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SELECTION FOR MASTITIS RESISTANCE AND SOMATIC CELL COUNTS TO IMPROVING MILK PRODUCTION IN EGYPTIAN BUFFALOES

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ABSTRACT

Estimates of (Co)variance components and genetic parameters by using MTDFREML program for milk yield (MY), somatic cell count (SCC) and mastitis (MAST) based on 1901 records of Egyptian buffaloes during the period from 2005 to 2008 at Mehallet Mousa Experimental farms were obtained. The mixed model used in the analysis included the fixed effects of month and year of calving and parity and the random effects of additive direct genetics and residual. Means of MY and SCC, were 2003 kg and 280,000 cells/ml, respectively in the animal without mastitis, 1230 kg and 1,500,000 cells/ml, respectively, in the animal with mastitis. Estimates of direct heritability for MY, SCC and MAST were 0.42, 0.30 and 0.32, respectively. Estimates of genetic correlation among MY with SCC and MAST were -0.26 and -0.45, respectively. Corresponding estimates of phenotypic correlation were -0.15 and -0.30, respectively between the same traits. Single-traits selection for MY resulted in genetic improve of 320.7 kg, -24990 cells/ml, -0.05 of MY, SCC and MAST, respectively. Comparisons between four selection indices in two methods of the relative economic values showed that the selection indices first and second in two methods which incorporated all studied traits and dropped MAST were the best indices. Ranking correlation between two methods was 0.95. Thus, it was recommend to use the method 2 of the relative economic values because its simplicity and ease of calculation.

Selection for MY with either SCC and MAST or SCC and MAST together lead to improve the efficiency of response of aggregate genotype compared with selection based on MY only. The selection indices which incorporated all studied traits and constructed by each the two methods of the relative economic values were recommended for use if selection is to the practiced at the end of the first lactation in Egyptian buffaloes.

Keywords: Genetic parameters, Somatic cell count, Mastitis, relative economic value, selection index and Buffaloes.

INTRODUCTION

Milk is an important part of the diet of human beings. The nutritional requirement of the human body is fulfilled by consuming about a quart of quality milk containing vitamin A, ascorbic acid, thiamine and calories of energy needed daily by an average individual (Bilal and Ahmad, 2004). Genetic selection towards increased milk production alone has reduced the genetic merit for health (Pryce et al., 1998). Selection index is a worthy method of choice to be used for determining the appropriate weights for traits included in a selection criteria. It allows appropriate consideration of the economic value and genetic and phenotypic parameters for the traits of concern (Rogers, 1993). Selection index is one of multi-trait criteria of

selection of females having optimum combination of production and reproduction traits, is practiced for bringing about simultaneous improved in more than one trait (Kaushik and Khanna, 2003). Windig et al., (2010) found that the accuracy of a selection index for SCM only was 0.664, while the accuracy of indices included sub clinical mastitis (SCM) and somatic cell score (SCS) early (up to 150 days) or SCS total (up to 100 days) or SCS late (151–400 days) were 0.819, 0.846 and 0.845, respectively.

Selection for improving udder health and milk traits is of primary importance in dairy industry (Interbul, 1999). An udder health index including somatic cell counts, clinical mastitis and udder health status is expected to give high selection response when compared with indirect selection based on somatic cell count only (De Jong and Lansbergen, 1996). Genetic improvement in several can be most effectively accomplished if the information about those traits is combined into an index of net merit or total score. The objectives of this study were determine genetic parameters for MY, SCC, DMY, MAST, UDHS and ML and construct all the combinations of selection indices between different studied traits by using two methods of the relative economic values.

MATERIALS AND METHODS

The data used in the present investigation were collected from the history sheets of lactating Egyptian buffaloes maintained at Mehallet Mousa Experimental farms of Animal Production Research Institute (APRI), Ministry of Agriculture. Data covered the period from 2005 to 2008. Number of records, buffalo cows, sires and dams were, 1901, 426, 118 and 373, respectively. Buffaloes were kept under semi-open sheds. Lactating buffaloes were milked by hand or machine twice daily at 7.00 a.m and 4.00 p.m throughout the lactation period, and milk production was recorded daily to the nearest 0.1 kg. Buffaloes were maintained under the same system of feeding in the farms. The animals were grazed on Egyptian clover (*Trifolium Alexandrinum*) during December to May with concentrate mixture and rice straw. During June to November, animals were fed on concentrate mixture, rice straw and limited amount of clover hay. Animals were feed according to their live weight, milk production and pregnancy status. The concentrate feed mixture was given twice daily before milking, while rice straw was offered once daily at 9.00 a.m, whereas clover hay or (silage) in Summer was offered at 11.00 a.m. Animals were allowed to drink water three times a day or free from water troughs. Multi mineral licking blocks were available for animals in the stalls. The somatic cell counts was measured by [Fossomatic 5000 (Foss Electric A/S 69, Stangerupade DK 3400 Hilleroed, Denmark Company)] from a sample of milk collected during the morning milking. The determinations of the somatic cell counts were performed in Dairy Services Unit which belong to the (APRI), somatic cell counts classified into nine levels. A case of clinical mastitis was that the veterinary treated case either with or without teat injury at any time between calving and the end of lactation, classed into two cases.

