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GENETIC PARAMETERS FOR MILK TRAITS AND MASTITIS SUSCEPTIBILITY IN FRIESIAN CATTLE

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ABSTRACT

This study aimed to explore the genetic parameters of milk traits and mastitis susceptibility in Friesian dairy cows. Data from 4,355 test days for somatic cell score (SCS), fat %, and protein % of 511 cows, 147 sires and 277 dams were analyzed. Medium heritability estimates were recorded for 305-day milk yield (0.25 ± 0.012), protein ($0.22\%\pm0.039$) and fat ($0.21\%\pm0.035$). A low heritability estimate was noted for SCS (0.02 ± 0.008). The estimated Predicted Breeding Value (PBV) for the 305-day milk yield (305dMY) trait varied widely. The range of breeding values was highest for protein and fat (0.264 and 0.131) of cows, and the highest for the 305dMY trait (2633.1 kg) for the sires. The negative environmental connection between 305-day milk yield and SCS suggests that sanitary methods and effective management might help maintain a suitable level of milk yield, while decreasing milk SCS and environmental mastitis incidence. This study recommends the use of more effective management practices aligned with the selection of cows that are more resistant to environmental factors to reduce the levels of SCS in milk by increasing the animals' resistance to mastitis. Furthermore, genetic characteristics for all analyzed features may be useful in developing selection indices to improve udder health and milk production in Friesian dairy cows.

Keywords: Genetic factors, milk yield, somatic cell score, Friesian cows.

INTRODUCTION

The dairy industry generally necessitates the adoption of strict hygienic measures in order to obtain healthy milk. Milk production and udder health (mastitis resistance) are vital traits, from an economic point of view, affecting dairy farming profitability. These polygenic features are regulated by a range of variables (for example, management tech-

environmental niques, circumstances, animal physiological stage) and are controlled by numerous genes with little impact on the observable phenotype (Snelling et al., 2013). Intense genetic selection, along with improvement in management and nutrition, can lead to increased milk production and subsequently reduce the prevalence of mastitis (Rupp and Boichard, 2003). The common and commercially most significant illness in dairy cattle is mastitis. Mastitis in dairy cattle is the leading source of economic losses in the dairy sector due to its widespread incidence.

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These losses include death and culling, veterinary costs, and decreased quantity and quality of milk yield, animal health and also interfering with milk processing and potentially endangering human health owing to antibiotic residues (Halasa *et al.*, 2007; Ezzat *et al.*, 2014; Kirsanova *et al.*, 2019).

Somatic cell count is a phenotypic indicator of the presence or absence of breast infection. SCC is widely utilized in cattle as a sensitive indicator of udder health and as a commercial milk quality criterion in bulk tank milk (Mehdid et al., 2019). Since the majority of subclinical mastitis patients lack clinical evidence, it is difficult to identify, making treatment and prevention more difficult. As a result, their decline in milk supply and quality causes the biggest economic loss on dairy farms (Kumari et al., 2018). Nevertheless, SCC has been widely employed as a significant strategy for indirect selection for increased resistance to mastitis in cows. (Martin et al., 2018) SCC and clinical mastitis frequently have a substantial hereditary link (Wolf et al., 2010) and to assess the quality of milk and payments of dairy producers. In addition, SCC is directly related to getting maximum milk production. The health of dairy cows, particularly the milk-producing mammary glands, is critical to the dairy business because of the crucial sanitary and economic factors involved in guaranteeing high production.

The objective of this study is to estimate the influence of genetic (heritability (h^2), phenotypic correlation (rP), genetic correlation (r_g) and predicted breeding value (PBV)) on (305dMY), protein %, fat %, and SCC in Friesian cows under Egyptian conditions, to study the impacts of genetic factors on predicting milk production in the upcoming lactation and as a sign of susceptibility to mastitis.

MATERIALS AND METHODS

Data source

Data were collected from the experimental farm Alkarda, situated in Kafr El-Sheikh, which belongs to the APRI, ARC, Egypt. Data from 4,355 test days for SCC, fat percentage, and protein percentage of 511 cows, 147 sires, and 277 dams were used in this study (Table 1).

