GENETIC AND PHENOTYPIC CORRELATION BETWEEN SOMATIC CELL COUNT AND MILK YIELD IN SAUDI DAIRY GOATS USING RANDOM REGRESSION ANIMAL MODEL

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ABSTRACT

The objective of the present study was to explaine thegenetic and phenotypic relationship between test-day somatic cell count and score (SCC& SCS), with daily milk yield in Gabali and Aradi Saudi goat using the random regression animal model. The total number of production records included in the present study was2021 dairy records. 942 dairy records for Aradi goats and 1079 dairy records for Gabli Goats. All available data were collected from Station of training and agriculture-veterinary research, King Faisal University. Polynomial random regression of the third order seemed adequate to explain variation in somatic cell count and test-day milk yield. Somatic cell count (SCC) wasexamined each 15-days using digital instrument DCC. The overall mean of daily production was 886±41 ml for Aradi goat and 738±36 ml for Gabli goat. Overall mean of somatic cell count for Aradi goats was $983x10^3$ cell\ml milk and for Gabila goats was $1127x10^3$ cell\ml milk. Lowest somatic cell count ($258x10^3$ cell\ml milk) obtained during early stage of the 1st lactation. While the highest somatic cell count, ($2541x10^3$cell\ml milk) obtained during the end of the 4th lactation. The 3rd parity showed the highest daily milk production (873 ml) and the 4th parity showed the highest somatic cell count ($1436x10^3$ cell\ ml milk). Additive, Phenotypic and permanent environmental correlations were estimated using random regression animal model. Additive genetic correlation between TDM and both of SCC and SCS were negative and ranged from -0.27 to -0.39 and -0.19 to -0.21, respectively. Estimates of additive genetic correlations between of somatic cell score decreased with increasing the interval between test-days. More details on estimates of different genetic parameters, estimates of permanent environmental and additive genetic correlations for all traits were tabulated.

Key words: Heritability- Correlation – milk - Somatic cell count – udder –goats.

INTRODUCTION

In several studies, somatic cell count reported asthe best indicator for early diagnostic of udder disease (Shook and Schutz, 1994). The SCC in milk is a reliable parameter to indirectly diagnose the health status of mammary glands (Blagitz, *et al*., 2012 and Olechnowicz, and Jaśkowski, 2012).Therefore, it is an effective tool to controlmammary gland disorders such as mastitis.White blood cells and some of epithelia cells from tissues of milking gland construct the main part of SCC in goat milk. Somatic cell count is significantly increase when udder tissue is becoming infected with mastitis (Moroni *et al*., 2005 and Koop *et al*., 2010). One important advantage of the test-day model for genetic evaluation is the most efficient use of serial observations, making better estimates of genetic values, and the possibility of using incomplete lactation records (Freeman, 1998). The ability of milk SCC to predictintra-mammary infection is lower in goat than in cattleand sheep (Boettcher *et al*., 2005). Accordingly, prediction rules would betterbased on repeatedSCC measures over lactation, as proposed by De Crémoux and Poutrel (2001). Many studies have shown that the level of somatic cells in milk influenced by many environmental factors. A study (Dohoo and Meek, 1982) showed that milk samples during the beginning, middle and end of lactation havea significant difference in the level of somatic cells. Milk samples start of lactation contained the highest levels of somatic cells. While the level of somatic cells in the milk of goats Saanen during the first lactation was morally low in comparison with the other lactations (Orman *et al*., 2011). Fuerst-Walt and Fuerst (2014) found that power of genetic inheritance for milk production were moderate to high (0.32 to 0.53) while for SCS were below 0.10 in dairy sheep of East Friesian and Lacaune. Also they found that, genetic correlations between repeated three measurements across lactation are high and ranged from 0.84 to 1.00 for milk production and very low for SCS.

The aim of the present study was to estimate genetic, phenotypic and permanent environmental correlations between test-day milk yield and somatic cell count in Saudi dairy goats using random regression analysis.