Statistical Analysis

Data were analyzed by using the MTDFREML program of Boldman et al., (1995) using multiple analysis animal model. Analytical model was used to determine the (Co)variance components, which included month and year of calving and parity as a fixed effects and the additive direct genetic effect of animal as random effects. The basic multiple model was:

$$Y = X\beta + Za + e$$

Where:

Y = a vector of observations, β = is a vector of fixed effect, a = vector of direct genetic effects, and e = vector of residual effects. X and Z are incidence matrices relating records to fixed genetic effects, respectively.

The variance-covariance structure for the model was as follows:

$$E(y) = Xb$$

And

$$V = \begin{bmatrix} a_1 \\ a_n \\ e_1 \\ e_n \end{bmatrix} = \begin{bmatrix} A\sigma^2 a_1 & \sigma a_1 a_n & 0 & 0 \\ \sigma a_2 a_n & A\sigma^2 a_n & 0 & 0 \\ 0 & 0 & In_1\sigma^2 e_1 & \sigma e_1 e_2 \\ 0 & 0 & \sigma e_2 e_n & In_2\sigma^2 e_n \end{bmatrix}$$

d, is the number of dams N is the number of records, A is the number relationship matrix among animals, $\sigma^2 a_1$, $\sigma^2 a_n$ is the additive direct genetic variance $\sigma\, a_i\, a_j$ is the direct genetic covariance items between any pair of the traits studies, $\sigma^2\ e_1$, $\sigma^2 e_n$ is the residual variance and I_a, I_n are identity matrices of appropriate order, the number of dam and number of animals with records respectively.

Matlab program (Matlab, 2002) were used to set up and construct the selection indices.

Estimation of direct and correlated responses

According to Falconer and Mackay (1996), expected direct (DR) and correlated (C_{RY}) response to selection for one trait based on first lactation records were calculated as:

$$DR = i^* h^2 * \sigma_p \text{ and}$$

$$C_{RY} = i^* h_x * h_y * r_g * \sigma_{py}$$

Where:

I = intensity of selection,

h^2 = the heritability estimate of trait X,

σ_p = the phenotypic standard deviation of each trait,

h_x = the square roots of heritability estimate of trait X,

h_y = the square roots of heritability estimate of trait Y,

r_g = the genetic correlation between the two traits, and

σ_{py} = the standard deviation of phenotypic values of trait Y.

The expected genetic change for one generation was calculated assuming selection based on cow side. Selection intensity and for a trait was set to be 1.00 for only the purpose of comparisons.

Estimate of the relative economic values for all traits studied were derived as:

1- Actual relative economic values (REV1)

The economic weight for each trait was calculated according to December 2013 prices based on the final net profit according to the following steps: (1) The net profit/kg of milk: the difference between cost of producing one kg of milk and its selling price in Egyptian pound (LE.) = 4 – LE 3.00 = LE. 1.00, (2) Losses in net profit due to elevated SCC: an average 193 day milk yield of 1544 kg realizes a net profit of LE. 0.332/ buffalo cow/day and (3) Cost of treatment and losses in milk production due to clinical mastitis infection: these costs were estimated as LE. 287 and LE. 400, respectively, which result in losses of LE. 4.44/infected buffalo cow/day and reduces the corresponding net profit to LE. 3.56.

2- Relative economic values of one standard deviation (REV2)

There is another method for estimation the economic value calculated as the relative economic value as $1/\sigma_P$, where σ_P is the phenotypic standard deviation of trait (Falconer and Mackay, 1996 and Cameron, 1997).The economic value of milk yield were set to unity and the relative economic values of other trait were calculated relatively as shown in Table (1).

Table (1) Economic values of different traits studied relative to that of milk yield.