 Table 1: Summary of data available for analysis

Item	Number	
Record	4355	
Cows' daughters	511	
Sires	147	
Dams	277	
Parity	6	
Year	6	
Season	4	

Studied traits

The understudied traits were 305 d MY, protein and fat percentage, and SCC; the hygiene trait was the frequency of mastitis infections throughout the lactation season. SCC data was categorized as milk test-day numbers, which were performed every 30 days throughout each lactation. To achieve data normality for the statistical analysis, the SCC was transformed into somatic cell linear scores (SCS) by applying the following equation: SCS = [log2](SCC/100)] + 3 animals, as proposed by Shook and Schutz, (1994). The trait was measured during 100, 150, 200 and 305 days of lactation. Protein and fat percentages were transformed to Arcsine by applying the following equation: θ =2arcsin \sqrt{X} as proposed by Kirk (2012), to estimate variance (V) and heritability (h^2) .

Herd management

In winter, the animals were fed a concentrate combination of wheat or rice straw, as well as Egyptian clover, and in summer, they were fed clover hay. Friesian heifers weighing roughly 305 kg were

artificially inseminated with verified Friesian sires' sperm. Pregnancy was detected after 60 days of service. The animals were milked by mechanical machines twice a day.

Statistical analysis

Variance components, heritability, permanent environmental and predicted breeding values were estimated by restricted maximum likelihood (REML) procedures using the multiple traits animal models (MTAM) program of Boldman *et al.* (1995). The model was:

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{p}_{\mathbf{e}} + \mathbf{e}$$

Where:

Y= vector of observations, $\boldsymbol{\beta}$ = vector of fixed effects including year (6 levels), parity (6 levels), and season (4 levels) with incidence matrix X; **a**= vector of direct additive genetic effect with incidence matrix (Z); **Pe**= vector of random maternal permanent environmental effects with incidence matrix (W); and e = the vector of random residual effects N (0, Is²e). The starting mixed model was obtained applying REML method of VARCOMP procedure of SAS (2003).

Analysis correlation BLUP and rank correlation was carried out. The value falls rapidly as the number of qualities analyzed increases. The transmission abilities (BLUP) estimated by DFREML, as well as their anticipated rankings, are used to calculate the product moment for BLUP and the Spearman for BLUP ranks. For the full set of animals, sires and dams, association (correlation) coefficients were calculated among the analyzed milk traits by SAS (2003).

RESULTS

Milk and somatic cell score traits

The mean for 305-day milk, protein %, fat %, and SCS₃₀₅ with standard deviation were 3001.88 ± 1114.67 kg, 2.92 ± 1.21 %, 3.57 ± 76 %, and 4.47 ± 1.54 , respectively, (Table 2). The coefficient of all variables ranged from 21.40 % to 41.30 %.

Table 2: Means, SD and CV% for study traits in Holstein cows

Traits	No	Mean	SD	CV%	Min	Max
305 (kg)	1476	3001.88	1114.67	37.13	1365.00	8423.00
Protein%	4355	2.92	1.21	41.3	1.08	8.60
Fat%	4355	3.57	0.76	21.4	0.90	8.25
SCS ₃₀₅	6719	4.47	1.54	34.5	1.00	10.300

SD = standard deviations and CV % =coefficients of variation.

Genetic parameters

Heritability estimate (h²_a)

The heritability for 305 d MY, protein %, fat %, and SCS is depicted in Table (3). Medium h_a^2 estimates were recorded for 305-day milk yield (0.25±0.012), protein % (0.22±0.039), and fat % (0.21±0.035). A low h²_a estimate was recorded for SCS (0.02 ± 0.008) . Differences in h²a estimates were due to the records utilized in estimation, the adjustment for non-genetic variables, the genetic makeup of the breed, management, different and models influencing genetic, climatic. and

environmental variances, as well as the estimation method (Fu XF *et al.*, 2017). Low heritability estimates ($h^2_a\pm$ se) were recorded for cumulative somatic cell score at 100 (0.001±0.010), 150 (0.02±0.011), 200 (0.02±0.009), and 305-day milk yield (0.02±0.008) (Table 3).