MATERIALS AND METHODS

Data consisted of 2021 test day records (TDR) on daily milk yield ($TDM_{ml/day}$), and somatic cell count (SCC). The current data set involved the first four parities

of Aradi and Gabali dairy goat reared in Training station of Agricultural and veterinary research at King Faisal University KSA. Somatic cell count (SCC) was examined each 15-days using digital instrument DCC (Delaval Cell Counter) .All studied traits were recorded on each test day between 5 and 230 days in milk (DIM). The animal must have at least two lactations. In general, the averageof lactations per animal was 3.7 with 7.16 test-day records. Data were recoded on does between 2011 and 2014. Number of TDR per lactation was not less than five observations. Lactational curve were Days in milk (DIM) were classified into 15 groups with 15 days interval. Estimates computed using raw data for test-day milk yield and somatic cell count were illustrated in Table (1).

Statistical analysis: Random regression (RR) models suggested for genetic analysis of test day (TDM) milk yields by Schaeffer and Dekkers (1994) were suggested because of their ability to model a separate lactation curve for every animal. Single trait RR models were applied to first lactation milk, fat and protein of test-day yield data with different functions for fixed and random regressions (Jamrozik and Schaeffer, 1997 and Jamrozik *et al.,* 1998). In the simulation study of Strabel and Misztal (1999), RR models were significantly better than an analysis of 305d in terms of correlation between estimated and true breeding values.To analysis the date of SCC trait, we normalized the SCC distribution by a logarithmic transformation. The SCS was computed as $SCS = log_2(SCC * 10^{-5}) + 3$ as reported in (Ali and Shook 1980 and Rupp *et al*., 2011).

The random regression model used in the study was

$$Y_{ijklm} = HTD_{il} + \sum_{n=1}^{n_p} \beta_{ilo} \chi_{klmo} + \sum_{n=1}^{n_p} \alpha_{klo} \chi_{klmo} + \sum_{n=1}^{n_p} \psi_{klo} \chi_{klmo} + \varepsilon_{ijklm}$$

Where:- $Y_{ijklm}$is them^{th} test day observation of k^{th} does in l^{th} lactation, $HTD_{il}$is theindependent fixed effect of i^{th} herd-test-date for l^{th} lactation, α_{klo} is theO^{th} random regression coefficient of additive genetic effect of k^{th} does in l^{th} lactation on DIM, ψ_{klo} is theo^{th} random regression coefficient of permanent environmental effect of k^{th} does in l^{th} lactation on DIM, $n_p$is the number of parameters fitted in days in milk function, $\beta_{jlo}$is the o^{th} fixed regression coefficient of j^{th} DIM of l^{th} lactation, $X_{klmo}$is the o^{th} dependent trait on DIM, and $\varepsilon_{ijklm}$is the random residual.

The following (co)variance structure was assumed:

$$V\begin{bmatrix}\alpha\\ \psi\\ \varepsilon\end{bmatrix} = \begin{bmatrix}G \otimes A & 0 & 0\\ 0 & P \otimes I & 0\\ 0 & 0 & E \otimes I\end{bmatrix}$$

Where: **G** = genetic covariance matrix between random regression coefficients and traits, **A**= additive numerator relationship matrix, **I=** identitymatrix, **P** = permanent environmental covariance matrix among random regression coefficients and traits, and **E** = residual variance for lactation and assumed to be constant throughout the lactation due to program limitations. Variance-covariance parameters for each of the current longitudinal traits (daily milk yield and milking duration) were estimated using the software package, DFREML (Meyer, 1998 Version 3ß). Random regression model used with cubic as the order of polynomial fit that achieved the highest correlations between random regression coefficients. Cubic random regression mostly used in several previous research works. Permanent environmental effect was presented as a ration between permanent environmental variance to total phonotypic variance.

RESULTS AND DISCUSSION

Averages of daily milk yield across the first four lactations in Saudi local dairy goatswere presented in Table (2). The overall mean of daily milk production were 886±41 ml and 738±36 ml for Aradi and Gabli goats, respectively. According to the results presented in Table (2) the existence of a gradual increase in the average daily milk production of the first lactation until the third lactation and then dropped in the fourth lactation. The average daily milk production in the second lactation increases by almost 22% than the first lactation, while the average daily milk production in the third lactation over the second lactation by 26%. On the other hand, the decline in milk production in the fourth season in comparison with the production of the third season was 9%.These results were in the agreement with the results obtained in the study of both Randy (1991) and Waldron, *et al*. (1997).

