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Genetic Parameters for some Productive and Reproductive Traits for First Lactation in Egyptian Buffalo

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ABSTRACT



A total of 2054 records of primiparous buffalo cows calved during 2000-2019 was collected from five Egyptian buffalo herds. The studied traits were birth weight (BW), total milk yield (TMY), lactation period (LP), age at first calving (AFC), gestation length (GL), days open (DO), and calving interval (CI). Year and season of calving, sex and herd were used as fixed effects. Genetic parameters were estimated using two models, the first model to estimate variance components and heritability, and the second model was estimated the genetic correlations among studied traits. Results showed that the heritability values were moderate for BW, LP and TMY (0.48, 0.23 and 0.50, respectively), suggesting that genetic improvement programs using the selection could be effective to improve these traits, but all reproductive traits were low, being 0.07, 0.02 0.0 and 0.12 for GL, DO, CI, and AFC, respectively, inferring that these traits could be improved using environmental and marginal conditions. The genetic correlation of the current study indicated that the selection for increasing BW of Egyptian buffalo could be followed by an improvement of TMY, longer LP and GL. The genetic correlation between productive traits and reproductive traits were positive ranged from 0.04 (TMY-AFC) to 0.91 (LP-DO and LP-CI). Selection of buffalo to reproduction traits would be ineffective or take long time because they are influenced by farm management, unlike productive traits.

Keywords: Buffalo; heritability; genetic parameter; first parity; Egyptian buffalo

INTRODUCTION

Egyptian buffaloes considered as dual-purpose animals, therefore improving traits related to milk and growth are important to farmers. Furthermore, Egyptian buffaloes considered as poor breeder because it is having poor fertility such as late maturity, long post-partum anestrous intervals, poor expression of estrus, poor conception rates and long calving intervals (Aziz et al., 2001). Consequently, estimation of population genetic parameters and genetic correlations among previous traits are crucial to design genetic improvement programs of Egyptian buffaloes. Most of animal data sets including multiple records of different traits regarded to the animal's productive and reproductive performance (Buzanskas et al. 2013). Multi-trait and repeatability animal models are convenient to studying these traits (Agudelo-Gómez et al., 2015). However, use of multiple-trait model to estimate the (co)variances components between parameters taken at different ages might vary, and over-parameterization of the model occurs when the number of traits is very large (Yakubu and Ayoade, 2009; Boligon et al. 2013; Agudelo-Gómez et al., 2015). Therefore, the aim of the current study were to evaluate genetic parameters for productive (BW, TMY, and LP) and reproductive (GL, CI, DO, and AFC) Traits of Egyptian buffaloes.

MATERIALS AND METHODS

Data set

Data were collected from five buffalo herds at Mehallet Mousa Experimental Stations belonging to the Animal Production Research Institute (APRI), Agricultural Research Center (ARC), Ministry of Agriculture and Land Reclamation, Egypt. Data of 2054 buffalo cow calved during 2000-2019 for first parity were collected. The traits of the study were birth weight (BW), total milk yield (TMY), lactation period (LP), age at first calving (AFC), gestation length (GL), days open (DO), and calving interval (CI).

Lactating Buffalo living under the same system of management, housing and feeding (El-Awady *et al.*, 2016) **Statistical analyses**

The Methodical environmental effects on studied traits were calculated as fixed effects using least squares methods perform in GLM procedure of SAS (2012). These fixed effects included the effects of season of calving (4 seasons), year of calving (20 years), sex (male and female) and herd (5 herds). The linear model was fitted as the follow:

$\mathbf{Y}_{ijklm} = \mathbf{\mu} + \mathbf{A}_i + \mathbf{B}_j + \mathbf{C}_{k} + \mathbf{D}_l + \mathbf{e}_{ijklm}$

Where, Y_{ijklm} : the phenotypic record of studied traits; μ : the effect of the intercept; A_i: the fixed effect of ith SC (1-4); B_j; jth YC; C_k; kth sex; D_i; lth herd and e_{ijklm}: the independent random residuals were assumed to be normally distributed with a mean of zero and a variance of σ^2_{e} . Significant fixed effects were used to form contemporary groups (CG), which were included in genetic analysis parameters.

Heritability and variance components were calculated using 2 models using Wombat software (Meyer, 2006).

