

GENETIC ANALYSIS OF THE RELATIONSHIP AMONG TEST-DAY MILK YIELD, SOMATIC CELL COUNT AND SOME UDDER CHARACTERISTICS OF HOLSTEIN FRIESIAN COWS

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SUMMARY

Genetic analysis of the relationship between test-day milk yield (TDM), somatic cell count and score (SCC&SCS) and ten udder-teat traits of Holstein Friesian cows was carried out using multi-trait animal model package. A total number of 3909 observations were collected on 2811 cows raised in four Egyptian dairy farms. Estimates of h^2_{TDM} ranged from 0.28 to 0.34, h^2_{TDM} increased markedly with advancing parity till the 3rd lactation, and varied according to stage of lactation ranging between 0.14 and 0.23. Overall h^2_{SCS} for all parities was 0.19. The highest h^2_{SCS} was obtained in the 1st parity whereas estimates of latter parities were obviously lower. Results indicated no clear effect of stage of lactation on h^2_{SCS} . Estimates of h^2 for udder and teat traits ranged from .29 to .54 and .46 to .61, respectively. Thus selection based on udder and teat measurements would be effective to improve these traits. Estimated correlation coefficients indicated a negative association between TDM and SCS. Genetic (r_g) and phenotypic (r_p) correlations among TDM and SCS showed generally low to intermediate values ranged from -.08 to -.28. There was a general trend towards slight increase in magnitude of $R_{gTDM*SCC}$ with advancing parity. This result may suggest that as SCC in milk increased, milk production will be in turn decreased, as a result of probable mastitis infected udder. Both rear udder width (RUW) and udder cleft (UC) showed genetically the highest positive association with TDM. This may indicate the possibility of indirect genetic improvement of TDM by selection for both RUW and UC. Estimates of R_{pSCS} with udder traits were all negative, indicating that cows with higher, more tightly attached udders and closer teats have lower SCS. R_{gTDM} with some udder-teat traits were positive and showed a general tendency towards increasing their magnitude with advancing parity. Other udder and teat traits showed, however, negative R_g with TDM and become greater in magnitude with advance in parity except with fore udder attachment (FUA). Udder depth showed the highest negative R_p (-.55) with TDM in the 4th lactation. Fore udder length (FUL) showed moderate positive R_p with TDM indicating that cows with longer fore-udders tend to produce more daily milk yield. For the other udder traits, particularly teat size (TS), the estimates of R_p with TDM were moderate and favorable and showed a tendency to increase in magnitude with parity. Genetic parameters for all studied traits are possible aids for constructing selection indices for improving udder health and milk yield.

Keywords: genetic parameters, test-day milk yield, somatic cell count, udder-teat traits

INTRODUCTION

Somatic cell count (SCC) in milk is one of the best indicators of udder health status both in pathogenic and non-pathogenic cases. Many recent research studies aimed, therefore, to declare how to use SCC and other economic traits in selection programs for improving udder health. Results of previous studies showed that h^2 estimates of milk yield ranged from 0.20 to 0.58, it was high in the 1st parity and decreased slightly thereafter with the advance of parity (Amin, 1997; Mohamed, 1998). Kennedy *et al.* (1982) showed that h^2_{SCC} in Holstein-Friesian cows ranged from 0.05 for ≤ 2 yr old to 0.10 for mature (≥ 6 yr) cows, and averaged 0.08 over all ages. Coffey *et al.* (1985) found that h^2 for $\log_2 SCC$ increased with parity. The authors noted that the substantially larger estimates in third and later parities suggests that SCC measured early and late in life may be genetically treated as different traits. Since adjustment for age was less than perfect, higher h^2 in third and later parities may be partly due to partial confounding of sires with age of cow. Seykora and McDaniel (1986) found that h^2_{SCC} of daughters were predicted with greater accuracy from averages of SCC of dams multiple lactations (0.16) than dams single lactation (0.12). They concluded that selecting healthy, older cows to be dams of bulls would have the effect of selection for reduced mastitis susceptibility. Banos and Shook (1990) showed that heritability estimates of SCC averaged 0.12 and were lowest in all three parities studied and was due to decreased sire variance in these subsets. Amin (2000) analyzed sample test-day SCS and milk production traits using four crossing groups among Hungarian Native Breed and Holstein Friesian. The author found that the highest h^2_{SCS} was obtained for crossbred group having 1/4 to 3/4 Holstein blood.

Monardes *et al.* (1990) showed that heritabilities of type traits were all smaller than 0.15; (fore-udder, 0.11; rear-udder, 0.13; fore-udder attachment, 0.12; rear-udder attachment, 0.14; median suspensory, 0.10; fore-teat placement, 0.13; and rear-teat placement, 0.09). Vanraden *et al.* (1990) reported heritability estimates as: fore udder attachment, 0.18; rear-udder height, 0.18; rear-udder width, 0.16; udder cleft, 0.15; udder depth, 0.25 and teat placement, 0.21. Gengler *et al.* (1997) used multiple diagonalization and a REML expectation-maximization algorithm with repeatability model for estimation of (co)variance components for linear and final type scores of Jersey cows in the US. Heritabilities were estimated as 0.26 for strength, 0.13 for foot angle, 0.13 for rear legs (side view), 0.27 for body depth, 0.31 for rump angle, 0.22 for fore-udder attachment, 0.28 for rear-udder height, 0.26 for rear-udder width, 0.32 for udder depth, 0.20 for udder cleft, 0.29 for front teat placement, and 0.31 for teat length.