The current results showed that summerbirthshave made the lowest average daily milk production of 541 ml. This result may be due to the inadequacy of the surrounding welfare and environmental conditions at this time of year, such as high temperature and high humidity. In addition, a decline the quality of the feed at this time of the year and add to that the low animal appetite to eat.

Overall mean for somatic cells count was 983 x 10^3 cell / ml.of milk and 1127 x 10^3 cell / ml. of milk for Ardi and Gabli goats, respectively (Table 2). Zeng and

Escobar (1996) study has pointed out that there are significant differences in somatic cells estimates among some of the local goat breeds.

Results (Table 2) indicate the existence of a significant increase in the content of goat's milk from somatic cells with the progress of the order of lactation. The highest content of somatic cells appeared in the fourth lactation and less milk content appeared in the first lactation of a difference of 573 x 10^3 ml milk. The rates of increasing somatic cells count from one lactation to the other were 25.5%, 4.6% and 31.2%. The differences between the second and third lactation wasvery lowand insignificant. Estimates have risen significantly in the fourth lactation.

During five consecutive lactation in the study Paap el al., (2007) achieved a significant increase in the content of goat's milk from somatic cells. A higher difference between the lactations in content of milk from somatic cells were obtained at the end of the lactation and before entering the dry period.In addition, Orman *et al*., (2011) reported thatthere were significant differences in the number of somatic cells in milk between first kindling goats and goats multiple kindling.

Estimates of somatic cell count through the different stages of the lactation curve illustrated in Figure 2. The results presented in the form of three stages shows change in the number of somatic cells in goat's milk during the beginning and middle and end of lactation.Overall means for number of somatic cells during the three phases were 511 x 10^3, 820 x 10^3 and 1436 x 10^3 cells / ml. milk. These results indicate a steady increase in somatic cell count with advancing stages of lactation curve. Overall average rates of increase in the level of somatic cells from one stage to another during lactation was 60.5% and 75.1% for the transition from the beginning to the middle phase and the transition from the middle to the end of the phase, respectively. Gomes *et al*., (2006) showed a significant increase in the number of somatic cells with the progression of the lactation curve. Where the averages of the various stages were 2.56 x 10^5, 6.50 x 10^5 and 8.52 x 10^5 cells /ml. of milk to the beginning, middle and end of lactation, respectively. It also has a study of Koop *et al*., (2010) indicate to the presence of a non-linear increase in the number of somatic cells with the progress of days in milk for some types of German dairy goats.

Phenotypic correlation between daily milk yield and somatic cells count: estimates of the phenotypic correlation coefficient between the daily milk production and somatic cell count was illustrated in a Table (3). In general the results showed a negative correlation (-0.36) between the milk yield and number of somatic cells.

Based on this result, phenotypic selection for animals with a high daily milk yield will accompanied by a low content of somatic cells.

This result agreed with a number of previous studies (Zeng *et al*., 1997; Moroni 2005; Petzer *et al*., 2008). Koop *et al*. (2010) found a negative correlation between milk production and the number of somatic cells in the group of infected animals with mastitis (the beginning of the injury).

The results of the current study haveshown that increased milk production may accompany with an increase in the number of somatic cells during the beginning phase of lactation (Figure 2 and Figure 3).Phenotypic correlation estimates (Table 3) confirms this conclusion. The results (Table 3) showed that all correlations were positive using either pooled data of all lactations or data of separate lactation during beginning of lactation curve. The highest estimate of the positive correlation coefficient between milk production and the number of somatic cells arrived at 0:57 (at the beginning of the third lactation), while the value of the lowest estimate of the correlation coefficient is 0.44 (at the beginning of the first lactation). This is due increasing milk production with progressing days in milk. Current results also showed a lack of state of the fluctuation in the value of the negative correlation coefficient completely within each milk season or within the various stages of lactation.

