ESTIMATION OF GENETIC PARAMETERS FOR TEST-DAY MILK YIELD AND SOMATIC CELL COUNT IN THE FIRST THREE LACTATIONS OF EGYPTIAN BUFFALO USING RANDOM REGRESSION

Manal M. El-Bramony[1], A. A. Nigm[2], Kawthar A. Mourad[1], M. A. M. Ibrahim[2] and U. M. El-Saied[1]

1- Animal Production Research Institute, Ministry of Agriculture and Land Reclamation, Dokki, Giza, Egypt, 2- Department of Animal Production, Faculty of Agriculture, Cairo University, Giza, Egypt

SUMMARY

Both fixed and random regressions were used to model test day records that are measured over the trajectory from days in milk (DIM) = 5 to 300-d of the first three lactations for Egyptian buffalo. The (co)variance components were estimated with a single trait animal model with REML algorithm for each of daily milk yield (DMY) and $\log_{10}$ SCC (LSCC) for a total of 3189 records. Records were taken from four buffalo experimental research herds belonging to the Animal Production Research Institute Egypt, between 1999 and 2004. The present study aimed at studying the pattern of inhertance, permanent environmental variance, and residual variance for DMY and LSCC in the first three parities of Egyptian buffalo.

Heritability estimates within each parity for DMY and LSCC had wide ranges in all parities. Average heritability estimates for LSCC was 0.15, 0.07 and 0.09 for the three parities, respectively. Estimates, in general, tended to increase toward edges of the trajectory. Permanent environmental variances for DMY were relatively low at early lactation and tended to increase toward the end of the trajectory. Residual variances for DMY were low at both edges of the 3rd parity contradicting the first and second parities. All variances (genetic, permanent environmental and residual) were very high for LSCC in the first parity while they were low in the second and third parities. This result may suggest that LSCC in first parity is not genetically the same as in the rest of parities. Genetic correlations among DIM for each of DMY and LSCC were generally high between adjacent records and tended to decrease when records were further apart. Permanent environmental and phenotypic correlations had the same trend.

INTRODUCTION

In Egypt, buffaloes are considered the main dairy animal. They contribute about 60% to the national milk production and therefore genetic improvement of buffalo milk yield is essential.

The test day model (TDM) has become the method of choice for genetic evaluation of production traits in dairy cattle. Test day models have the advantage of accounting more precisely for short-term variation than lactation models and therefore it is considered more efficient resulting in a more accurate evaluation (Reents *et al.,* 1995; Robert-Granie *et al.,* 2002 and Mrode and Swanson, 2003). Moreover, TD models are a step towards a more biological view for individual variation of the lactation curve (Swalve, 1995 and 1998; Jamrozik *et al.,* 1997).

Ptak and Schaeffer (1993) suggested a repeatability TDM that accounts for the shape of the lactation curve assuming the fixed herd-test date effect. The repeatability model, however, assumes that genetic correlation between repeated records is considered to be equal to unity and a constant variance at all observations. Such models are often used for its simplicity. The multivariate model have been also suggested to analyze longitudinal traits, however, it assumes that subsequent observations to be separate traits. Modeling the covariance structure of repeated measurements correctly is important for drawing correct inference from such data.

Schaeffer and Dekkers (1994) extended a random regression (RR) of TD for genetic analysis because it has the ability to model a separate lactation curve for each animal by the inclusion of random regression coefficients. The lactation curve for an individual cow is split into two sets of regressions on days in milk (DIM). Fixed regressions set to describe the general shape of lactation curve for all cows in the same subclass and the random regressions set is peculiar to each cow (deviations from the average curve), which allows cows to have differently sharper lactation curves. Kirkpatrick and Heckman (1989) and Kirkpatrick *et al*. (1990) added that RRMs facilitate more accurate modeling of the variance-covariance structure of traits that change over a trajectory, are able to predict covariance structure at any point along a continuous scale and will lead to more accurate prediction of BVs and therefore a higher genetic progress would be expected.