Studies dealing with genetic analysis of udder traits and somatic cell count of Holstein Friesian cattle in Egypt are scarce. The present study aimed at estimating genetic parameters for test-day milk yield, somatic cell count, and some udder and teat traits along with their interrelationships in Holstein Friesian cows in Egypt.

MATERIAL AND METHODS

The numbers of Holstein Friesian cows used in the present study were 723, 737, 1061, and 290 at Al-Salhia, Dunia, Delta Misr farm number 1 and Delta Misr farm 2, respectively. The numbers of test-day observation were 2958 distributed as 1237 at the 1st parity, 749 at the 2nd parity, 534 at the 3rd parity, and 438 at the 4th parity. Pedigree information were partly known in most farms. Productive traits studied were test-day milk yield (TDM) and somatic cell count and score (SCC & SCS). In addition, monthly measurements of udder and teat traits were taken, according to the score classes proposed by Hungarian Association of Animal Breeding. These traits were as follows:

Fore-Udder Length(FUL)	Teat Placement Rear View (TPRV)
Fore-Udder Attachment (FUA)	Teat Placement Side View (TPSV)
Rear-Udder Height (RUH)	Teat Size (TS)
Rear-Udder Width (RUW)	Udder Cleft (UC)
Udder Depth(UD)	Udder Balance(UB)

The first measurement on the cow was obtained three weeks after parturition. Information on dates of first calving, parity, source of the cow (imported as pregnant heifer or locally born in Egypt), calving date, dates of all available test-day observations and date of drying off were recorded for all animals. Stage of lactation was divided into four groups (lactational quarter year: LQY) going from the first month of lactation up to the 12th month with three months interval each. Determination of milk somatic cell was performed after Gary (1985). VLS_{SCC} was converted to expected somatic cell count (E_{SCC}) according to Barillet *et al.* (1984). For statistical analysis E_{SCC} was further expressed as expected somatic cell score (E_{SCS}) using log₂ E_{SCC} (Rogers *et al.*, 1991).

Data were analyzed using MTDFREML (Multitrait Derivative Free Restricted Maximum Likelihood) animal model (Boldman *et al.*, 1997). The general linear animal mixed model in matrix notation is given by $y = Xb + Z_1a + Z_2c + e$. Where: y is the vector of observations, X is the known matrix, b is the vector of fixed effects (parity and/or age at calving, cow source, farm, season and year of calving), Z_1 , Z_2 are the known incidence matrices, a , and c are non-observable sire and cow random vectors, respectively.

Expectation and variances are defined as:

$$E \begin{bmatrix} a \\ c \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix} \quad \text{var} \begin{bmatrix} a \\ c \\ e \end{bmatrix} = \begin{bmatrix} A \sigma^2_a & \sigma_{au} & \dots & \dots & 0 & 0 \\ \sigma_{au} & B \sigma^2_c & \dots & \dots & I \sigma^2_{e_1} & \\ 0 & I \sigma^2_{e_1} & \dots & \dots & I \sigma^2_{e_2} & \end{bmatrix}$$

Where: A and B are the numerator relationship matrix among animals of sire and cow within sire, I is the identity matrix, σ^2_a and σ^2_c are the direct random additive genetic effect of the sire and cow, respectively. $\sigma^2_{e_1}$ and $\sigma^2_{e_2}$ is the sire and

cow population error variance, respectively. Multi-trait Derivative Free Restricted Maximum Likelihood (MTDFREML) procedure developed by Boldman *et al.* (1997) was used to estimate additive and non-additive variances and co-variances for all studied traits. A variance structure from the sire model in general terms is:

$$\sigma_p^2 = \sigma_s^2 + \sigma_e^2,$$

where σ_p^2 is the total phenotypic variance, σ_s^2 is the sire component of variance between paternal half sibs which involve one quarter of the additive genetic variance (sire model) and σ_e^2 composed of 3/4 the additive genetic variance along with the non-additive genetic variance and environmental variance. The cow model was used in a separate analysis of variance and the structure of variance component was

$$\sigma_p^2 = \sigma_c^2 + \sigma_e^2, \quad \sigma_c^2 = \sigma_a^2 + \sigma_{E_p}^2,$$

where σ_p^2 is the total phenotypic variance, σ_c^2 is the cow component of variance, σ_a^2 is the additive genetic variance, $\sigma_{E_p}^2$ is the permanent environmental variance and σ_e^2 is the residual variance. Heritability (h^2), genetic (R_g) and phenotypic (R_p) correlation between any two traits was estimated as

$$h^2 = \frac{4\sigma_s^2}{\sigma_p^2}, \quad R_g = \frac{\sigma_{s_{ij}}}{\sqrt{\sigma_{s_i}^2} \sqrt{\sigma_{s_j}^2}}, \quad R_p = \frac{\sigma_{p_{ij}}}{\sqrt{\sigma_{p_i}^2} \sqrt{\sigma_{p_j}^2}}$$

Where $\sigma_{s_{ij}}$ and $\sigma_{p_{ij}}$ are the sire genetic and phenotypic covariance between the i^{th} trait and the j^{th} trait, respectively and are estimated from the analysis of measurements of the two traits on the same animal. $\sigma_{s_i}^2$, $\sigma_{s_j}^2$ are sire genetic variance and $\sigma_{p_i}^2$, $\sigma_{p_j}^2$ are phenotypic variances for both traits i and j , respectively.