Additive genetic correlations between measurements of somatic cell across days in milk are illustrated in Figure (3). Estimates of additive genetic correlations between of somatic cell score (Ra_{SCS}) decreased with increasing the interval between test-days. Correlations between measures of somatic cell score during the first three DIM groups and late DIM near to end-lactation were negative. Negative estimates of Ra_{SCS} ranged from -0.08 to -0.51. The highest negative correlation occurred between the 1st measure of SCS with the corresponding measurements near to end-lactation and ranged from -0.18 to -0.51. Additive genetic correlations for milk somatic cell score during beginning, middle, and late of lactation were approximately near to unity. These results indicate that similar additive gene expression exists no longer than three months in sequins of lactation. From another genetic point of view, consider milk somatic cell score could as different traits across lactation.

Boettcher *et al*. (2005) estimated the repeatability of SCS at 0.34 using a finite mixture model and 0.31 using a linear mixed model. Maroteau *et al*. (2014) found that estimates of repeatability for test-day milk were 0.58 and 0.71 in Alpine and Saanen, respectively.

Additive genetic correlations between measurements of test-day milk yield (Ra_{TDM}) across days in milk are illustrated in Figure (3). Results in Figure 3 shows Ra_{TDM} increased among different measurements during 2nd half of lactation. Estimates of

Ra_{TDM}ware more than 0.60 at the beginning the 2nd half of lactation and 0.90 during the end-lactation. This result indicate to TDM can be treated as repeated trait especially during the 2nd half of lactation. The additive genetic correlation between measures of TDM during early and late lactation was negative and ranged from -0.06 to -0.27. This negative correlation is not strong and not indicate to high reduction will occur during end-lactation.Therefore, selection for high production during early lactation will not associated with greater reduction during late of lactation.

Estimates of genetic (Rg) and phenotypic (Rp) correlations between test-day milk yield (TDM) and both somatic cell count (SCC) and somatic cell score (SCS) are presented in Table (2). Estimates values indicate a clear trend of a negative association between TDM and both SCC and SCS. Both Rg and Rp between TDM and each of SCC and SCS showed intermediate and slightly high values ranged from -0.16 to -0.44. This may indicate a decrease in SCC with increasing milk 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 turn decreased. This may be due to the destruction of milk producing tissues in the udder due to mastitis infection. The magnitude of association between TDM and SCS was, however much lower than that with SCC across and within parities. The present result indicates that negative correlation estimates became increasely negative as parity advanced. Rupp *et al*. (2011) and Maroteau *et al*. (2014) reported that the genetic correlation between milk production and somatic cell score were positive, low, not significantly different from zero in Saanen and Alpine goats. The results of the present study are in agreement with that reported by (Rupp *et al*., 2003 andRiggio *et al*., 2007) in dairy sheep and by (Amin, 2000 and Mangwiro *et al*., 2000) in dairy cattle.

Estimates of heritability and permanent environmental effect for some udder-teat traits presented in Table (3). Heritability for teat placement either side view or rear view increased with progressing order of lactation from 0.32 to 0.59 and 0.35 to 0.60 for TPRV and TPSV, respectively. The highest heritability for teat length was 0.67 obtained during the 2nd parity and was moderately low during the 4th lactation (0.42).

In general, all suggested udder-teat traits in the current study obtained high heritability. In addition, estimate of permanent environmental effect (Table 3) for udder-teat trait are small except for teat placement during the first lactation only. Therefor selection for improving udder-teat traits can achieved during either early of later parities.

Estimates of heritability for teat length and teat placement in the current study agree with that reported in several studies (Manfredi *et al*., 2001; Clément *et al*., 2006 and Rupp *et al*., 2011) during the first lactation. On the other hand, Wiggans and Hubbard (2001) found that estimates of heritability for teat placement and teat size were 0.22 and 0.12 for some dairy goats in the United states. Mavrogenis *et al*. (1988) found that heritability estimate for teat length in Chios sheep was (0.64) in the range of the estimates reported in the current study.