RRM would permit better modeling of the repeated milk yield TD records throughout the lactation period and therefore it becomes the model of choice for genetic evaluation for such cases (Swalve, 1998). Such models have been also used for genetic analysis of test-day SCS (Haile-Mariam *et al.,* 2001; Negussie *et al.,* 2002 and Mrode and Swanson, 2003). The objective of this work was to study variance-covariance structure for daily milk yield and LSCC throughout the trajectory of DIM in the first three parties of Egyptian buffalo using the RRM.

MATERIAL AND METHODS

Animals and Management:

Buffalo cows were kept under semi-open sheds. Amounts of rations given to the animals were determined according to animal body weight and level of milk production. The ration was offered twice daily and clean water was available all the

time. Buffalo cows were hand-milked twice a day at 7 a.m. and 4 p.m. throughout the lactation period in Gemiza and Mehallet Mousa experimental stations while machine milking was practiced at Nattaf Kadeem and Nattaf Gedeed. Buffalo cows were naturally mated in a group-mating system. Rectal palpation was applied to check pregnancy. As a rule, buffalo heifers were to be first mated at 24 mo of age or 330 kg of weight, and milking buffalo cows were to be dried 2 mo before their expected calving dates and allowed to be re-mated 2 mo postpartum.

Data:

Data used in this study were collected at monthly intervals over the period from October 1999 through June 2004 from four buffalo experimental farms belonging to the Animal Production Research Institute (APRI), Egyptian Ministry of Agriculture and Land Reclamation. A total of 3189 test day records of milk yield and SCC (thousands/ml) of buffaloes in the first three parities were collected.

TD records from first three lactations between 5 and 300 DIM were considered in the statistical analysis. Buffalo cows with less than 4 TD records/lactation were excluded from the data to insure better estimation of the lactation curve. Table 1 presents some statistics of the data analyzed in this study. After editing, the percentage of 82% of TD records was kept in the file.

Table 1. Structure of the data analyzed in the first three parities of Egyptian buffalo

Item	Parity		
	First	**Second**	**Third**
Buffaloes with records	139	198	174
Test-day records (TDR)	878	1242	1069
Average TDR / buffalo	6.32	6.27	6.14
Total number of animals in pedigree file	422	247	222
Number of sires with progeny	37	32	33
Number of dams with progeny	48	19	20
Mean (SD) for DMY, Kg	6.55 (2.68)	7.77 (3.15)	7.96 (3.11)
Phenotypic range for DMY, Kg	2 - 16	1 – 18	1.5 – 18
Mean (SD) for LSCC	4.74 (0.53)	4.80 (0.52)	4.83 (0.53)
Phenotypic range for LSCC[1]	4.00 – 6.86	4.00 – 6.74	4.00 – 6.60
SCC: thousands/milliliter (SD)	140.6 (405)	143.4 (275)	153.7 (272)
Average age at calving mo (SD)	37.1 (6.3)	53.9 (9.2)	68.0 (9.2)
Phenotypic range for age at calving, mo	25 – 62	39 – 99	49 – 125

LSCC[1]: $\log_{10}$ SCC.

Ten DIM classes were defined. The first class included test days between 5 and 30 DIM and all the subsequent tests were of 30d interval up to 300 DIM. SCC was measured following an alternative a.m.-p.m. monthly recording scheme by automated method of infrared absorption spectrophotometry (Milk-o-Scan; Foss Electric, Hillerφd, Denmark) at the Dairy Services Unit, Animal Production Research Institute, Sakha, Kafr El-Sheikh Governorate. Individual SCC records for each test day were transformed to $\log_{10}$ scale to meet the characteristics needed by hypothesis testing (Ali and Shook, 1980).

Statistical model:

Data were analyzed by REML with a derivative-free algorithm using the computer package (DF-REML, Version 3β) developed by Meyer (1998) with the following single trait animal model for each of first three lactations:

$$Y_{ijkl} = HTD_i + \sum_{m=1}^{4} \beta_{km} Z_{jlm} + \sum_{m=1}^{4} a_{jm} Z_{jlm} + P_j + e_{ijkl}$$

Where:

Y_{ijkl} = record l on DMY or LSCC within lactation made on HTD subclass i for the jth buffalo cow belonging to k^{th} subclass, where k ranged from 1 to 10 starting with k = 1 and incrementally by 1 every 30 days thereafter along the trajectory from 5 to 300-d,