RESULTS AND DISCUSSION

Heritability estimates for TDM and SCS

Estimates of heritability and sire variance component for TDM and SCS across and within parities are presented in Table 1. Overall h^2_{TDM} was higher in farm "Delta Misr 1" compared with farm Al-Salhia (0.34 vs. 0.28). This reflects a rather higher additive genetic variance in the first farm. Intermediate heritability estimates have been generally observed for TDM in the 1st or subsequent parity. Estimates of h^2_{TDM} found in the present study are generally close to estimates of Monardes and Hayes (1985).

Table 1. Estimates of sire variance components and heritability (\pm SE) of test-day milk yield (TDM) and somatic cell score (SCS) in different parities

Parity	Al-Salhia Farm			Delta Misr Farm 1			Overall		
	σ^2_s	σ^2_e	$h^2 \pm SE$	σ^2_s	σ^2_e	$h^2 \pm SE$	σ^2_s	σ^2_e	$h^2 \pm SE$
TDM									
All	3.56	47.30	.28 \pm .08	6.37	68.57	.34 \pm .11	5.61	67.41	.31 \pm .14
1 st	2.33	49.45	.18 \pm .07	8.15	93.73	.32 \pm .08	7.12	122.36	.22 \pm .09
2 nd	4.11	52.58	.29 \pm .11	6.09	167.91	.14 \pm .09	5.66	102.02	.21 \pm .11
3 rd	6.18	71.07	.32 \pm .17	4.37	55.91	.29 \pm .11	5.79	74.61	.29 \pm .12
4 th	5.28	170.72	.12 \pm .08				5.28	170.72	.12 \pm .08
SCS									
All	14432	247968	.22 \pm .10	22431	538344	.16 \pm .07	9871	197890	.19 \pm .09
1 st	18835	282525	.25 \pm .11	25436	510059	.19 \pm .12	14611	263693	.21 \pm .11
2 nd	8423	272344	.12 \pm .08	15413	1012120	.06 \pm .00	7539	369411	.08 \pm .04
3 rd	10032	276597	.14 \pm .07	1432	42630	.13 \pm .04	10398	309540	.13 \pm .05
4 th	9258	327396	.11 \pm .04				9258	327396	.11 \pm .04

Overall h^2_{SCS} for all parities was 0.19 (Table 1). The highest h^2_{SCS} was obtained in the 1st parity, whereas estimates of the later parities are obviously lower. These estimates are similar to those reported for Holsteins by Coffey *et al.* (1985) and Seykora and McDaniel (1986) who found that h^2_{SCS} for mixed parities was 0.18. The present results suggested a general trend toward decreasing h^2_{SCS} with advance in parity. This may be due to decreasing additive genetic variance with progressing parities. Similarly, Banos and Shook (1990) reported a decreasing trend in heritability of SCS with increasing lactation number, mainly due to decreased sire variance and increased residual variance. The results of Strandberg and Shook (1989) indicated that direct selection for mastitis and indirect selection on the basis of somatic cell score gave similar responses in terms of reducing the rate of mastitis incidence.

Heritability estimates for TDM and SCS as affected by month of lactation

Estimates of sire variance component and h^2 for TDM and SCS in different segments of month of lactation are presented in Table 2. h^2_{TDM} varied according to month of lactation ranging between 0.14 and 0.23, being highest at the mid-lactation. Estimates of h^2_{TDM} found in the present study agree generally with the corresponding values reported by Tijani *et al.* (1999) who obtained heritability estimates for milk yield ranging from 0.10 and 0.22. They also concluded that h^2_{TDM} in mid-lactation were higher than at the beginning or end of lactation. Gengler *et al.* (1999) reported that h^2_{TDM} increased with lactation stage.

Heritability estimates for SCS in Table 2 indicate no clear trend of month of lactation effect on the estimates of h^2_{SCS} . Results in Table 2 agree generally with those reported by Mrode and Swanson (2001) who reported that h^2_{SCS} increased slightly with days in milk in all parities.

Table 2. Estimates of sire σ_s^2 and residual σ_e^2 variance components and heritability ($h^2 \pm SE$) of test-day milk yield (TDM) and somatic cell score (SCS) as affected by stage of lactation

Lactation Months	TDM			SCS		
	σ_s^2	σ_e^2	$h^2 \pm SE$	σ_s^2	σ_e^2	$h^2 \pm SE$
Overall	9.15	165.14	0.21 \pm 0.10	9871.42	197890.00	0.19 \pm 0.09
0 <3	4.51	124.35	0.14 \pm 0.10	10652.35	462770.22	0.09 \pm 0.01
$\geq 3 < 6$	11.28	184.89	0.23 \pm 0.11	12723.39	411377.00	0.12 \pm 0.05
$\geq 6 < 9$	8.23	211.24	0.15 \pm 0.08	12987.14	419913.00	0.12 \pm 0.09
$\geq 9 - 12$	7.11	142.57	0.19 \pm 0.07	15643.84	268775.18	0.22 \pm 0.11

Heritability estimates for udder and teat traits

Estimates of sire variance component and heritability of studied udder and teat traits in different parities are given in Table 3. Estimates of h^2 for udder traits (FUA, FUL, RUW, RUH, UD, UC, and UB) were medium to high and ranged from 0.29 for RUH to 0.54 for RUW. The magnitude of h^2 values indicates the possibility of improving udder traits through selection. Heritabilities found in the present study did not differ greatly from estimates obtained by Gengler *et al.* (1997) who reported that h^2 was 0.28 for RUH and 0.32 for UC.

