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ESTIMATION OF VARIANCE COMPONENTS AND SOME GENETICS PARAMETERS FOR MILK YIELD IN WATER BUFFALO POPULATION RAISED IN ISTANBUL

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ABSTRACT

This study aims to estimate variance components, heritability, and repeatability of lactation yield (270 day), as well as estimated breeding value for 879 water buffalo lactation records for 615 animals belonging to the water buffalo breeding project using BUGA software. The model was constructed by using all available the pedigree information. Herd, season and year were used as fixed effects while lactation length and age were used as covariate. Random environment variance, genotypic variance and permanent environment variance values were estimated as 48388.61±0.0003 kg^2, 12003.08±0.0003 kg^2 and 9567.92±0.0003 kg^2 while heritability (h^2) and repeatability (r) of lactation yield were estimated as 0.17 ±0.162 and 0.30, respectively. The study concluded that the heritability of milk yield was low and in order to achieve more effective genetic improvement, the project should be organized in a way that allows for the identification of sire records for the animals involved. In addition, the environmental conditions in which buffalos are raised must be brought closer to the conditions required by the animals.

Key words: water buffalo, estimated breeding value, BUGA software, genetic parameter

INTRODUCTION

Water buffalo is one of the livestock species that adapt to very different environmental conditions, including marginal topographic conditions such as swamps and diseases. However, on the other hand, they are pretty vulnerable to heat stress due to the characteristics of their skin and sweat glands. It is more capable than cattle in terms of utilizing poor-quality roughage. In addition, the dry matter content of its milk is higher than that of cow's milk, and the composition of its meat is richer. Although its milk has still a very low proportion (%0.19) (Turan *et al.*, 2022) in total milk production, its milk has a great potential for sustainable water buffalo breeding. Due to its specific content, it is favourable for some products, such as yogurt and ice cream. While this rich content of milk causes it to be marketed at a higher price, it also provides an economic advantage to the producer. This animal species, which has the potential to be used as draught animal, especially in underdeveloped countries, as well as for its meat and milk, is decreasing in number in Türkiye, like the situation in many countries. This decrease in the numerical abundance of buffaloes can be associated with their slow development and late reaching of puberty, and the fact that the duration of pregnancy and drying time varies greatly depending on breed, climatic conditions, and geographical location. Another disadvantage compared to cattle is the low milk yield, which prevents the breeder from governmental subsidies, even though milk has a high price (Aköz *et al.*, 2017). The milk produced per buffalo in Türkiye is also quite low. Nevertheless, Türkiye is the 20th and 10th country in the world in terms of buffalo presence and buffalo milk production, respectively (Özger and Karadaş, 2022). Buffalo farming in Türkiye is conducted intensively, particularly by small-scale family farms. In the 1970s, the buffalo population in Türkiye was around 111,700, but by 2010, it had decreased to 87,000. As a result of the projects for the improvement of Anatolian buffalo under the supervision of the Ministry of Agriculture and Forestry's General Directorate of Agricultural Research and Policies, this number increased to 142,000 in 2016 and 165,000 in 2023. The Anatolian buffalo breeding program is implemented in 18 provinces, and approximately 30,000 buffaloes are registered in the 'Buffalo Star' database. On a national scale, it is important to apply selection programs based on the selection of individuals with high genetic merit to increase milk yield in the Anatolian buffalo population.

Estimating genetic parameters is essential for achieve this goal. Modern methods of parameter estimation use the animal model which uses all relationships between an animal and the other recorded individuals in the population, using a genetic relationship matrix (A). There are several additional variance components that can be estimated from such data using the animal model. Sohail and Qureshi (2010) reported that the heritability estimate of first lactation milk yield in dairy buffalos was 0.62 ± 0.28. They also found that the heritability estimate of overall mean lactation milk yield was 0.38 ± 0.21. While Malhado *et al* (2013) found that the heritability coefficient estimates were 0.28 for Murrah buffaloes raised in Brazil, Garcia *et al* (2013) reported that heritability estimates for milk yield in Buffalo were 0.15 for milk yield. Shalaby, *et al* (2016) studied estimation of heritability, genetic and phenotypic correlations and genetic trend in Egyptıan buffaloes the heritability values estimated for the productive traits in the first three parities were generally low and ranged between 0.03 to 0.19.