HTD_i = fixed effect of test date i (146, 178 and, 169 levels for the first three parities, respectively),

P_j = random effect of permanent environment associated with all TD yields of the jth buffalo,

e_{ijkl} = random residual effect associated with Y_{ijkl} and

β_{km} and a_{jm} = fixed and random regression coefficients, respectively, of DMY or LSCC on DIM where m = the number of covariates appeared as: X_1 = age of buffalo cow at calving and X_2, X_3 and X_4 are three parameters describing the lactation curve according to Gamma type function of Wood (1967). These coefficients were used to fit the covariance structure for additive genetic and permanent environmental effects. Gamma function was successfully used to fit the shape of the lactation curve for Egyptian (Samak *et al.,* 1988; Mansour *et al.,* 1993 and Sadek *et al.* 1998) and Indian (Kumar and Bahat, 1979 and Yadav *et al.,* 1995) buffaloes with R^2 values reaching 99%. All known relationships among individuals were considered in the animal model.

RESULTS AND DISCUSSION

Heritabilities and variances:

Heritability estimates for DMY at selected DIM in the first three parities are shown on the diagonal of Table 2 and graphically represented in Figure1. Estimates were low at the beginning of the first parity (DIM= 5 to 180), and gradually increased to the end of the lactation trajectory. Estimates were higher in the second parity and tended to increase up to DIM=60 then decreased for DIM between 180 and 210 and increased gradually thereafter to the end of lactation. The third lactation had a quite different trend in which estimates were very high at the beginning of lactation (DIM= 5) then dropped DIM= 90 and sharply increased thereafter to the end of lactation. Similar trends were reported by Strabel and Misztal (1999), Alnajjar (2001) and El-Saied (2004) for dairy cows.

Figure 1. Estimates of heritability at selected days in milk (DIM) for daily milk yield in the first three parities.
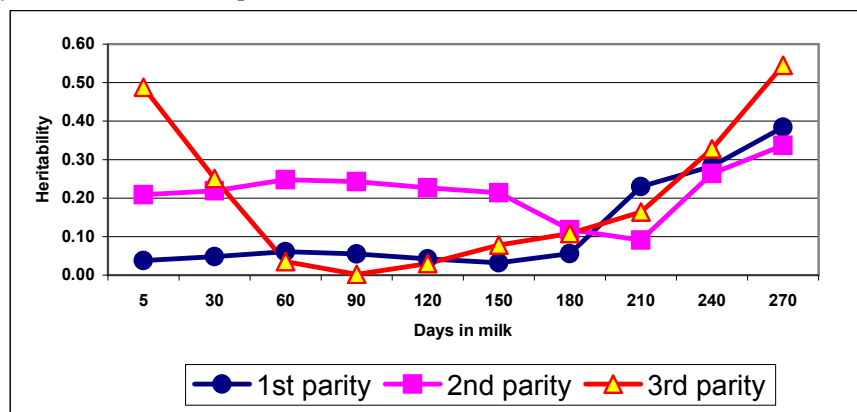

Heritability estimates for individual TD records ranged from 0.032 to 0.384, from 0.091 to 0.337 and from 0.002 to 0.545 in 1st, 2nd, and 3rd lactations, respectively. These ranges are slightly higher than those reported by Alnajjar (2001), in the first three parities of dairy cows with respective means of 0.123, 0.215 and 0.203. Similar estimate (0.216) of the first parity was reported by Mayeres *et al.* (2004).

In general, heritability estimates for DMY, within each parity, had wide ranges and in all parities tended to increase toward the edges of the defined lactation trajectory. Most heritability estimates obtained by RR are high at the edges and low in middle of the lactation trajectory (Jamrozik and Schaeffer, 1997 and El-Saied, 2004). Strabel and Misztal (1999) explained that relatively smooth genetic and permanent environmental variances with two-parity model suggested the large swings of heritabilities could be artifacts of single-trait RRM.