Table 3. Estimates of sire σ_s^2 and residual σ_e^2 variance components and heritability ($\pm SE$) of udder and teat traits in different parities

	FUA	FUL	RUW	RUH	UD	UC	UB	TPRV	TPSV	TS
σ_s^2	25.26	27.25	21.29	1.06	14.44	18.38	26.06	28.34	32.95	49.71
σ_e^2	18.94	19.75	136.41	128.70	171.88	185.84	241.22	218.09	22.51	276.26
h^2	.49 \pm .13	.50 \pm .11	.54 \pm .14	.29 \pm .09	.31 \pm .09	.36 \pm .11	.39 \pm .14	.46 \pm .15	.52 \pm .19	.61 \pm .17
1 st	.32 \pm .11	.22 \pm .09	.42 \pm .11	.24 \pm .11	.18 \pm .10	.42 \pm .12	.34 \pm .15	.32 \pm .11	.35 \pm .20	.55 \pm .12
2 nd	.35 \pm .13	.28 \pm .08	.55 \pm .18	.32 \pm .12	.22 \pm .09	.45 \pm .14	.42 \pm .11	.42 \pm .19	.45 \pm .18	.67 \pm .22
3 rd	.55 \pm .18	.61 \pm .19	.55 \pm .20	.28 \pm .09	.35 \pm .11	.19 \pm .11	.46 \pm .12	.55 \pm .11	.51 \pm .11	.58 \pm .24
4 th	.47 \pm .16	.62 \pm .16	.43 \pm .18	.28 \pm .14	.35 \pm .14	.21 \pm .12	.23 \pm .09	.59 \pm .13	.60 \pm .12	.42 \pm .18

FUA= fore udder attachment, FUL= fore udder length, RUW= rear udder width, RUH= rear udder height, UD= udder depth, UC= udder cleft, and UB= Udder balance TPRV= teat placement rear view, TPSV= teat placement side view, and TS= teat size.

Estimates of h^2 for teat traits (TPRV, TPSV, and TS) ranged from 0.46 for TPRV to 0.61 for TS overall parities. These values lead to the conclusion that selection based on teat measurements would be effective to improve teat traits. When considering parity, the results reflect a general trend towards increasing h^2 values with advance in parity. The current heritability estimates for teat traits agree with those of Gengler *et al.* (1997) but are somewhat higher than those of Mrode *et al.* (2000).

Correlations among studied traits

Genetic (r_g) and phenotypic (r_p) correlations between TDM and both SCC and SCS are presented in Table 4. Estimated values indicate a clear trend of a negative association between TDM and both SCC and SCS. Both r_g and r_p between TDM and each of SCC and SCS showed generally low to intermediate values which ranged from -0.08 to -0.28. This indicates a decrease in SCC with increasing yield or conversely a decline in milk production with increasing level of SCC in milk. This result suggests that as SCC in milk increased, milk production will be in turn decreased, as a result of probable mastitic infected udder. This may be due to the destruction of milk producing tissues in the udder as a result of mastitis infection. The magnitude of association between TDM and SCS was, however, much lower than that with SCC across and within parities. The present results indicate that negative correlation estimates became increasingly negative as parity advanced. Kennedy *et al.* (1982) came to the same conclusion and observed that $r_{p\text{ SCC}^*\text{TDM}}$ increased with progressing lactation age. They reported an average value of -0.13 for $r_{p\text{ SCC}^*\text{TDM}}$. Mrode and Swanson (1996) reported that the estimates of r_p tended to be more negative in later parities than in the first parity. The present results are also consistent with those of Amin (2000); Mangwiro *et al.* (2000).

Table 4. Estimates of genetic (r_g) and phenotypic (r_p) correlation of test-day milk yield (TDM) with somatic cell count (SCC) and score (SCS) across parities

Parity	$r_g \pm SE$		$r_p \pm SE$	
	SCC	SCS	SCC	SCS
All	-0.23±0.10	-0.13±0.07	-0.27±0.13	-0.15±0.07
1 st	-0.17±0.10	-0.12±0.05	-0.15±0.11	-0.09±0.04
2 nd	-0.19±0.09	-0.12±0.07	-0.15±0.09	-0.08±0.04
3 rd	-0.24±0.11	-0.15±0.04	-0.28±0.15	-0.14±0.07
4 th	-0.26±0.12	-0.15±0.03	-0.25±0.11	-0.23±0.10

Correlations of TDM and SCS with udder and teat traits

Overall correlation coefficients either genetic or phenotypic of studied udder and teat traits with TDM and SCS are shown in Table 5. Results indicated a consistent trend of direction of both r_g and r_p between TDM and each studied udder and teat trait, except with RUW, where r_p but not r_g was negative. Results in Table 5 indicated marked variation in both direction and magnitude of estimated r_g and r_p between TDM and studied traits. Both RUW and UC traits showed genetically the highest positive association with TDM. This may indicate the possibility of indirect genetic improvement of TDM by direct selection for both RUW and UC traits. The positive r_g and r_p of some udder and teat traits with TDM are in a accordance with those reported by Rogers *et al.* (1989) and van Nickerk *et al.* (2000). Similar to the present results, Misztal *et al.* (1992) reported negative genetic correlation of milk yield with FUA (-0.44), UD (-0.31) and front teat placement (-0.03) and concluded therefore that selection for only increased milk yield would cause deterioration of some udder traits.