Phenotypic and genetic correlation

The estimated genetic (r_g) and phenotypic (r_p) correlations of 305-day milk yield, protein %, fat %, and SCS are illustrated in Table (4). All examined traits had positive correlations, with the exception of SCS,

which had negative correlations with 305dMY and P%. 305-dMY demonstrated a modest positive correlation with P%, F%, and SCS. P% had positive r_g with different SCS traits and fat %, while F % had low r_g with SCS.

Table 3:	Heritability,	Permanent	environment	for	305-days	milk	yield,	protein,	fat	percentage
	and somatic	cell count in	n four classes	of l	actation in	n Fries	sian cat	ttle		

Traits	$\mathbf{h}^{2}_{\mathbf{a}}$	\mathbf{P}^2_{e}	e ²
305dayMY	$0.25 \pm .0.012$	0.007 ± 0.004	0.74 ± 0.002
P%	0.22±0.039	0.0017 ± 0.007	0.78±0.039
F%	0.21±0.035	0.0091 ± 0.008	0.78±0.034
SCS ₁₀₀	0.001±0.010	0.94 ± 0.017	0.74±0.012
SCS150	0.02±0.011	0.04±0.013	0.94±0.013
SCS250	0.02 ± 0.009	0.022±0.009	0.96±0.009
SCS305	0.02 ± 0.008	0.19 ± 0.008	0.96 ± 0.008

 h_a^2 =heritability, p_e = Permanent environmental, e = environmental, SCS_{100} = somatic cell score at 100 days, $SCS_{150, =}$ = Cumulative somatic cell score at 150 days, SCS_{250} = Cumulative somatic cell score at 250 days and $SCS_{305=}$ = Cumulative somatic cell score at 305 days,

Table 4: Correlation coefficient between of 305- days milk yield, protein %, fat% and SCS in Friesian cows

Phenotypic correlation								
	305dayMY	P%	F%	SCS				
305 d MY	1							
Р%	0.026	1						
F%	0.031*	0.337***	1					
SCS	-0.071*	-0.005	0.016	1				
	BLUP corr	relation						
305d MY	1							
Р%	0.221***	1						
F%	0.174^{***}	0.464***	1					
SCS	0.036	0.023	0.076	1				
	Rank correlation							
305d MY	1							
Р%	0.205***	1						
F%	0.175***	0.434***	1					
SCS	0.042	0.047	0.078	1				

Ns; non-significant *, ** and ***; significant at 0.05, 0.01 and 0.001 respectively

Predicted breeding value (PBV)

The PBV values as mean, SE, Mini & Max for 305-dMY, protein, fat, and SCS₃₀₅ for all animals (cow, sire and dam) of Friesian cattle are presented in Table (5). The PBV values for the studied traits varied widely; the range of PBV of sire for 305 DMY (2633.1 kg) was higher than both cow (2111.2 kg) and dam (2171.6 kg). The ranges of PBV of cow for protein and fat (0.264 and 0.131) were higher than both sire (0.026 and 0.013) and dam (0.022 and 0.015). On the other hand, the range of PBV of dams for SCS (0.56) was higher than both cows (0.29) and sires (0.44). The present results showed wide differences in PBV among cows, sires and dams for the studied traits, which indicate the possibility of selection for 305d-MY.