Estimates of genetic and phenotypic correlation between TDM and some udder-teat traits across different stage of lactation presented in Table (4). Overall estimates of genetic correlations for relationship between TPM with TPRV, TPSV, and were 0.22±0.09, 0.23±0.07 and 0.24±0.11, respectively. Estimates of genetic correlations were higher than the corresponding phenotypic. The highest estimates of R_g between TDM and teat placement obtained during early and mid-lactation. On the other hand, the highest R_g between TDM and TL obtained during end-lactation. These results indicate to selection for improving teat placement and length can be achieve indirect improvement of milk production.

Estimates of R_g for SCS with TPRV were negative and decreased with progressing days in milk (Table 3). These results may indicate to animals with irregular status of teat placement are more susceptible for mastitis disease. Estimates R_g of SCS with TL increased up wared end of lactation and arrived to 0.46. Therefor selection for reducing somatic cell count during end-lactation can achieve accurate reduction in teat length and may causes problems using automatic milking. Rupp *et al*. (2011) found moderately positive genetic relationship between somatic cell score and each of teat length (0.29) and teat placement (0.15).

To avoid these problems more studies on SCC in dairy goats are required, especially aspects related to infection status and production and technological aspects of milk that could justify the inclusion of SCS into the breeding program.

Table 1. Distribution of production records on groups of days in milk across lactation.

Days in milk groups	# Records	Days in milk groups	# Records
≤ 5	93	96-105	134
6-20	109	106-120	125
21 - 35	137	121-135	133
36 - 50	147	136-150	127
51 - 65	137	151-165	130
66 – 80	169	166-180	123
81-95	140	181-195	120
		> 195	197

Table 2. Estimates of means of daily milk production (Mk) and somatic cell count (SCC: 103 cell/ml milk) across lactations, season of kindling and goat breed.

	CV[2]	Mk[1]	CV[2]	SCC[1]
Overall mean	46	793±38	24	1046±32
Order of lactation				
1st Lactation	21	569±28[d]	20	761±24[c]
2nd Lactation	45	695±32[c]	21	718±27[c]
3rd Lactation	38	873±29[a]	24	1023±37[b]
4th Lactation	67	794±42[b]	23	1436±37[a]
Season of kindling				
Winter	61	975±23[a]	21	1341±21[a]
Spring	54	811±27[b]	21	1011±32[b]
Summer	31	541±21[d]	18	712±18[d]
Autumn	47	611±24[c]	20	947±21[c]
Breed				
Aradi	67	886±41[a]	22	983±37[b]
Gabli	29	738±36[b]	17	1127±41[a]

1: Mean ± standard error, 2: Coefficient of variability

Table 3. Phenotypic relationship between somatic cell count and daily milk yield across lactation curve.

Interval	Overall	Lactation			
		1st	2nd	3rd	4th
All Lactations	-0.36±0.09	-0.31±0.07	-0.38±0.02	-0.32±0.00	-0.36±0.07
Star-lactation	0.54±0.14	0.44±0.09	0.49±0.09	0.57±0.14	0.47±0.09
Mid-lactation	-0.53±0.12	-0.43±0.11	-0.55±0.11	-0.56±0.14	-0.41±0.11
End-lactation	-0.57±0.11	-0.39±0.12	-0.59±0.11	-0.59±0.11	-0.47±0.11

Table 4. Estimates of genetic (Rg) and phenotypic (Rp) correlations between test-day milk yield (TDM) with both of somatic cell count (SCC) and somatic cell score (SCS) across the first four parities.

Parities	$R_g \pm SE$		$R_p \pm SE$	
	SCC	SCS	SCC	SCS
All	-0.32±0.10	-0.22±0.04	-0.37±0.11	-0.17±0.03
1st	-0.27±0.10	-0.19±0.04	-0.31±0.09	-0.16±0.00
2nd	-0.27±0.09	-0.17±0.10	-0.30±0.11	-0.17±0.07
3rd	-0.36±0.11	-0.23±0.14	-0.42±0.09	-0.19±0.02
4th	-0.39±0.11	-0.21±0.11	-0.44±0.12	-0.21±0.07