Traits	Net profit	Actual economic value	Phenotypic SD	1/ σp	Economic value (1/ σp)
MY	1.00	1.00	763.5	1/763.5	1.00
SCC	-0.332	-0.332	270.76	1/270.76	-2.82
MAST	-3.56	-3.56	0.30	1/0.30	-2545

The index value was calculated as:

$$I = b_1p_1 + b_2p_2 + \ldots\ldots\ldots + b_np_n = \sum_{i=1}^{n} b_i p_i$$

Where:

bi = partial regression coefficient and,

Pi= phenotypic value of traits

Regression coefficients (b) of all selection indices were estimated as:

$$Pb = Ga \text{ or } b = P^{-1}Ga$$

Where: P is the phenotypic variance-covariance matrix,

G is the genetic variance-covariance matrix,

b is a vector of partial regression coefficients to be used in the index,

a is a vector of constants representing the economic values of the traits, and

P^{-1} is the inverse of phenotypic variance-covariance matrix

Values of partial regression coefficients and phenotypic variance–covariance matrix P were used to calculate index variance as $\sigma^2_I = \underline{b}' \underline{P} \underline{b} = \underline{b}' \underline{G} \underline{a}$ where b' is the transpose of (b) vector of partial regression coefficients. Variance of the total aggregate genotypic was estimated as $\sigma^2_H = a'Ga$, where σ^2_H, is aggregate genotypic variance, and a' is the transpose of economic value column vector. Accuracy of the index (R_{IH}) defined as the correlation between aggregate genotypic value (H) and the selection index value (I), was $\sigma_{IH} = \sigma_I/\sigma_H = \sigma_{IH}\ (\sigma_I * \sigma_H)$, since $\sigma_{IH} = \sigma^2_I$. The expected genetic gain (ΔG) for any one of the traits was i $R_{IH}\ \sigma_I$, where i is the selection intensity, which was set to 1.00 for the purpose of comparisons, or was calculated according to Tabler and Touchberry, (1959) $\Delta G = \sigma_I * i * B_{YI}$ where i is the selection intensity assuming that the selection differential equals one unit of standard deviation and B_{YI} is the regression of each trait in the index on the index value. $B_{YI} = \underline{b}'ci / \underline{b}'Pb$ where ci is the i th column of G matrix. To compare indices and determine traits which combine best into an index, relative efficiency of the selection index (RE) was calculated for each index based on R_{IH} relative to the complete index (I_1). Estimates of genetic and phenotypic variances and co variances of traits were used for constructing various selection indices using Henderson's modifications of Hazel's method (1943).

RESULTS AND DISCUSSION

Overall means

Phenotypic means and their standard deviation (SD) and coefficient of variability (C.V) for milk yield and somatic cell count, are presented in Table 2. The present values for milk yield is nearest the value estimated by Abu El-Naser, (2008 and 2014) in another set of data on Egyptian buffaloes (2054 and 2100 kg), respectively, while the mean of SCC was higher 280,000 cells/ml than obtained by him (182,000 and 261.200 cells/ml), respectively. Generally, average of SCC in buffalo was low compare with found in cows milk as reported by El-Arian and El-Awady, (2008) (426,000 cells/ml), working on Friesian cows in Egypt.

Table (2) Means, standard deviation (SD) and coefficient of variation (C.V) for milk yield (MY) and somatic cell counts (SCC) with and without mastitis incidence.

Variable	Normal (with out mastitis)				With mastitis			
	N	$\bar{x}$	SD	C.V	N	$\bar{x}$	SD	C.V
MY	2644	2003	716.9	35.79	98	1230	413.3	33.6
SCC*10^{-3}	2644	280.0	222.8	79.57	98	1500.0	1114.0	74.3

Covariances component and heritability

Estimates of variance and covariance components and heritability for different traits studied are in Table 3. Heritability estimates for MY (0.42), SCC (0.30) and MAST (0.32), respectively.

Table (3) Estimates of (Co)variance components and heritability for milk yield (MY), somatic cell count (SCC) and mastitis (MAST) in Egyptian buffaloes.

Estimate	Traits		
	MY	SCC	MAST
σ^2_a	670.00	845.00	1.82
σ^2_e	920.00	1941.00	3.92
σ^2_p	1590.00	2786.00	5.74
h^2a	0.42	0.30	0.32
e^2	0.58	0.70	0.68

σ^2_a = direct additive genetic variance, σ^2e = residual (temporary environmental variance) σ^2_p = phenotypic variance, h^2_a= direct heritability, e^2 = fraction phenotypic variance due to residual effects.