Total variance is the sum of genetic, permanent environmental and residual variances. Heterogeneity of variances through the lactation can occurs in each of these components. Figure 2 presents additive genetic variance for DMY in the first three parities. In general, additive genetic variance across the three lactations had different trends at the beginning of the trajectory (low in the 1st, medium in the 2nd and high in the 3rd). Variances tended to be low up to (DIM= 180) and then gradually increased to the end of the trajectory. Similar trend was found by Jamrozik and Schaeffer (1997), Jamrozik *et al.* (1997) and Alnajjar (2001) for the first three parities of Holstein Friesian cows. Van der Werf et al. (1998) noted that genetic variances estimated directly from RR were higher in the edges of lactation. Kettunen *et al.* (1998) concluded that the overestimated genetic variances at the edges of the defined lactation trajectory curve may be due to mathematical characteristics of random regression sub-models. In general, random regression was efficient to detect fluctuations of genetic variance along lactation.

Figure 2. Estimates of additive genetic variance at selected days in milk (DIM) for daily milk yield in the first three parities.
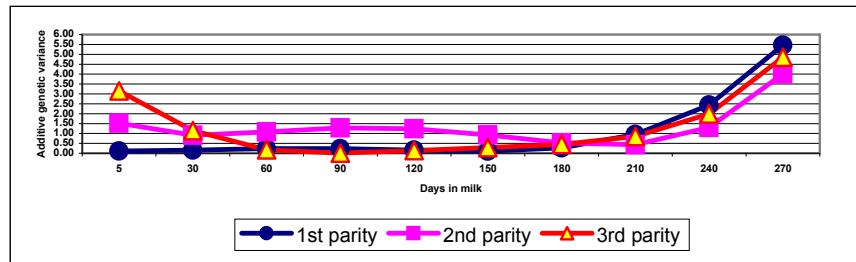
In Figure 3, estimates of permanent environmental variance are presented through DIM for the first three parities. In general, permanent environmental variances were relatively low at early lactation (DIM=5); increased gradually up to (DIM=120), remain without notable change up to (DIM=210) and then increased to the end of the trajectory. Second and third parities had a similar trend. Permanent environmental variance of the 1st parity increased sharply from (DIM=210) to the end of the trajectory. These results are in agreement with results reported by Strabel and Misztal (1999); Alnajjar (2001) and Mayeres *et al.* (2004).

Additive genetic variances ranged from 0.109 to 5.460, 0.434 to 4.010 and 0.011 to 4.850 for the first three parities, respectively while permanent environmental variances ranged from 0.139 to 5.556, 0.498 to 2.480 and 1.440 to 3.170, respectively. Average of the variances for TD milk yield were 1.013, 1.320 and 1.310 for the additive and 1.980, 1.680 and 2.010 for permanent environmental variances in the first three parities, respectively. Rekaya *et al.* (1999) noticed that estimates for genetic variance tended to be very high at the beginning and the end of lactation, while permanent variances did not change significantly from the first to later lactation extent at the edges.

Figure 3. Estimates of permanent environmental variance at selected days in milk (DIM) for daily milk yield in the first three parities.
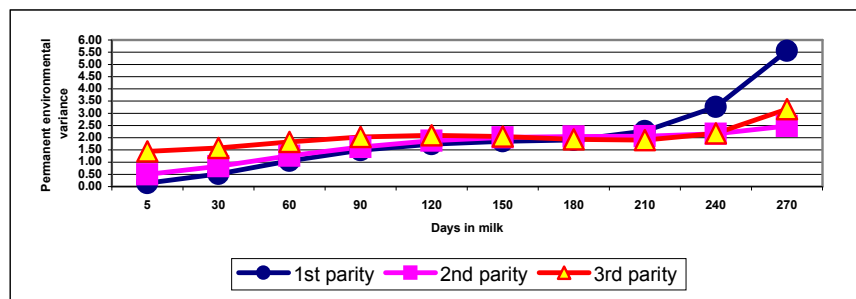
Residual variance for DMY (Figure 4) tended to be low at both edges in the 3rd parity oppositely to the 2nd parity, which had high estimates at both edges. First parity was more similar to the second and tended to be high at both edges with fluctuated

estimates during the trajectory of DIM. Mean estimates of residual variances were 2.35, 2.55 and 2.01 for the three parities, respectively. The same trend was reported by Jensen et al. (2001), who modeled the residual variance in 14 different classes of DIM in the first three parities for dairy cows. They found that variance generally increased with parity number. Similar trends were also reported by Jamrozik and Schaeffer (1997) and Jamrozik *et al.* (1997) and Alnajjar (2001).