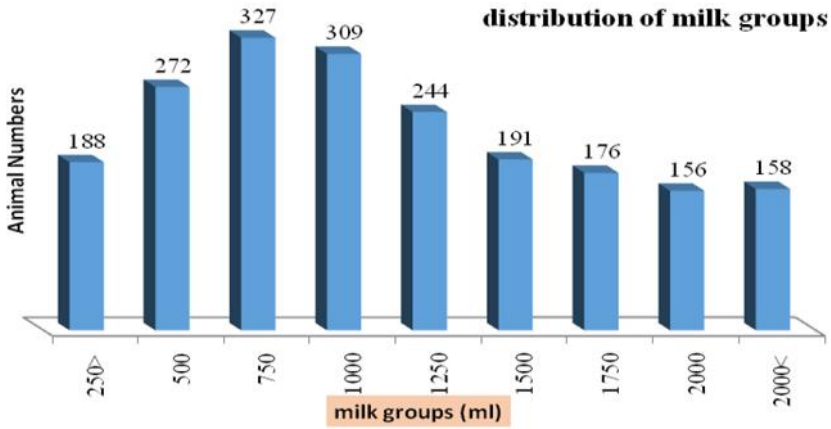

Figure 1. Distribution of daily production records on nine milk production groups.

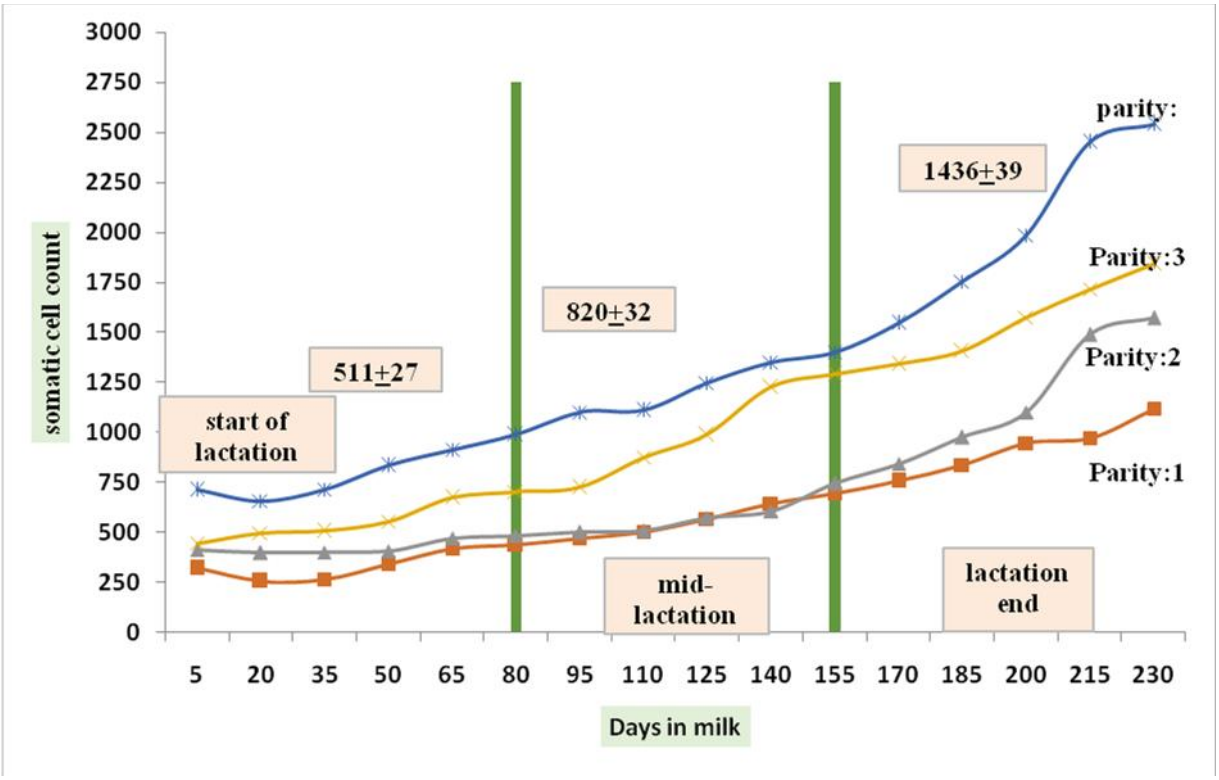

Figure 2. Estimates of somatic cell count (1000 cells / ml. milk) during the various stages of the lactation curve within the first four parities.