The present estimate nearly obtained in Egyptian buffaloes, by Abu El-Naser, (2008) reported that estimates of heritability for MY was (0.39) and SCC (0.23) and Abu El-Naser, (2014) found that estimates of heritability and fraction phenotypic variance due to residual effects for MY, SCC and MAST were 0.41, 0.28 and 0.30, and 0.58, 0.70 and 0.68, respectively.

El-Awady and Oudah, (2011) with Friesian cow, obtained the direct heritability h^2 for MY, SCC, MAST being 0.31, 0.11 and 0.18, respectively.

Correlations

Different correlations and ratios among different studied traits are given in Table 4. The estimate of genetic correlation between SCC and MAST was positive (0.56). The genetic correlation between MY with SCC and MAST were moderate and negative. The phenotypic correlation between MY with SCC and MAST were negative (-0.15 and -0.30), while the phenotypic correlation between SCC and MAST was positive (0.37).

Table (4) Different correlations and ratios among milk yield (MY), somatic cell count (SCC), and mastitis (MAST) in Egyptian buffaloes.

Trait		Correlations and ratios between and among traits		
$Trait_1$	$Trait_2$	r_{a1a2}	r_{p1p2}	r_{e1e2}
MY	SCC	-0.26	-0.15	-0.11
	MAST	-0.45	-0.30	-0.22
SCC	MAST	0.56	0.37	0.30

r_{a1a2} = genetic correlation between trait1, 2 and so on, r_{p1p2} = phenotypic correlation between traits 1, 2 and so on and r_{e1e2} = residual environmental ratio between traits 1, 2.

Mrode and Swanson, (1996) found that the negative (re) between milk yield traits and Log SCC.

El-Awady, (2009a) and EL-Awady and Oudah, (2011) on Friesian cows, estimated the high and positive genetic and phenotypic correlations between MY with SCC and MAST), ranged from (-0.75, to -0.39), while the correlations between (SCC and MAST) was strong and positive. Abu El-Naser, (2014) on Egyptian buffaloes, estimated genetic correlations between MY with (SCC, MAST) were negative (-0.24 and -0.41) and genetic correlation between SCC and MAST was positive 0.41. Also phenotypic correlation between MY with (SCC, MAST) were negative (-0.15 and -0.27)

and phenotypic correlation. The residual environmental ratios ranged from (-0.10 to 0.27).

Direct and correlated response to selection

The direct selection for each traits MY, SCC and MAST could be expected to increase of 320.67 kg, 81.23 cells/ml, 0.10, respectively, per generation. Single-traits selection for MY resulted in genetic improve of 320.67 kg, - 24990 cells/ml, and –0.05, respectively Table 5. El-Awady, (2009b) working on Egyptian buffalo, found that the direct selection for each of TMY, FY, PY and Lactose yield could be expected to increase of 258.96, 12.10, 10.61 and 16.31 Kg, respectively per generation for examined Egyptian buffalo herds. He added that, the selection for TMY resulted in increase of 258.96 kg of milk, while increased fat, protein and lactose by 8.51, 10.09 and 14.30 kg, respectively.

Table (5) Expect direct and correlated response per generation to selection for a single trait for different traits studied (maximum responses on diagonal) in Egyptian buffaloes.

Trait	MY	SCC*10^{-3}	MAST
MY	320.67	-24.99	-0.05
SCC*10^{-3}	-70.46	81.23	0.05
MAST	-125.96	46.98	0.10

Selection index

Ranking selection index based on accuracy (rIH), partial regression coefficients (b's), relative efficiency (RE) and the expected genetic change in different traits (ΔG)/generation are in Tables 6 and 7. Four selection indices were constructed for milk yield, somatic cell count and mastitis in the present study. Comparisons between all the selection indices when using the actual economic values (REV1) showed the selection index I_{1A} and I_{2A} which incorporated all traits (full index) and (dropped MAST from full index) was the best indices (RE=100), following by index I_{3A} (dropped SCC from original index), I_{4A} relative efficiency (RIH = 0.63 and RE= 98.44) and decline in relative efficiency values down to RE= 89.1 in I_{4A} (dropped MY from full index) ,that lowest accuracy (R_{IH}) and relative efficiency. The highest expected genetic gain in one generation obtained through selection index I_{3A} which lead to by MY increased 16.3 kg and the highest expected genetic gain for SCC and MAST in index I_{4A} (-14.22*10-3 cells/ml).