	Minimum			Maximum			Range
	PBV	SE	Accuracy	PBV	SE	Accuracy	
			Cow				
305d MY	-941.3	253.8	0.84	1169.9	350.1	0.68	2111.2
Protein	-0.014	0.01	0.88	0.25	0.01	0.87	0.264
Fat	-0.12	0.01	0.82	0.011	0.01	0.70	0.131
SCS ₃₀₅	-0.014	0.17	0.68	0.28	0.19	0.52	0.294
			Sire				
305d MY	-817.6	246.8	0.85	1815.5	244.9	0.86	2633.1
Protein	-0.01	0.01	0.78	0.016	0.01	0.83	0.026
Fat	-0.006	0.001	0.89	0.007	0.01	0.80	0.013
SCS305	-0.29	0.15	0.75	0.15	0.19	0.52	0.44
Dam							
305d MY	-641.7	244.7	0.86	1529.9	316.4	0.75	2171.6
Protein	-0.009	0.01	0.72	0.013	0.01	0.60	0.022
Fat	-0.007	0.01	0.60	0.008	0.01	0.55	0.015
SCS ₃₀₅	-0.28	0.2	0.50	0.28	0.17	0.64	0.56

Table 5: Minimum, Maximum, PBV, SE, accuracy and range of predicted BV of studied traits in Friesian cattle

Range = (Maximum - Minimum).

DISCUSSION

The overall means of 305 d-MY, protein %, fat %, and somatic cell score were reported by Allam (2011); Faid-Allah (2018); Bobbo *et al.* (2020); Romano *et al.* (2020). The somatic cell score (SCS₃₀₅) obtained from the current study was higher than the SCS reported for dairy cows. The mean of 305 d-MY for cows was 4229 kg (Allam, 2011). The mean of 305-day milk yield, fat %, and protein % for Holstein cattle were 8715.52 kg, 3.32 ± 0.49 %, and 3.06 ± 0.19 %, respectively (Romano *et al.*, 2020).

The mean and standard deviation for clinical mastitis cases per lactation (time/parity) were 1.99±1.62 (Zavadilová et al., 2015), 0.38±0.4861 (Zavadilová et al., 2017), 0.712±0.91 (Faid-Allah, 2018), 2.64±1.39 (Romano et al., 2020), and 3.17±1.90 (Bobbo et al., 2020). In Friesian cattle, the average and standard deviation of cumulative milk output in 90, 150, and 180 days were 1837±512, 3392±744, and 1999) 3777±902 kg (Atil. and 1475.49±527.49, 2337.08±860.78, and 2931.45±963.42 kg (Zein, 2014), respectively.

Estimates of genetic parameters are required to develop the selection criteria and future breeding methods. Heritability estimation is necessary for the breeder to pick the breeding program, the type of selection to be followed, and to anticipate the subsequent genetic gain (Cobuci et al., 2007). Estimates of h^2a were low to moderate, consistent with the majority of prior research. (Allam, 2011; Valencia-Posadas et al., 2022). In general, the estimates of h²a for productive traits in this study were moderate; this implies the availability of adequate genetic variety and the potential for future development through genetic selection, as well as improved management levels (Worku et al., 2022). A moderate heritability estimate of milk yield was recorded by Guler et al., (2010), which was 0.23, Yilmaz et al., (2011), which was 0.22., Abo-Gamil et al., (2021), which was 0.24 Worku et al., (2022), which was 0.17 and Ratwan et al., (2022), which was 0.28. Higher heritability estimates were observed for milk output for the Chilean cow breed (0.29) (Montaldo et al., 2017). Heritability was estimated at 0.49, 0.31, 0.50, and 0.32 for 305-d MY, average F %, average P %, and average SCS, respectively, for Thai dairy cattle (Buaban et al., 2022). On the other hand, the heritability estimate for mastitis score recorded by many researchers (Allam, 2011) showed that h2a values for mastitis score in Friesian cows were 0.25 and 0.12, respectively. Also, Carlen et al. (2004) and Bloemhof et al. (2009) found values 0.03 and the were 0.03. respectively. Heritability estimates of SCS were 0.070±0.007 in Holstein (Pérez-Cabal et al., 2009). While they were 0.11: 0.13 again for the number of mastitis cases per lactation (Wolf et al., 2010), 0.03:0.05 for clinical mastitis (Jamrozik et al., 2013), 0.04 for clinical mastitis and 0.05 for the number of cases of clinical mastitis in (Pérez-Cabal Holstein cows and Charfeddine, 2013), 0.09 (Zavadilová et al., 2015), 0.02 and 0.09 (Faid-Allah, 2018).