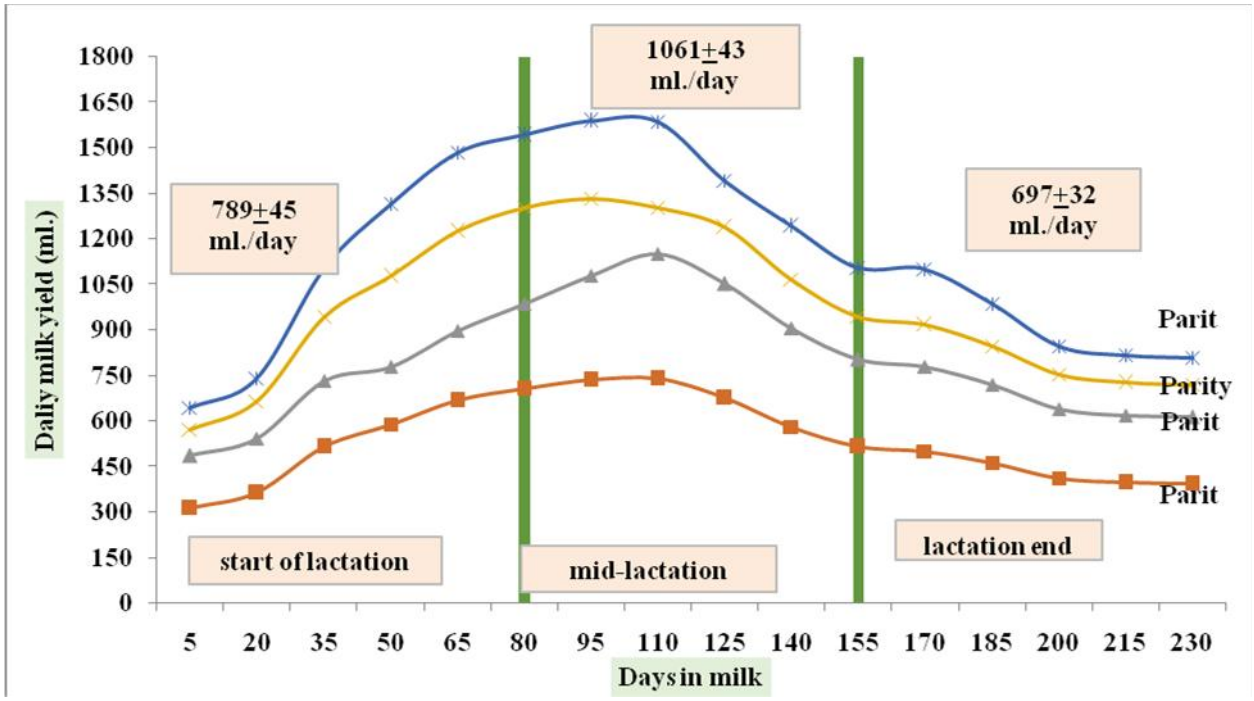

Figure 3. Estimates of means of daily milk yield (4 lactations) across different stages of lactation curve.