However, estimates of genetic parameters related to milk yield in the Anatolian buffalo are limited. This study examined the estimation of genetic parameters such as heritability and EBV's for recorded lactation milk yields of Anatolian buffaloes raised in Istanbul.

MATERIALS AND METHODS

To estimate genetic parameters and variance components the data of lactation milk yield was obtained from "Manda Yıldızı" database (Tekerli, 2019). The data within the scope of the "Anatolian Buffalo National Breeding Project" which is supported by the Directorate General for Agricultural Research and Policies (TAGEM) and consisted of pedigree and production records belonged to a total of one thousand animals calved between 2020-2023 in fifty farms in four different districts (Arnavutköy, Eyüp, Çatalca and Silivri) of Istanbul (41° 28' 35" N ve 28° 27' 41" E). Milking is carried on twice daily, in the morning and evening. Milk records of buffaloes are collected with a weighing scale with a precision of 10 g/50kg. Animals with a lactation period of less than 100 days or more than 320 days were eliminated from the data set. The same animal has at least 2 and at most 3 lactation records Monthly control intervals (minimum of 3 and a maximum of 10 test-day records) were identified, and it was assumed that the control day falls exactly in the middle of the control period. The basic principle of the test interval method of calculating production records and averaging the milk weights for successive test days and multiplying the average by the number of days between the two test dates ICAR (2017). After eliminated animals, 879 lactation record from 615 animals remained belonging to 36 different farms were included in analysis. The number of animals per farm ranged from 2 to 64. All the pedigree information that were obtained were fitted. Pedigree records include animals born between 2010 and 2021. As a result of the variance analysis performed by using environmental conditions such as calving date, parity, calving date, calving season, calving age, lactation length, and herd, only effects of lactation length, parity and herd were found statically significant ($p<0.05$). Therefore, these three factors whose effects were found to be significant were included in the model. Only the first 10 parities were taken into account and evaluated at five levels.

While lactation order and herd were used as fixed effects, lactation length was included as covariate in the model. Model used is given as Equation 1.

$Y_{ijk} = \mu + h_i + p_j + b_{yx}X_{ijk} + e_{ijk}$ [1] where

Y_{ijk} : Milk production of any water buffalo (k) in the herd (h) i and parity (p) j,

μ : Overall mean,

h_i : Effect of herd (i=1, 2, 3 … and 37),

p_j : Effect of parity (j=1, 2, 3, 4 and ≥5),

b_{yx} : Partial regression coefficient of Y with respect to X

X_{ijk} : Lactation length (day) of any water buffalo (k) in the herd (h) i and parity (p) j,

e_{ijk} : Random residual error

Additionally, the model given below (Equation 2) was used to estimate of genetic parameters.

$y = Xb + Zu + Wpe + e$ [2] where

y: vector of milk yields, b: vector of fixed effects (herd and parity) and covariate (lactation length),

u: vector of random animal effects,

pe: vector of random permanent environmental effects, and

e: vector of random residual effect. X, Z and W are incidence matrices relating records to fixed, animal and permanent environmental effects, respectively.

Analysis was performed BUGA software (Yazgan, 2023) by using AI-REML algorithm (Gilmour *et al.,* 1995). Additionally, the analyses were repeated using the WOMBAT (Meyer, 2007), and it was observed that the results were exactly the same.

RESULTS

According to results obtained from pedigree analysis given on Table 1. As can be shown from the Table 1, there were animals belonged to 350 dams, all sires remained unknown. The community-based Anatolian buffalo breeding program, which is implemented at the national level, is carried out in 18 provinces with a population of 900 head of adult buffalo in each province. This national project started about 10 years ago in 18 provinces and is recorded in the national "buffalo star" named database. Water buffalo farming at present condition mostly , is based on pasture resource exploitation; on the contrary, bıg herds (around 100 heads) are located near to the big cities and buffaloes in this case receive concentrate supplemented feed (maize, wheat, barley, cottonseed and sugar beet by-products) when available. Artificial insemination is not applied in villages The larger farms with 40-50 females maintain their own males and the villages usually share a common male. Natural mating keeping two sires within the herd continuously is practised. So, it is not possible to appoint a sire at the initial stage of this project. One of the aims of this project was to estimate the genetic parameters of the herd with the data of the Istanbul population, which is one of the subpopulations at the provincial level, with a newly developed genetic value calculation software called BUGA.