Estimates of r_p of SCS with UD, UB, FUA, RUW, and RUH were all negative. These results broadly support the conclusion of Rogers *et al.* (1991) that cows with higher, more tightly attached udders and closer teat placement have lower SCC in their milk. They suggested the inclusion of udder characteristics in addition to SCC in an index as indirect means of reducing mastitis incidence.

Correlation estimates in different parities

Results in Table 5 indicated that r_g of TDM with UC, FUL, RUW, RUH, TPSV and TS were all positive and showed a general tendency towards increasing their magnitude with advancing parities. The other udder and teat traits showed, however, negative r_g with TDM and became greater in magnitude with progressing parity except with FUA. Rogers *et al.* (1998) concluded that bulls that transmit more milk would have daughters with more mastitis and a tendency to have deeper udders. van Nickerk *et al.* (2000) reported a negative r_g between UD and milk yield ranging from -0.44 and -0.53 and a positive but rather higher r_g than those found in the present study between milk yield and both RUW and RUH.

Phenotypic correlations presented in Table 5 increased in magnitude with progressing parity, except those of UC which decreased with parity. The highest estimate was -0.55 obtained for $r_{p\ TDM*UD}$ in the 4th lactation. This may suggest that cows with deep udders tend to produce lower milk yield as a greater risk of a probable result of mastitis infection. In the present study, FUL showed a moderate and positive r_p with TDM ranged from 0.28 in the 1st lactation and 0.53 in the 4th lactation. Therefore, cows with longer fore-udder tend to produce more daily milk yield. For the other udder traits, particularly TS, the estimates of r_p with TDM were moderate and favorable and showed a tendency to increase in magnitude with parity.

Correlation coefficients between udder and teat traits with SCS increased in absolute magnitude with advancing parity, except FUA and RUW in the 4th parity, where they showed lower values. The strongest negative genetic estimates were found for $r_g\ SCS*UD\&FUA$ in the 4th and 3rd lactation, respectively. Generally, estimates of r_p of udder and teat traits with SCS are lower than those of r_g . These results may suggest that the surrounding environmental conditions may play an important role in controlling the relation between SCS and most udder and teat traits. The strongest estimate was 0.38 for $r_{p\ SCS*FUL}$ in the 3rd parity. Udder depth also had a moderate r_p with SCS (-0.32). This result indicates that more shallow udders (those higher in relation to the hock) are generally associated with reduced mastitis incidence. All r_p of teat traits with SCS of the first four parities were positive. Closer teat distances (front and side) were associated with lower SCS and lower mastitis incidence, but estimates of r_p were rather lower and ranged from low to intermediate. For the other teat traits, particularly $r_{p\ TS*SCS}$ were low but tended to be favorable. The present results are in accordance with those reported by Monardes *et al.* (1990) who found positive r_g and r_p between SCC and UC, TPSV, and TPRV. Rogers *et al.* (1998) showed that correlation coefficients between sire evaluations for SCS and udder depth were -0.02 and -0.20 in the 1st and 2nd lactation, respectively, while those with fore-udder attachment were -0.10 and -0.26, in the same order. The present results for these two traits are very close to their estimates showing the same trend to be increased with advancing parity.

Correlation estimates across stage of lactation

Genetic and phenotypic correlations of udder and teat traits with TDM and SCS within classes of month of lactation are given in Table 6. Positive r_g between studied udder traits and TDM showed a general trend to increase with advancing months of lactation (r_g between TDM and UC, RUW, and RUH). This result was also observed with TS where r_g with TDM increased substantially with stage of lactation. Estimates of r_g of other udder traits with TDM were inconsistent and showed no clear trend with stage of lactation. Results in Table 6 indicate that r_p between TDM and each of UC, RUH and TS traits were positive and increased in magnitude with advancing stage of lactation from 0-3 mo to >9-12 mo. RUW showed a negative r_p with TDM with a tendency to drastic increase in magnitude with progressing months of lactation.

Results in Table 6 showed that estimates of r_g between SCS and udder and teat traits increased gradually in magnitude with progressing lactation except those with UC, TPRV and TPSV. The strongest estimates of genetic correlation were found between SCS and each of UD, FUL and FUA, where they were -0.52, 0.53, and -0.51 in the >9-12mo class for the three traits, respectively. Regarding the r_p of udder and teat traits with SCS per month of lactation groups, the results revealed that the r_p ranged from low to intermediate values with a tendency to be lower at the first group (0-3 mo). Generally, estimates of r_p for all traits increased with month of lactation except those for UC and RUH where they showed a slight decline in the fourth class (>9-12 mo) and TPRV, and TPSV showing lower estimates in the >6-9 and >9-12 classes of month of lactation. Among udder traits estimates of $r_{p\text{SCS*UC\&FUL}}$ per month of lactation class were positive, meanwhile the other r_p estimates were negative. No comparable estimates for the effect of stage of lactation on the association between SCS and udder and teat traits were found in the literature.