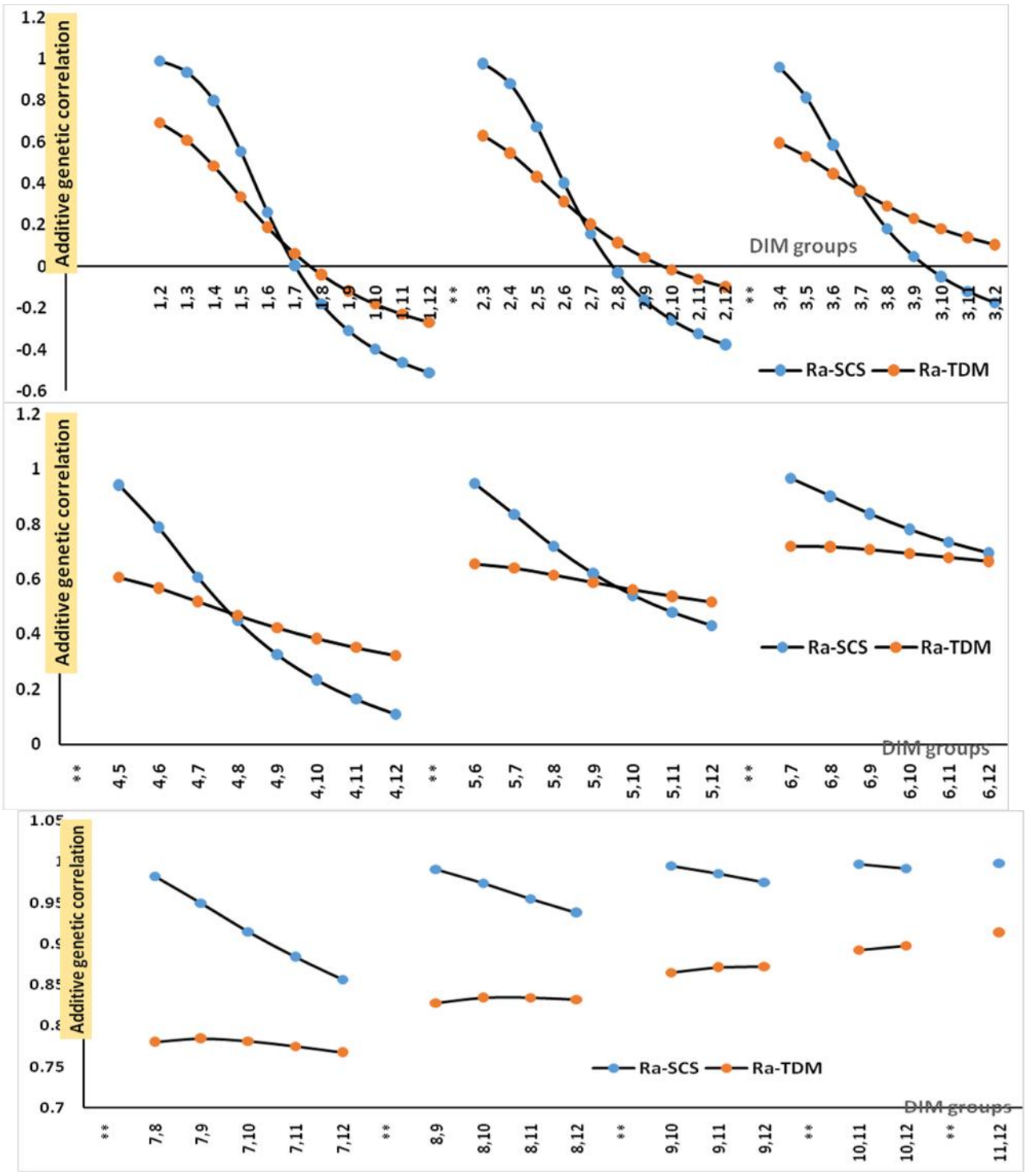

Figure 4. Estimates of additive genetic correlation (Ra_{ij}) among measurements of somatic cell score (SCS) and test-day milk yield (TDM) at i^{th} DIM with j^{th} reminder DIM across lactation.

Conclusion: In the current study, genetic and phenotypic parameters for somatic cell count, test-day milk yield, and some udder-teat traits in Saudi dairy goats were reported. Reducing the loss in production and understanding the mechanism of evaluating the purchased goats either phenotypically or genetically will be of assistance. Early examination ofmilk somatic cell could be an esteemed tool for predicting and reducing loss caused by mastitis in an early stages of productive life. Dairy goats with abnormal udder form especially for teat

characteristics are not desired for increasing milk production. The current results suggest that, reducing somatic cell count in goat milk and enhancing udder health can be achieved by selection.

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