Undoubtedly, the more information sources available in the pedigree are used in the estimation of genetic value, the more accurate the estimation will be. From this point of view, at the provincial level, the birth weight of the calves born by the project animals, that is, the broodstock buffaloes, the weight of 6 months, the weight of one year is obtained and the monthly milk yield controls of the broodstocks are carried out, and then these data are uploaded to the software database called "buffalo star" at the national level. Those whose lactation is completed below a certain milking period are evaluated. Then, an index selection is applied by weighting the milk yield of the mother and the growth values of individuals.

Beginning stage of countryside community-based breeding programmers (CBBPs) for Anatolian Buffalo populatıon have become the main focus for testing and disseminating improved genetics. These schemes have the ability to do detail into local farming structures and to support technical changes that may be necessary. Traditional breeding pyramids adapted to the local water buffalo production condition. All the recording and selection decision are carried out in nucleus are informed by the owner in the resulting in multipurpose water buffaloes suitable for local farmers CBBPs .Criteria for selection indices will be informed by the CBBPs with groups of herds of water buffalo at the base of what looks like a traditional breeding pyramid. All the recording and selection decisions are carried out in the nucleus and bulls with elite genetics passed down from the nucleus, through a multiplier level to the CBBPs. According to these findings it can be said that there was no half sib sister from dam animal analyzed.

Lactation milk yield average was estimated as 1287.72 ± 18.101 kg. (Table 2). Random environment variance, genotypic variance and permanent environment variance values were estimated as 48388.61±0.0003kg^2, 12003.08±0.0003 kg^2 and 9567.92±0.0003 kg^2 while heritability (h^2) and repeatability (r) of lactation yield were estimated as 0.17 ±0.162 and 0.30, respectively. The plots belong to additive genetic, permanent environment and residual effects are given on Figure 1, 2 and 3, respectively. Lactation milk yield was found to be linearly and positively correlated with lactation length which ranged between 100-329 days as expected. Additive genetic effects of the animals ranged from 405.88 to -134.82 kg (Figure 1).

Table 1. Descriptive statistics for the pedigree used in the study

Item	Value
Number of animals in the pedigree	879
Number of individuals that have become parents	350
Percentage of individuals that have become parents among all animals (%)	39.81
Number of individuals without performance records in the pedigree	264
Number of individuals with performance records in the pedigree	615
Percentage of animals with performance records among all animals (%)	69.96
Among individuals with performance records:	
Number of individuals with known sire	0
Number of individuals with known dam	350
Number of individuals with unknown dam	0

Table 2. Descriptive statistics for milk yields in the dataset

Item	Value
Maximum	4992.8
Minimum	266.75
Mean	1287.72
Standard Deviation	518.978
Standard Error	18.101
Coefficient of Variation (%)	40.3