Heritability estimates were low for SCS that ranged from 0.04 to 0.14 in the Romanian Black and White cattle population (Pelmuş et al., 2022). In contrast, medium to high heritability estimates of SCS were reported by Jimenez-Granado et al., (2022).Heritability estimates were 0.05 ± 0.01 for somatic cell score, 0.22±0.01 for 305dayMY, 0.27±0.02 for fat %, and 0.17±0.02 for protein % (Bobbo et al., 2020). While, h_a^2 estimates were 0.19±0.01 for SCS, 0.22±0.01 for 305-dayMY, 0.61±0.02 for fat %, and 0.65±0.02 for protein %, as reported by Romano et al., (2020). Low heritability values for SCS at 100 (0.03), 150 (0.02), 200 (0.05), and 305-dayMY (0.05) were revealed by Zavadilová et al., (2017) and Bobbo et al., (2020) confirming the high influence of environmental factors on this trait. This demonstrates that we should prioritize thorough environmental management (diet, milking circumstances, surroundings, and facilities) alongside genetic selection for this characteristic. It is worth noting that, while the genetic gain is minor, it is substantial, given the large number of animals with low levels of mastitis and the development of animals with phenotypically immune glands.

negative environmental correlation Α between SCS and milk output has also been documented in other populations (Haile-Mariam et al., 2001). The negative environmental correlation between 305 d MY and SCS implies that sanitary methods and effective management would be useful in maintaining a suitable level of milk production while managing the SCS of milk (Koivula et al., 2005). Taking SCS before and after clinical mastitis as two distinct features, the positive genetic correlation between milk production and SCS was 0.17 and 0.25, respectively (Carlen et al., 2004). Other investigations revealed negative environmental а correlation between SCS and protein production, ranging from -0.11 to -0.14 (Samoré et al., 2008). It is obvious that the interactions of different illnesses on SCS can alter the correlation coefficients between 305d-MY, protein, and fat percentage with SCS. Following the occurrence of clinical or subclinical mastitis and subsequent elevation of the SCS, the total protein content of milk may rise or remain stable. Following udder infection, the genetic correlation between protein output and SCS was substantial and positive at the beginning of the earliest phases of first lactation but neared zero or negative as lactation progressed (Samoré et al., 2008). Some research found that SCS during the first half of lactation had a greater genetic association with clinical mastitis (Bloemhof et al., 2009). In general, the greater the number of somatic cells in milk, the lower the protein and fat content (Garcia et al., 2015). The current study found that cows with a high genetic potential for milk, fat, or protein supply tended to have a high SCS. The negative environmental correlation between SCS vield attributes suggests that and environmental elements that improve milk output might also serve to reduce SCS.

The calculated genetic factors in the present study might be beneficial in developing a selection index for the genetic improvement of Friesian cattle.

The PBV of sires had a broad range for the 305 dMY trait. This might be ascribed to the export of sires from diverse sources throughout the world for Friesian cows, and a shift in breeders' intended goals from milk production characteristics to functional and hygienic traits. The greater genetic variety, the higher the the prediction of superior sires in PBV through selection. The ranges represent values for traits that are less than those recorded by Faid-Allah, (2018). Furthermore, the PBV for dams showed a narrower range than sires for all analyzed features, which might be related to the selection of superior cows within the farms, in agreement with those of Faid-Allah, (2018). High genetic diversity was detected among the PBV of sires, according to Kumar et al. (2008), Moges et al., (2009) and Faid-Allah, (2018). The predicted BV for the mastitis trait ranged from -0.0785 to 0.0965 for clinical mastitis (CM) and from -0.2184 to 0.3884 for the number of cases for clinical mastitis (NCM) (Pérez-Cabal et al., 2009). While Pelmus et al. (2022) differed from the current study, which revealed that the BV for the best cows for somatic cell score was between -35.566 and -191.358 for the Black and White Romanian cattle population.

