12	4,90	17,44	50,54
Dual traits, two generations	DA_a	824	34,02	0,17	4,75	16,64	46,65
	DA_y	824	34,73	0,16	4,62	18,27	48,10
	AA_a	824	116,13	0,82	23,54	62,39	197,44
	AA_y	824	112,48	0,73	20,84	45,00	244,09
Three traits, two generations	DA_a	418	33,26	0,21	4,20	19,83	43,47
	DA_y	418	34,88	0,21	4,38	20,01	47,37
	AA_a	418	109,07	1,04	21,20	51,01	199,09
	AA_y	418	109,26	0,83	16,88	38,43	176,05
	BY_a	418	188,68	1,87	38,26	82,05	363,70
	BY_y	418	193,12	1,56	31,92	61,69	303,60

Table:1 Descriptive statistics on birth, six, and one-year weights in terms of single, double, and triple traits in two generations (damand offspring).

DA_a Birth weight of the dam, DA_y: Birth weight of the offspring, AA_a: Sixth month weight of the dam, AA_y Sixth month weight of the offspring, BY_a One-year weight of the dam BY_y: One-year-old weight of the offspring

Traits	DA_a	DA_y	AA_a	AA_y	BY_a	BY_y
DA_a	**1**	0,189 (0,001)	0,127 (0,001)	0,018 (0,612)	0,088 (0,072)	0,066 (0,178)
DA_y		**1**	-0,006(0,860)	0,252 (0,001)	-0,023(0,636)	0,298 (0,001)
AA_a			**1**	0,060 (0,083)	0,830 (0,001)	0,023 (0,643)
AA_y				**1**	0,043 (0,377)	0,763 (0,001)
BY_a					**1**	0,040 (0,413)
BY_y						**1**

Table 2: Phenotypic correlation coefficients and standard errors of growth traits

The numbers at the top of the diagonal indicate the phenotypic correlation coefficients, and the values given in parentheses indicate the importance levels. DA_a :Birth weight of dam, DA_y :Birth weight of offspring, AA_a Sixth month weight of dam, AA_y:Sixth month weight of offspring, BY_a:One-year weight of dam, BY_y:One-year weight of offspring

Özellik Adı	n	h^2
Birth weight	1597	0,39
Sixmonths weight	824	0,12
Yearling weight	418	0,08

Table 3: Degrees of heritability of growth traits

Traits	Birth weight	Sixth month weight	One-year weight
Birth weight	1	0,06	0,25
Sixth month weight		1	0,67
One-year weight			1

Table 4: Genetic correlations between traits

The numbers on top of diagonal show the genetic correlation coefficients.

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