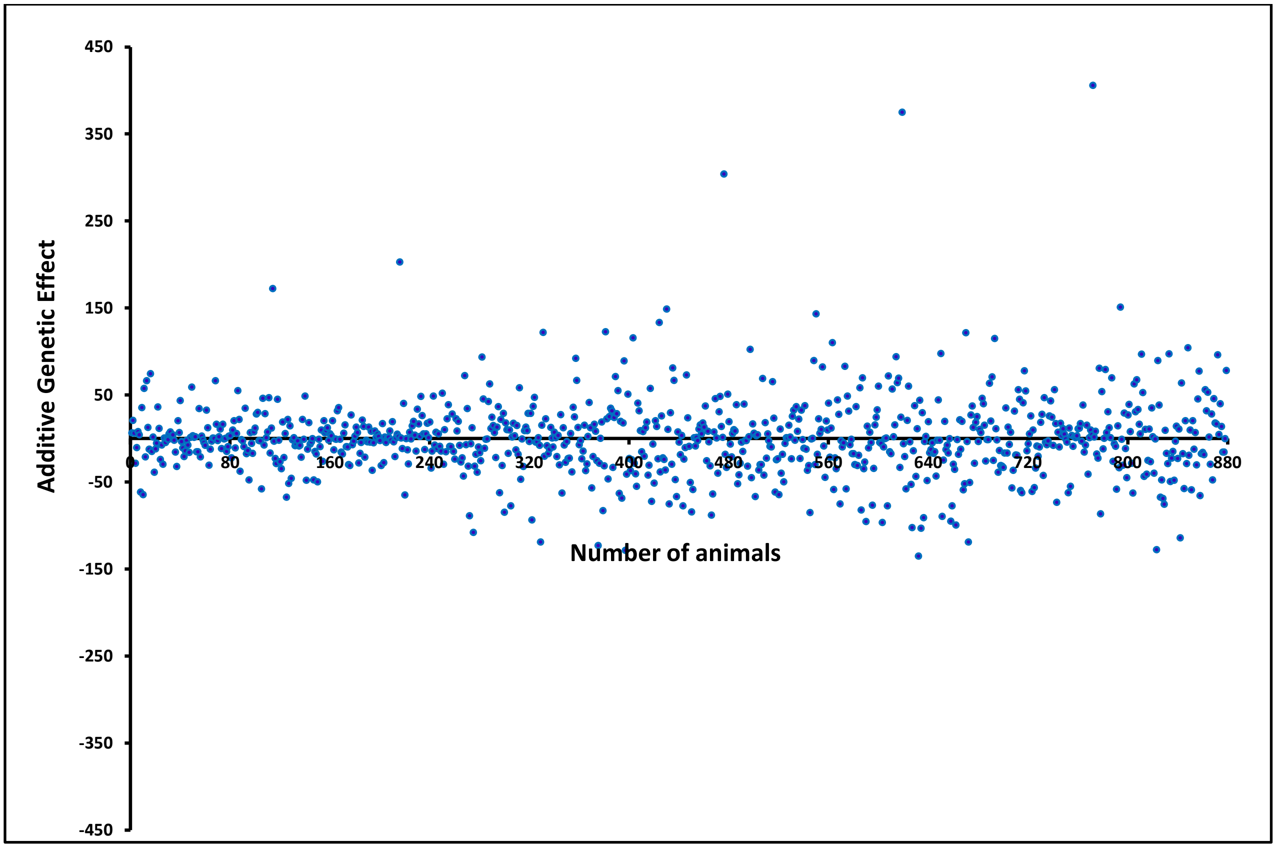

Figure 1. Estimated additive genetic effects of the animals

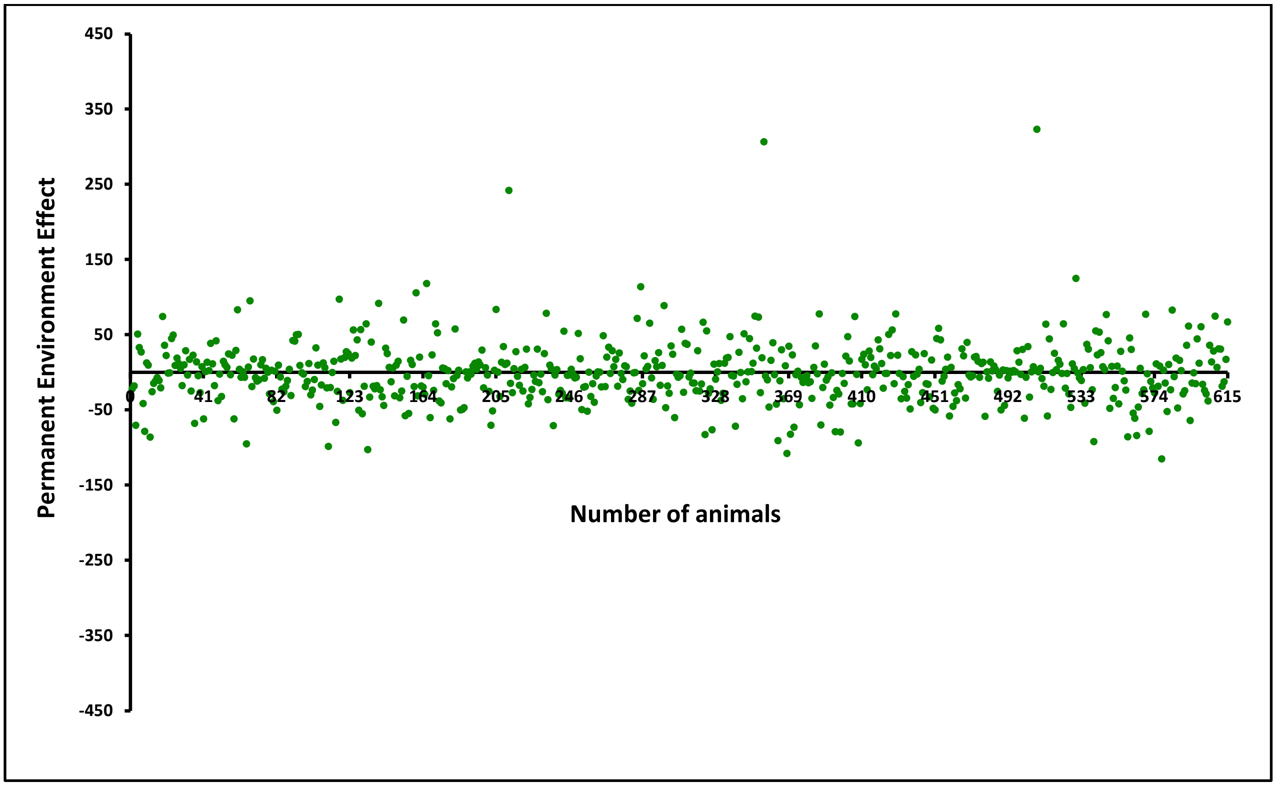

Figure 2. Permanent environment effects of the animals

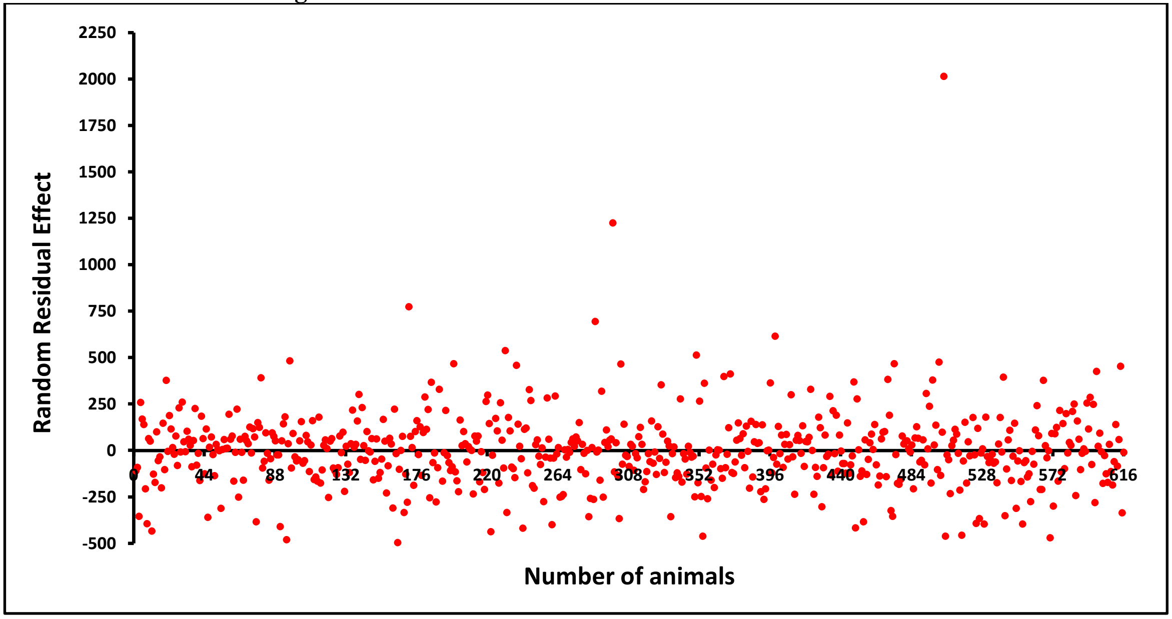

Figure 3. Random residual effects

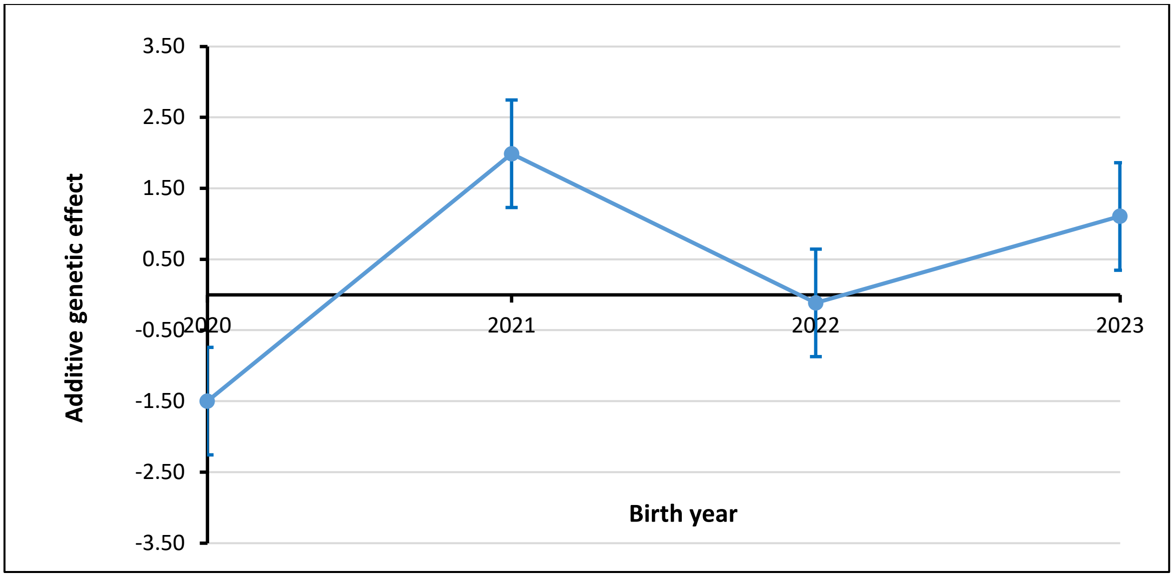

Figure 4. Average change in additive genetic effects by birth years

DISCUSSION

Average lactation milk yield found here was similar to those found in the previous study which was carried out in Anatolian Water Buffalo raised in İstanbul within the scope of the Anatolian Water Buffalo Breeding Project (Soysal *et al.,* 2018) while in the other previous study, conducted on animals raised in another province of the same project, average lactation milk yield found well below when comparing our finding (Berkin and Esen, 2017). Again, in the studies conducted in Türkiye with and Italian buffaloes (Soysal *et al.,* 2016) and Murrah X Anatolian water buffalo crosses raised in Institution conditions (Cetin *et al.,* 2022) average lactation milk