CONCLUSION

The current study recommended that improvement through genetic selection based on genetic parameters, along with improving management levels, are possible aids for improving udder health, milk yield, decreasing SCS levels in milk and reducing environmental mastitis incidence. Although genetic advancement in Friesian cattle has been significant, it has been sluggish, and it is recommended that improvement genetic initiatives and suitable management techniques should be established.

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المعالم الوراثية لصفات إنتاج اللبن وقابلية الإصابة بإلتهاب الضرع في الأبقار الفريزيان

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تهدف هذه الدراسة إلى تقدير المعالم الوراثية لصفات انتاج اللبن وقابلية التهاب الضرع في قطيع ابقار الفريزيان. سجلت بيانات انتاج اللبن اليومي لمدة ٢٣٥٥ يوم لاختبار عدد الخلايا الجسدية (SCS) ونسبة الدهون ونسبة البروتين لـ ٥١١ بقرة و ١٤٧ طلوقة و٢٧٧ أم. تم تقدير المكافئ الوراثي وكان قيمته متوسطة لإنتاج الحليب في ٣٠٥ يوم (٢٠٠ ± ٢١٠٠) ونسبة البروتين (٢٢٠ ± ٣٩٠٠) ونسبة الدهون (٢٠٠ ± ٣٠٥٠). في حين كانت قيمة المكافئ الوراثي منخفضة لصفة عدد الخلايا الجسدية لـSCS فكانت (٢٠٠٠ ± ٢٠٠٠). القيمة التربوية المتوقعة المقدرة (PBV) ونسبة البروتين (٢٠٣٠ ± ٣٩٠٠) ونسبة الدهون (٢٠٠ ± ٢٠٠٠). في حين لصفة البروتين والدهن (٢٢٠٠ و ٢٢٠٠) للأبقار والأعلى بالنسبة لصفة ٢٠٠ يوم على نطاق واسع. كانت القيم التربوية الأعلى لصفة البروتين والدهن (٢٦٢٠ و ٢٠١٠) للأبقار والأعلى بالنسبة لصفة ٢٠٠ يوم (٢٠٣٠ ع. يشير الارتباط البيئي السلبي بين (٣٠٠ يوم و SCS) الى أن الرعاية الصحية والإدارة الجيدة ستكون مفيدة في الحفاظ على مستوى عالي من انتاج اللبن بالإضافة إلى التحكم في عدد الخلايا الجسدية SCS التها التربوية الأعلى الحمد (٢٢٣٠٠) للأبقار والأعلى بالنسبة لصفة ٢٠٠ يوم (٢٣٠٠) للأباء. المواظ على مستوى عالي من انتاج اللبن بالإضافة إلى التحكم في عدد الخلايا الجسدية SCS البن للحد من حالات التهاب الضرع البيئي. توصي هذه الدراسة باستخدام ممارسات إدارية أكثر فعالية تتوافق مع الانتخاب للأبقار التهاب الضرع البيئي. توصي هذه الدراسة باستخدام ممارسات إدارية أكثر فعالية تتوافق مع الانتخاب للأبقار التهاب الضرع البيئي. توصي هذه الدراسة باستخدام ممارسات إدارية أكثر فعالية تنوافق مع الانتخاب للأبقار التهاب الضرع البيئية لنقايل مستويات عدد الخلايا الجسدية SCS في اللبن عن طريق زيادة مقاومة التهاب الضرع البيئي من انتاج اللبن بالإضافة المارسات إدارية أكثر فعالية تنوافق مع الانتخاب للأبقار التهاب الضرع البيئيت معام الوراشة المعروم الصفات المدروسة مساعدات محتملة لاستخدام أدلة التحوان لالتهاب الضرع أبيئية لتعاليل مستويات عدد الخلايا الجسدية SCS في اللبن عن طريق زيادة مقاومة الحيوان لالتهاب الضرع أبيئية مومات إنتاج اللبن في أبقار الفريزيان.

الكلمات المفتاحية: العوامل الور اثية، صفات إنتاج اللبن ، عدد الخلايا الجسدية، أبقار الفريزيان،