Single treat model was applied for first parity in order to estimate variance components and heritability for all traits as follow:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_1\mathbf{a} + \mathbf{e}$$

y: observation's vector, *b*: fixed-effects vector with incidence matrix *X*, *a*: random animal effects vector with incidence matrix *Z*₁, and *e*: random residual effects vector with mean equals 0 and variance σ_{e}^2 . Additive (animal) effects vector (*a*) was assumed to be $N \sim (0, A \sigma_a^2)$, where *A* is the numerator matrix relationship between animals in the pedigree file and σ_a^2 is direct genetic variance. Residual (environmental) effects vector (*e*) was assumed to be $N \sim (0, I_n \sigma_{e}^2)$, where I_n being the order identity matrix equal to the number of records, and σ_e^2 is the environmental variance.

The genetic correlations estimated with the 2nd model among studied traits using bivariate animal model as the follow:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} x_1 & 0 \\ 0 & x_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} z_1 & 0 \\ 0 & z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Where y_i = observations vector, b_i = fixed effects vector, a_i = random animal effects vector for the ith trait, e_i = random residual effects vector for the ith trait, and X_i and Z_i are incidence matrices relating records of the ith trait to the fixed and the random animal effects, respectively.

It is assumed that:

var	a_1	=	$[g_{11}A]$	$g_{12}A$	0	0]
	a_2		$g_{21}A$	$g_{22}A$	0	0
	e_1		0	0	r_{11}	r_{12}
	$ e_2 $		L O	0	r_{21}	r_{22}

Where g_{11} is the genetic variance for trait $1, g_{22}$ is the genetic variance for trait 2, $g_{12} = g_{21}$ is the genetic covariance between both traits, r_{11} is the residual variance for trait 1, r_{22} is the residual variance for trait 2, $r_{12} = r_{21}$ is the residual covariance between both traits.

RESULTS AND DISCUSSION

Buffalo cows with BW between 22 and 46 kg, TMY between 653 and 3427.5 kg, LP between 123 and 360 days, AFC between 620 and 1235 days, a GL between 286 and 318 days, a DO between 42 and 312 days, and a CI between 316 and 620 days were retained in the final analysis (Table 1).

Descriptive statistics of studied traits are presented in Table 1. The averages of BW, TMY and LP were 30.9 kg, 1295.86 kg and 205.69 days, respectively. The averages of reproductive traits including AFC, GL, DO and CI were 1045, 299.95, 146.95 and 442.36 days, respectively.

Table 1. Description of data set for birth weight, productive and reproductive traits of Egyptian buffaloes.

Trait	Number	Mean	Standard deviation	Min	Max
Birth weight (kg)	2370	30.9	3.15	22	46
Total milk yield (kg)	923	1295.86	6 465.01	653	3427.5
Lactation period (days)	939	205.69	51.89	123	360
Age at first calving (days)	2054	1045	175	620	1235
Gestation length (days)	1763	299.95	8.5	286	318
Days open (days)	1675	146.95	72.97	42	312
Calving interval (days)	1721	442.36	75.76	316	620

The significant fixed effects that used to form CG for each trait are presented in Table 2. The CG for BW included effect of herd and year of calving, while the CG for MY, LP, AFC, GL and CI included effect of herd, and season and year of calving. For DO, the CG involved the effect of season and year of calving.

 Table 2. Fixed effects that composed contemporary group for each trait.

Traits	Herd	Season of calving	Year of calving
Birth weight (kg)	Х		Х
Total milk yield (kg)	Х	Х	Х
Lactation period (days)	Х	Х	Х
Age at first calving (days)	Х	Х	Х
Gestation length (days)	Х	Х	Х
Days open (days)		Х	Х
Calving interval (days)	Х	Х	Х

The variance components and heritability of studied traits are presented in Table (3). The heritability values were moderate for BW, LP and TMY (0.48, 0.23 and 0.50), showed that genetic improvement programs using selection could be effective to improve these traits. However, all reproductive traits were low, being 0.07, 0.02 0.0 and 0.12 for GL, DO, CI and AFC, respectively.