Interrelationships among udder and teat traits

Estimates of r_g and r_p of teat traits with udder traits are presented in Table 7. Estimated correlations ranged generally from low to intermediate values. As long as the r_g is concerned, results in Table 7 showed that $r_{g\text{TS*RUW}}$ acquired the highest value (0.28) while that $r_{g\text{TS*UB}}$ was the lowest (0.03). Regarding the r_g between TPSV and udder traits, it was found that the association with UD, FUA and RUH were all negative. Teat size (TS) also showed negative r_g with both UD and FUA while its correlation coefficient with RUW was positive. Udder traits showed generally similar trend for r_p with teat traits as that observed for r_g . Estimates of $r_{p\text{TPRV*UD\&FUA}}$ are very close to those estimates reported by van Niekerk *et al.* (2000) on South African Jersey cattle. The corresponding r_g values were, however, much lower than their estimates although being similar in direction. Vanraden *et al.* (1990) obtained rather higher estimates for both r_g and r_p and found that r_g and r_p between FUA and TPRV was 0.58 and 0.40, respectively.

Table 7. Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients (\pm SE) between studied udder-teat traits

Trait	UD	UC	UB	FUL	FUA	RUW	RUH	TPRV	TPSV	TS
UD		.17 \pm .10	-.32 \pm .11	.33 \pm .12	.53 \pm .17	.67 \pm .23	.51 \pm .21	.21 \pm .13	-.13 \pm .19	-.17 \pm .11
UC	.30 \pm .09		.29 \pm .11	.17 \pm .09	.51 \pm .18	.39 \pm .14	.09 \pm .04	.11 \pm .07	.11 \pm .09	.07 \pm .10
UB	-.49 \pm .13	.31 \pm .11		-.17 \pm .11	-.22 \pm .10	.34 \pm .12	-.11 \pm .09	-.13 \pm .07	.09 \pm .01	.03 \pm .09
FUL	.45 \pm .11	.22 \pm .07	-.13 \pm .09		.39 \pm .13	-.21 \pm .11	-.14 \pm .06	-.16 \pm .11	.13 \pm .07	.15 \pm .04
FUA	.73 \pm .14	-.13 \pm .11	-.11 \pm .04	.33 \pm .12		-.21 \pm .13	-.34 \pm .11	.24 \pm .03	-.11 \pm .07	-.06 \pm .11
RUW	.51 \pm .19	.49 \pm .22	.33 \pm .11	-.26 \pm .10	-.38 \pm .11		-.31 \pm .15	.09 \pm .01	.07 \pm .09	.28 \pm .10
RUH	.67 \pm .24	.41 \pm .30	-.09 \pm .17	-.37 \pm .13	-.44 \pm .12	-.48 \pm .13		.09 \pm .09	-.07 \pm .11	.19 \pm .07
TPRV	.13 \pm .01	.07 \pm .11	-.09 \pm .01	-.12 \pm .09	.24 \pm .14	.11 \pm .01	.05 \pm .01		.16 \pm .09	-.17 \pm .07
TPSV	-.12 \pm .11	.09 \pm .10	.14 \pm .09	.09 \pm .09	-.16 \pm .11	.03 \pm .07	-.09 \pm .04	-.11 \pm .07		.21 \pm .11
TS	-.19 \pm .04	.13 \pm .09	.00	.11 \pm .09	-.19 \pm .22	.25 \pm .13	.13 \pm .07	.14 \pm .07	.18 \pm .07	

Relationships among udder traits

Estimates of r_g and r_p between studied udder traits are given in Table 7. Results indicated moderate to high positive correlations either phenotypic or genetic between UD and the other udder traits. Genetic as well as phenotypic correlations between UD and the other traits increased generally with advancing parity order. The present results are in accordance with those reported by Gengler *et al.* (1997) and van Niekerk *et al.* (2000) though opposed in the sign of r_g and r_p between UD and RUW, where their estimates were negative. Genetic correlations of UC with FUA and RUW found in the present study are generally in close agreement with the corresponding values reported by Misztal *et al.* (1992). Their estimate of r_g between UC and each of FUA and RUW were 0.51 and 0.41, respectively. The profile of variability in estimates of both r_g and r_p among udder traits found in the present study might be explained by different genetic factors controlling these traits in different parities. The present estimate of r_p between UC and FUA showed remarkable differences from those estimates given by van Niekerk *et al.* (2000). In addition, managerial conditions may influence the correlations between traits in later parities, where cows could be subjected to different housing systems, milking practices etc. resulting in unstable association among udder traits in different time intervals throughout animal's life. The limited number of observations available for the present study may of course have its impact on the estimates obtained for the relationships among studied udder traits.

CONCLUSION

Genetic analysis of the relationship between test-day milk yield (TDM), somatic cell count and score (SCC&SCS) and ten udder-teat traits (UTT) of Holstein Friesian cows was carried out. The highest estimates of $h^2_{TDM, SCC \& UTT}$ were 0.34, 0.23, and 0.61, respectively. High estimates of genetic correlations were obtained between milk production and UTT. These results indicate to selection based on UTT would be effective to improve milk production. SCC in milk increased, milk production will be in turn decreased, as a result of probable mastitis infected udder. Genetic

parameters for all studied traits are possible aids for constructing selection indices for improving udder health and milk yield.