yield was found to be quite high. In terms of genetic parameter estimates both heritability (h^2) and repeatability (r) of lactation yield were found low. Similarly, there are various previous studies in that found low (0.03- 0.20) heritability (Rosati and Van Vleck, 2002; Thevamanoharan *et al.,* 2002; Garcia *et al.,* 2013) for milk yield related traits including lactation milk yield while the parameter was found as moderate for the traits by different investigators (0.20-0.28) (Baldi *et al.,* 2011; Kaplan and Tekerli, 2023). The magnitude of heritability not only indicates genetic variance of a certain trait in a population, but also indicates the influence of the environmental effects and accuracy (Falconer and Mackay, 1996). Scilicet, there may be different reasons of the low value of heritability. In a recent study, in which a meta-analysis of genetic parameters for milk production traits including lactation milk yield was performed, also exposed h^2 value ranging from low to medium for the trait in buffalos Medrado *et al*, (2013). In the other recent study that carried to evaluate genetic parameters in water buffalo belonging to breeding project herds in Yozgat Türkiye heritability of lactation milk yield was estimated as 0.25 (Kaplan and Tekerli, 2023). This value is very slightly higher than what we found in presented study. It could be explained by higher recording quality for both milk yield and pedigree. Also, Similar to our study, when the overall mean lactation milk yield was considered, the error of heritability was also found high (0.38 ± 0.21) by the researchers as mentioned earlier. Additionally our findings very close to findings of research conducted by Shalaby, *et al* (2016).

Figure 4 shown that Average change in additive genetic effects over years. Accordingly, while the average of the additive genetic effects of the population was below zero in 2020, it increased dramatically a year later and reached around 2 kg in 2021. However, this value was not reached again in the following years. This result may have been caused by the negative change in environmental factors.