Table 3. Variance components and heritability estimates for birth weight, milk and reproductive traits in Egyptian buffaloes

	Egypuan	Dunaloes.		
Traits	σ^2_a	σ^{2}_{e}	$\sigma^{2}p$	$h^{2}a$
BW	0.4112	0.440	0.0.851	0.48 (0.013)
LP	1208.2	3531.08	4398.29	0.23 (0.094)
TMY	2605.29	2637.78	524306	0.50 (0.011)
GL	16.1123	202.248	218.361	0.07 (0.04)
DO	242.369	11566.4	11808.7	0.02 (0.03)
CI	2887.50	35114.5	38002	0.08 (0.04)
AFC	0.036	0.277	0.307	0.120(0.041)

 σ_a^2 = direct genetic variance; σ_e^2 = residual variance; σ_p^2 =phenotypic variance; h_a^2 = direct heritability. BW: birth weight; LP: lactation period; TMY: total milk yield; GL: gestation length; DO: days open; CI: calving interval; AFC: age at first calving.

Our results are in agreement with Abu El-Naser (2020), who observed estimates of heritability of 0.25 and 0.18 for TMY and LP in Egyptian buffalo, respectively. Also, Barros et al. (2016) found heritability estimate of 0.24 for MY in Murrah Buffalo, but estimate of heritability for LP was smaller (0.09) than corresponding value in the current study. On the other hand, Morammazi et al. (2007) found estimates of heritability 0.7 and 0.04 for TMY and LP, respectively that were smaller than those reported in our study. Low heritability estimates were found for all fertility traits, inferring that these traits could be improved using environmental and marginal conditions and first parity records are not good indicator to predicate it in next parities. These results are in agreement with those reported by previous studies. The low heritability estimates were reported previously in Japanese Black cattle (Setiaji and Oikawa, 2019), Holstein cattle (Muuttoranta et al., 2019), in Murrah buffalo (Barros et al., 2016) and Iranian buffalo (Morammazi et al., 2007).

The genetic correlation of the current study indicated that the selection for increasing BW of Egyptian buffalo could be followed by an improvement of TMY, longer lactation period and GL. These results were supported by Jamrozik and Miller (2014). Moreover, Gupta et al. (2015) estimated a highly positive genetic correlation (0.83 and 0.74) for BW-MY and BW-LP, respectively, in Murrah buffalo. The genetic correlation between milk traits (TMY and LP) and reproductive traits (CI, DO, GL and AFC) were positive and ranged from 0.04 (TMY-AFC) to 0.91 (LP-DO and LP-CI). The obtained genetic correlation between milk

and reproductive traits in the current study indicated that the selection for increasing milk traits may be associated with deleterious effect on reproductive traits. These results are in agreement with the previous studies (Pryce *et al.*, 2004; Gupta *et al.*, 2015; Barros *et al.*, 2016; Ayalew *et al.*, 2017). Despite the fact that most genetic selection programs in dairy cattle focus on production, many non-productive and reproductive traits are also necessary to extend longevity of the animal and reduce losses due to health disorders and mortality (Szücs *et al.*, 2009). Milk yield improvement is not straight forward, as selecting for a single trait as quantity might leads to lower milk quality and/or reproductive efficiency (Barros et al., 2014).

There were positive genetic correlations among the reproductive traits in this study that ranged from 0.04 (GL-DO) to 0.99 (CI-DO), which revealed that buffalo cows reproduced earlier tended to have shorter GL, CI, DO (Table 4). These results were comparable with the finding of others (Gutierrez *et al.*, 2007; Eaglen *et al.*, 2012; Brzáková *et al.*, 2019; Lopez *et al.*, 2019; Setiaji and Oikawa, 2019; Abu El-Naser, 2020).

 Table 4. Genetic correlation among studied traits

	BW	LP	TMY	GL	DO	CI
LP	0.98					
	(0.003)					
TMY	0.74	0.99				
	(0.407)	(0.446)				
GL	0.76	0.33	0.60			
	(0.413)	(0.285)	(0.424)			
DO	0.08	0.91	0.53	0.04		
	(0.626)	(0.006)	(0.015)	(0.394)		
CI	0.29	0.91	0.27	0.05	0.99	
	(0.109)	(0.006)	(0.151)	(0.120)	(0.213)	
AFC	0.99	0.16	0.04	0.15	0.37	0.38
	(0.003)	(0.388)	(0.079)	(0.313)	(0.067)	(0.066)

BW: birth weight; LP: lactation period; TMY: total milk yield; GL: gestation length; DO: days open; CI: calving interval; AFC: age at first calving.