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تحليل وراثي للعلاقة بين إنتاج اللبن اليومي، تعداد الخلايا الجسدية وبعض خصائص الضرع والحلمات لأبقار الهولستين فريزيان

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تم إجراء تحليل وراثي باستخدام النموذج الحيواني متعدد الصفات للعلاقة بين صفات إنتاج اللبن اليومي، عدد الخلايا الجسدية مع بعض صفات الضرع والحلمات. كان عدد المشاهدات الكلية 3909 تم تجميعها من 2811 بقرة في أربعة مزارع لإنتاج اللبن. تراوحت قيمة المكافئ الوراثي لإنتاج اللبن اليومي بين 0.28 الى 0.34. ارتفعت قيمة المكافئ الوراثي مع تقدم ترتيب موسم الحليب حتى الموسم الثالث واختلفت قيمته خلال المراحل المختلفة من منحنى الحليب وتراوحت قيمته بين 0.14 الى 0.23. التقدير العام للمكافئ الوراثي للخلايا الجسدية كان 0.19. اعلى تقدير للمكافئ الوراثي للخلايا الجسدية ظهر في الموسم الاول بينما انخفضت هذه القيمة في المواسم الاخيرة بدرجة واضحة. تقديرات المكافئ الوراثي لصفات الضرع والحلمات تراوحت بين 0.29 الى 0.54 و0.46 الى 0.61 على التوالي. لذلك فان الانتخاب على اساس مقاييس الضرع والحلمات سوف يكون فعال جدا لتحسين هذه الصفات. تشير نتائج الارتباط الى ان هناك علاقة تلازم سالبة بين انتاج اللبن وعدد الخلايا الجسدية في اللبن فقد تراوحت قيمة الارتباط بين -0.08 الى -0.28 مع تزايد طفيف في قيمة الارتباط الوراثي مع تقدم ترتيب موسم الحليب. وهذه النتيجة تشير الى ان ارتفاع عدد الخلايا الجسدية في اللبن سوف يصاحبه انخفاض في انتاج اللبن كنتيجة لاحتمال اصابة الحيوان بمرض التهاب الضرع. كان هناك ارتباط وراثي قوى وموجب بين انتاج اللبن اليومي وكل من عرض الضرع من الخلف والحاجز العرضي للضرع. لذلك فان الانتخاب لصفات الضرع السابقة قد يحسن بطريقة غير مباشرة من انتاج اللبن. الارتباط المظهري للخلايا الجسدية مع صفات الضرع كانت جميعها سالبة مما يشير الى ان الابقار ذات الضرع المشمور ذو الارتباط القوى بالجسم والحلمات المتقاربة تميل الى انتاج لبن منخفض في محتواه من الخلايا الجسدية. الارتباط الوراثي لإنتاج اللبن مع بعض صفات الضرع والحلمات كان موجب ويميل الى الزيادة مع تقدم ترتيب موسم الحليب. اما الارتباطات الأخرى فكانت سالبة ومتزايدة ايضا مع تقدم ترتيب موسم الحليب باستثناء صفة شدة ارتباط الأرباع الامامية. وكانت العلاقة بين انتاج اللبن وعمق الضرع من اعلى الارتباطات الوراثية السالبة (-0.55) في الموسم الرابع. وتشير نتائج الارتباط ان الحيوانات ذات الضرع المتدلية يصاحبها دائما نقص في انتاج اللبن كنتيجة محتملة للاصابة بالتهاب الضرع. أظهر امتداد الضرع للامام ارتباطاً مظهرياً موجباً ومعتدلاً مع محصول اللبن اليومي تراوح بين 0.28 في أول موسم الى 0.53 في الموسم الرابع. ارتباط صفات حلمات الضرع مع انتاج اللبن اليومي كانت قيمته متوسطة وزادت مع تقدم ترتيب موسم الحليب. التقديرات الوراثية لجميع الصفات المدروسة تم حسابها وعرضها هنا كخطوة نحو تكوين أدلة انتخاب لتحسين العائد الاقتصادي الكلي لمزارع ماشية اللبن.

Table 5. Estimates of genetic (r_g) and phenotypic (r_p) correlation of udder and teat traits with test-day mil k yield (TDM) and somatic cell score (SCS) and ranges across parities