The main possible reasons can be considered as environmental conditions that are not suitable for the animal's needs, high number of animals whose sires are unknown, possible mistakes made during registration days and lack of information about dry time, and calving interval in the data for our study. Moreover, the low value of h^2 would be caused from significant amount of the phenotypic variation arising from small herd size where data obtained. The similar situation was reported by Thevamanoharan *et al*., (2002) who estimated low h^2 for Nili- Ravi buffaloes. When these limitations are taking in to account, low genetic parameters estimated here is obvious in nature. A recent study worth mentioning conducted on dairy cows revealed that, the heritability was estimated to be high in high milk yielding groups and low in low milk yielding groups (Wahinya *et al.,* 2020)

Another noteworthy situation is that the standard error of h^2 was estimated to be very near to itself in the presented study. As well known the standard error of heritability measures the precision of the estimation for heritability (Falconer and Mackay, 1996; Lynch and Walsh., 1998; Hill and Weir, 2004; Kor Oldenbroek and Liesbeth van der Waaij, 2015). In this case, it could be considered as a natural consequence of the previously mentioned limitations, which may be influential in estimating the low heritability level. This inconsistent situation might also be considered as an indication that the estimated heritability is unreliable. In this case, where the heritability was estimated so low and questionable, it should not be a surprise that the estimated repeatability (r) is also low. However, according to these results it is not possible to say that genetic improvement may be obtained by selection. Although the software is not able to yet estimate repeatability (r), it can be easily seen that the proportion of permanent environmental variance in the total variation is 30%.

The buffalo breeding system should be improved by environmental arrangement and developing of more reliable recording system to increase selection accuracy and accordingly to achieve genetic gain. To increase the reliability and precisely of the estimated heritability, the analysed sample size should be also expanded. Serious effects of non-additive genetic and environmental factors have been already demonstrated on the lactation milk yield (EL-Hedainy *et al.,* 2020). In this content including various factors that known to be source of variations such as sire and dry season in the model could increase the reliability of the results obtained.

All these situations are largely due to the current structure of Buffalo breeding in Türkiye. It has been put forward by many researchers interested in buffalo breeding systems and economy. It is clear that environmental conditions for the breeding of the species is not optimized as much as needed. It has already been determined that regular records are not kept (Karlı *et al.,* 2018). In these studies, it was emphasized that milk yield should be improved for profitability in Türkiye (Karlı *et al.,* 2018; Yılmaz and Kara, 2019). First of all, environmental improvement would be suggested in order to estimate useful genetic parameters as previously researchers have been suggested for similar traits in different livestock species (Barros *et al*., 2016).

The investigations were also carried out to estimate genetic diversity among water buffalo reared in Türkiye. While they stated that there was a significant genetic diversity in the species, they also pointed out that the significant deviations from Hardy-Weinberg equilibrium could be due to nonrandom mating (Gargani *et al*., 2016; Ünal *et al*., 2021). This genetic diversity is an opportunity for the intense selection which contribute to genetic progress while possible non random mating would be a threat. Accurate recording would also ensure genetic diversity, which is essential for selection.

In addition to these recommendations, which are known to everyone, the introduction of software that would make recording and genetic parameter estimation in accordance with Türkiye's production conditions easier, more accurate and faster will make a great contribution.

In this context, the use of a software that has a Turkish interface, works under Excel, has the ability to arrange data and has high data analysis potential may be a great opportunity (Yazgan, 2023). There is a software called BUGA that has already been developed and shown to be useful (Yazgan and Soysal, 2023). The use of this software named as BUGA in breeding programs should be evaluated

Conclusions: The buffalo population in Türkiye is generally organized in family farms, and the stakeholders' herds are grazed together in a communal village pasture. Therefore, it has not been possible to identify a sire in the initial phase of the project. In the later stages of the project, to achieve more effective genetic improvement, an organization that allows for the identification of sire records for the animals involved is necessary, as well as bringing the environmental conditions in which the buffalos are raised closer to the conditions required by the animals. However, since it is essential to estimate the breeding values of the animals under the current conditions, this has been carried out using software named BUGA (Best linear unbiased estimation and variance element determination toolkit with REML method). Although there are other methods for estimating genetic parameters beyond animal models, this is the best approach for estimating genetic parameters under the current conditions. In the future, as more performance records and sire records are obtained, more reliable and effective breeding studies can be conducted."

Conflict of Interest: The authors declare that there are no conflicts of interest.

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