Table (6) Ranking of the selection indices (I,s A) according to accuracy (RIH), partial regression coefficients (b,s), relative efficiency (RE%) and the expected genetic change (ΔG)/per generation of various traits based on the relative economic value (REV1).

Ranking of selection indices	Traits						SD_I	R_{IH}	RE%
	MY(Kg)		SCC		CM				
	b	ΔG	b	ΔG	b	ΔG			
I_{1A}	0.42	15.48	-0.10	-10.50	-1.85	-0.52	20.34	0.64	100
I_{2A}	0.42	15.74	-0.10	-8.16		-0.45	18.37	0.64	100
I_{3A}	0.41	16.13		-6.49	-1.59	-0.46	17.56	0.63	98.44
I_{4A}		5.46	-0.09	-14.22	-1.45	-0.61	6.88	0.57	89.1

In Table 7 when using the economic value by one phenotypic standard deviation (REV2), the highest accuracy of selection indices and relative efficiency were I_{1S} and I_{2S} which incorporated all traits (full index) and I_{2S} (dropped MAST from full index) (RE=100), while the indices I_{3S} (dropped SCC from full index) and I_{4S} (dropped MY from full index) were the lowest accuracy (r_{IH}=0.56) and relative efficiency (RE=98.24).

The highest expected genetic gain in one generation obtained through selection index I_{2S} which lead to by MY increased 9.93 kg and the highest expected genetic gain for SCC index I_{2S} (-13.97*10-3 cells/ml). while the highest expected genetic gain for MAST index I_S (-0.74).

The rank correlation coefficient among complete indices when using the two methods (REV1 and REV2) was 0.95, which indicated that quite similarity of the buffalo cows indices values under the two methods of the economic value (REV1 and REV2). Thus it might be related to REV2 because of its simplicity and high applicability.

Table (7) Ranking of the selection indices (I,s S) according to accuracy (RIH), partial regression coefficients (b,s), relative efficiency (RE%) and the expected genetic change (ΔG)/per generation of various traits based the relative economic value by using one standard deviation (REV2).

Ranking of Selection indices	Traits						SD	R_{IH}	RE%
	MY(Kg)		SCC		CM				
	b	ΔG	b	ΔG	B	ΔG			
I_{1S}	10.31	8.82	-6.30	-9.90	-684.52	-0.74	0.0019	0.57	100
I_{2S}	0.56	9.93	-0.79	-13.97		-0.46	0.0022	0.57	100
I_{3S}	10.62	8.85		-8.00	-720.81	-0.73	0.0019	0.56	98.24
I_{4S}		7.53	-6.75	-9.81	-725.59	-0.72	0.0019	0.56	98.24

El-Awady et al., (2014) analyzed another set of data on Egyptian buffaloes using model including the additive, permanent, maternal and residual effects, in two methods of the relative economic values to comparisons between fourteen selection indices in two methods of the relative economic values, showed that the selection index I_1 which incorporated all studied traits [(milk yield (MY), somatic cell count (SCC), daily milk yield (MY), mastitis (MAST), udder health status (UDHS) and milk losses (ML)] was the best index, while the lower indices of accuracy (R_{IH}) and relative efficiency in two method of the relative economic values was selection index I_{14}. They added that the ranking correlation between two methods was 0.91 indicating the use of method 2 of the relative economic values was recommend because its simplicity and ease of calculation.

El-Awady, (2009a) working on Friesian in Egypt, calculated twelve indices by using four traits (MY, SCC, CM, and UDHS), found that the highest accuracy and relative efficiency for indices (MY and UDHS, MY, CM and UDHS and MY and CM), respectively and the lowest from index included (CM and UDHS). He added that the correlation between the economic relative value and relative economic of one phenotypic standard deviation was 0.96.

Windig et al., (2010) resulted that the used of direct information on clinical mastitis lead to increased the accuracy. The magnitude of the increase depended on how many other SCC traits (SCS early, SCS total, and SCS late), also the index included and how many offspring had information on clinical mastitis. When only SCM was used in the index, adding CM information for all offspring lead to increase the accuracy by 18.8%.

El-Awady, (2004) on growth traits of Friesian calves from birth to weaning, found that the inclusion of the maternal genetic effect in the model resulted in large expected genetic change in all traits studied and increased the accuracy of the selection index by 9 to 12%.