Trait	Genetic Correlation \pm SE						Phenotypic Correlation \pm SE					
	TDM			SCS			TDM			SCS		
	Overall	Min	Max	Overall	Min	Max	Overall	Min	Max	Overall	Min	Max
<i>UD</i>	-.30 \pm .01	-.10	-.28	-.41 \pm .22	-.18	-.37	-.48 \pm .17	-.24	-.55	-.29 \pm .17	-.12	-.32
<i>UC</i>	.35 \pm .09	.12	.39	.53 \pm .18	.10	.43	.28 \pm .12	.26 ⁴	.41 ¹	.23 \pm .07	.11	.25
<i>UB</i>	-.17 \pm .07	-.08	-.14	-.22 \pm .17	-.16 ²	-.26	-.31 \pm .11	-.24	-.28 ³	-.23 \pm .01	-.10	-.19
<i>FUL</i>	.29 \pm .11	.18	.38	.44 \pm .19	.29	.33	.35 \pm .09	.28	.53	.35 \pm .09	.14 ⁴	.38 ³
<i>FUA</i>	-.20 \pm .04	-.10 ⁴	-.38 ¹	-.43 \pm .22	-.28	-.48 ³	-.29 \pm .11	-.22	-.42	-.27 \pm .11	-.16	-.28 ²
<i>RUW</i>	.41 \pm .12	.16	.39	-.18 \pm .04	-.11 ⁴	-.26 ³	-.55 \pm .17	-.11	-.42	-.20 \pm .11	-.12	-.28 ³
<i>RUH</i>	.30 \pm .11	.16	.26	-.17 \pm .07	-.08	-.20	.29 \pm .19	.12	.26	-.15 \pm .10	-.12 ⁴	-.17 ²
<i>TPRV</i>	-.21 \pm .07	-.09	-.11	.11 \pm .07	.10 ²	.18	-.17 \pm .22	-.13	-.28	.16 \pm .09	.12	.23
<i>TPSV</i>	.13 \pm .00	.04	.13 ³	.12 \pm .00	.10 ²	.20	.23 \pm .09	.10 ²	.32	.22 \pm .07	.18	.32
<i>TS</i>	.31 \pm .07	.12	.20	.20 \pm .11	.12	.25	.35 \pm .10	.21	.42	.29 \pm .14	.22 ⁴	.28 ³

Unlabeled estimates means minimum values are presented in the 1st parity and maximum values are presented in the 4th parity

Table 6. Estimates of genetic r_g (\pm SE) and phenotypic r_p (\pm SE) correlation of udder and teat traits with TDM and SCS per month of lactation

Trait	0-3mon		>3-6 mon				>6-9mon				>9-12 mon					
	r_g		r_p		r_g		r_p		r_g		r_p		r_g		r_p	
	SCS	TDM	SCS	TDM	SCS	TDM	SCS	TDM	SCS	TDM	SCS	TDM	SCS	TDM	SCS	TDM
UD	-.15 ¹ (.11)	-.40 ² (.18)	-.39 (.10)	-.21 (.10)	-.21 (.10)	-.44 (.17)	-.53 (.21)	-.33 (.13)	-.34 (.13)	-.52 (.14)	-.57 (.19)	-.44 (.13)	-.18 (.06)	-.52 (.23)	-.33 (.22)	-.47 (.24)
UC	.17 (.07)	.63 (.23)	.14 (.10)	.16 (.15)	.22 (.09)	.51 (.19)	.16 (.10)	.14 (.12)	.37 (.17)	.45 (.16)	.19 (.10)	.24 (.11)	.39 (.15)	.32 (.11)	.21 (.13)	.21 (.11)
UB	-.32 (.11)	-.18 (.10)	-.20 (.10)	-.19 (.10)	-.26 (.12)	-.18 (.09)	-.17 (.08)	-.23 (.12)	-.14 (.09)	-.20 (.06)	-.14 (.10)	-.27 (.11)	-.12 (.03)	-.20 (.11)	-.09 (.04)	-.29 (.10)
FUL	.28 (.12)	.23 (.10)	.26 (.11)	.20 (.10)	.31 (.14)	.34 (.11)	.37 (.19)	.23 (.09)	.30 (.11)	.46 (.18)	.28 (.11)	.33 (.19)	.27 (.12)	.53 (.16)	.22 (.11)	.39 (.19)
FUA	-.18 (.09)	-.31 (.12)	-.24 (.14)	-.10 (.15)	-.18 (.09)	-.32 (.14)	-.26 (.17)	-.12 (.10)	-.27 (.14)	-.49 (.20)	-.34 (.10)	-.29 (.10)	-.18 (.03)	-.51 (.24)	-.21 (.07)	-.31 (.10)
RUW	.12 (.04)	-.14 (.08)	-.25 (.13)	-.18 (.15)	.21 (.10)	-.16 (.06)	-.36 (.13)	-.18 (.07)	.37 (.13)	-.15 (.06)	-.49 (.10)	-.22 (.15)	.52 (.19)	-.19 (.07)	-.63 (.22)	-.22 (.07)
RUH	.18 (.09)	-.15 (.09)	.19 (.10)	-.13 (.04)	.29 (.16)	-.19 (.09)	.27 (.10)	-.17 (.06)	.45 (.15)	-.19 (.01)	.42 (.10)	-.17 (.07)	.55 (.16)	-.16 (.09)	.49 (.09)	-.14 (.09)
TPR	-.29 (.12)	.17 (.04)	-.24 (.09)	.23 (.11)	-.29 (.10)	.19 (.03)	-.21 (.09)	.25 (.10)	-.18 (.09)	.09 (.04)	-.14 (.07)	.14 (.01)	-.17 (.03)	.08 (.01)	-.12 (.01)	.14 (.04)
V	.18 (.04)	.14 (.01)	.19 (.07)	.28 (.08)	.20 (.10)	.14 (.00)	.34 (.11)	.28 (.11)	.19 (.11)	.08 (.00)	.21 (.03)	.20 (.10)	.10 (.01)	.08 (.01)	.20 (.03)	.18 (.03)
TPSV	.11 (.02)	.12 (.07)	.19 (.12)	.19 (.10)	.19 (.06)	.16 (.07)	.27 (.08)	.21 (.11)	.45 (.12)	.24 (.10)	.37 (.11)	.32 (.19)	.46 (.11)	.26 (.14)	.41 (.41)	.35 (.11)