CONCLUSION

We estimated genetic parameters in first parity for productive and reproductive traits in Egyptian buffalo. Our results show that low direct heritability estimates were found for all reproductive traits, first parity records are not good indicator to predicate it in next parities. Therefore, the selection of buffalo to reproductive traits would be ineffective or take long time and these traits are mainly influenced by farm managing practice, in reverse to the productive traits. Genetic correlations estimates indicated that the selection to decrease AFC with suitable age and DO would accompany by shorter CI. The results of this study could be utilized to design breeding programs for buffalo cluster in Egypt.

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المعالم الوراثية لبعض الصفات الانتاجية و التناسلية خلال موسم الحليب الاول في الجاموس المصرى ايمن فواد عاشور1 و محمد السيد الشعراوي² 1قسم بحوث التكنولوجيا الحيوية - معهد بحوث الانتاج الحيواني – مركز البحوث الزراعية - مصر 2قسم الانتاج الحيواني – كلية الزراعة – جامعة كفرالشيخ- مصر

تم جمع 2054 من بيانات الموسم الأول للجاموس من عام 2000 إلى عام 2019 من خمسة قطعان الجاموس للمحطات البحثية التابعة لمعهد بحوث الإنتاج الحيواني. كانت صفات المدروسة هي وزن العجل عند الميلاد، وإجمالي إنتاج اللبن، وفترة الحلب ، والعمر عند أول ولادة، وطول فترة الحمل ، والفترة المفتوحة والفترة بين الولادتين . تم استخدام السنة وموسم الولادة والجنس والقطيع كتأثيرات ثابتة. تم تقدير المعالم الوراثية باستخدام نموذجين ، النموذج الأول لتقدير المعلق حد والجنس والقطيع كتأثيرات ثابتة. تم تقدير المعالم الوراثية باستخدام نموذجين ، النموذج الأول لتقدير المعات المدروسة . كانت قيمة المكافىء الوراثي متوسطة لصفات الموزن عند الميلاد و طول فترة الحلس والقطيع كتأثيرات ثابتة. تم تقدير المعالم الوراثي ، أما النموذج الثاني فقد استخدم لتقدير الارتباطات الوراثية بين الصفات المدروسة. كانت قيمة المكافىء الوراثي متوسطة لصفات الوزن عند الميلاد و طول موسم الحليب و محصول اللبن كلاتى (0.44 و 20.3 و 0.50) على التوالى ، مما يشير إلى أن استخدام برامج التحسين الوراثي عن طريق الانتخاب يمكن أن تكون فعالة في تحسين هذه الصفات (الوزن عند الميلاد و طول مقتره الجاموس المعات (الوزن عند الميلاد و طول مقرول اللبان). بينما كان المكافىء الوراثي عن المريق الانت عن أوراثي عان الزن عند الميلاد و طول موسم الحليب و محصول اللبن كلاتى (19.5 و 20.3 و 0.50) على التوالى ، مما يشير إلى أن استخدام برامج التحسين الوراثي اصفات الخصوبة (طول مقرول المنوالى ، مما يشير إلى أن استخدام برامج التحسين ولاراثي عن المريق الانت المعلى والفتره المن والوراثي الماد والوراثي عان ماديوب (طول مول فترة الحمل و 0.50) على التوالى، وبذلك يمكن أن الخصوبة (طفر و فعالة في تحسين ولادتين والعمر عند اول ولاده كانت منخفضه (0.00 ، 0.00 ، 0.00 و 1.00) على التوالى، وبذلك يمكن أن عاصوبة (طول قترة المول و العلاق و لوراثية للدر الله بين عن مول و قترة الحموس المصوبي ويمكن أن الخصوبة (طفر و فالفتره بين ولادتين والعمر عند اول ولاده كانت منخفضه (0.50 ، 0.00 ، 0.00 و 1.00) على ولوراثى، وبذلك يمكن أن الخصوبة (طول قترة الحمل و لاده كان مار تحلو و لولاده كانت منخفضه (0.00 ، 0.00) مال ولوالى و يندني و ولول فترة الحموس ولفول قترة الحموس المصر ي يمكن أن الحصوب فلولو فالغز و العلام و ولول يقر الع لالما مول من الارتباط الو