Strandberg and Shook, (1989) found that a selection index that includes SCS was nearly as effective as an index that included clinical mastitis. The rate of increase in mastitis was diminished by 80% of the reduction accomplished by selection on clinical mastitis. Sørensen et al., (2010) found that the selection of milk yield, somatic cell score, udder depth, teat placement, and foot angle improved efficiency of response in the aggregate genotype by 1% to 4% over selection for milk yield only. Norman et al., (2010) constructed four US genetic-economic indices for dairy cattle, found the net merit index produced more milk (219 kg) and lower somatic cell score. They added that, one way to reduce costs is through the improvement of functional traits, like somatic cell score (SCS).

El-Awady et al., (2014) on Egyptian buffaloes, concluded that the selection for MY with either one or more of the udder health traits lead to improve the efficiency of response of aggregate genotype by 8.5 to 19% over selection for MY alone.

CONCLUSION

The present results had shown that the estimates of correlation between SCC and MAST was high and positive. Also correlations between milk yield both SCC and MAST were moderate and negative, thereby improvement in MAST and SCC following upturn to another traits. Selection for MY would resulted in correlated changes in different traits more than the direct selection of each SCC and MAST.

Including selection for SCC and MAST in any selection index was recommended. Selection for MY with either one of SCC and MAST or jointly lead to improve the efficiency of response of aggregate genotype over selection for MY alone. The selection indices constructed by any each the two methods taken of the economic value were recommended for use if selection is to the practiced at the end of the first lactation in lactating Egypt buffaloes.

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الانتخاب للمقاومة لالتهاب الضرع وأعداد الخلايا الجسمية لتحسين إنتاج اللبن فى الجاموس المصري

ست الحبايب شلبي عوض
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قدرت مكونات التباين والمعايير الوراثية باستخدام برنامج الـــ MTDFREML لصفات إنتاج اللبن، عدد الخلايا الجسدية والتهاب الضرع لعدد ١٩٠١ سجل للجاموس المصري خلال الفترة من ٢٠٠٥ حتى عام ٢٠٠٨م بمحطة بحوث الإنتاج الحيواني بمحلة موسى. تم استخدام النموذج المختلط والمشتمل على شهر و سنة الولادة والموسم كعوامل ثابتة و التأثيرات العشوائية متمثلة فى التأثير الوراثي المضيف للحيوان والخطأ العشوائي.

كانت المتوسطات لكل من ناتج اللبن، عدد الخلايا الجسدية في حالة عدم وجود التهاب الضرع هى ٢٠٠٣، ٠٠ ٢٨٠.٠ ألف خلية جسدية / ملى ، في حالة وجود التهاب الضرع ١٢٣٠ كجم، ١.٥٠٠ ألف خلية جسدية / ملى.

كانت تقديرات المكافئات الوراثية المباشرة لناتج اللبن، عدد الخلايا الجسدية و التهاب الضرع هي ٠.٤٢، ٠.٣٠ و ٠.٣٢على التوالي. بينما كانت الارتباطات الوراثية بين كمية اللبن وكلا من عدد الخلايا الجسدية والتهاب الضرع كانت -٠.٢٦ و – ٠.٤٥على التوالي. والارتباطات المظهرية بين كمية اللبن و نفس الصفات السابقة كانت -٠.١٥و ٠.٣٠- على التوالي.

أدي الانتخاب المباشر لكمية اللبن إلى تحسن وراثي بـــ ٣٢٠.٧ كجم و -٢٤,٩٩٠إلف خلية/ملى و-٠.٠٥ لكل من ناتج اللبن، عدد الخلايا الجسدية و التهاب الضرع على التوالي. كانت الاستجابة نتجه الانتخاب المباشر لإنتاج اللبن أفضل من الانتخاب المباشر لكل صفة من الصفات على حدة وكان أفضل الأنلة الانتخابية الدليل الكامل والدليل الكامل بعد إسقاط التهاب الضرع من حيث دقة الدليل والكفاءة النسبية . الانتخاب لإنتاج اللبن مع صفة واحدة أو أكثر من التهاب الضرع وعدد الخلايا الجسدية أدى إلى تحسين الكفاءة النسبية للوراثة عن الانتخاب لإنتاج اللبن بمفردة. ونظرا لان معامل ارتباط الرتب بين الطريقتين المستخدمتين بلغ ٠.٩٥ فان الأنلة الانتخابية المشتقة باستخدام الطريقة الثانية (وحدة واحدة من الانحراف المعياري) يوصى باستخدامها اذا ما تم تطبيق الانتخاب في نهاية الموسم الأول في الجاموس المصري لبساطتها وسهوله حسابها.