Figure 4. Estimates of residual variance at selected days in milk (DIM) for daily milk yield in the first three parities.
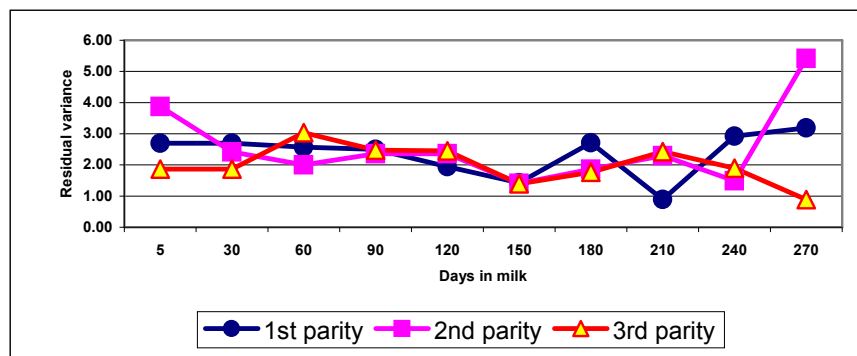
Estimates of heritability at selected DIM for LSCC in the first three parities are presented on the diagonal of Table 3 and graphically represented in Figure 5. Estimates tended to increase with DIM in the 1st parity up to (DIM=120) while they decreased in the 2nd and 3rd parities up to DIM=150. Then estimates tended to increase to the end of trajectory for all parities. Then, estimates tended to increase to the end of the trajectory for all parities. Similar pattern was reported by Negussie *et al.* (2002) and De Ross *et al.* (2003) for dairy cows. Average heritability estimates for test day SCC was 0.15, 0.07, and 0.09 for the first three parities, respectively. No previous estimates were found in the literature for dairy buffaloes, however, these estimates are in agreement with those reported for dairy cows by Reents et al. (1995), Haile-Mariam *et al.* (2001), Mrode and Swanson (2003) and Ødegåd *et al.* (2003). Therefore, recommendations similar to those practiced for dairy cows, such as maintenance of hygienic conditions and the culling of sires on genetic basis when their daughters are predisposed to high SCC, are also recommended for dairy buffaloes to reduce SCC.

Figure 6, 7 and 8 represent estimates of additive genetic, permanent environmental and residual variances at selected days in milk (DIM) for LSCC in the first three parities. Average additive genetic variances were 0.842, 0.020 and 0.030 for the three parities, respectively. The corresponding permanent environmental and residual variances were 1.42, 0.04 and 0.03 and 2.48, 0.17 and 0.19, respectively. The trend of additive genetic and permanent environmental variances for the first parity tended to increase toward the end of lactation, however, residual variance had a different trend. Variances in second and third parities were very close with very low estimates. Similar results were found by Haile-Mariam *et al.* (2001).

Figure 5. Estimates of heritability at selected days in milk (DIM) for log$_{10}$ somatic cell count in the first three parities
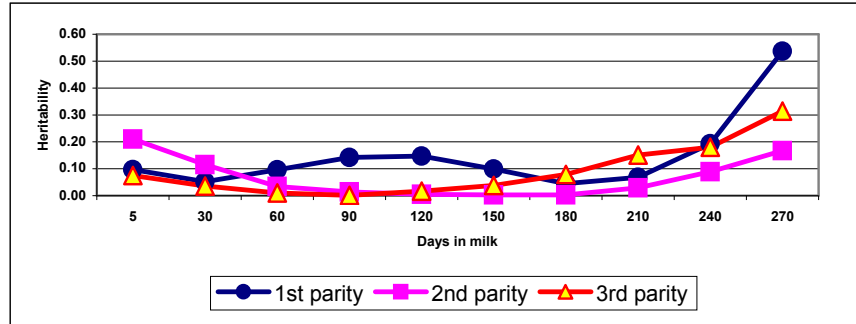
In general, heritabilities for LSCC were low in early lactation and tended to increase as DIM advanced. Haile-Mariam *et al.* (2001), who had a similar trend, stated that the increase in heritability with DIM was a combined by a large decrease in environmental and residual variances. De Ross *et al.* (2003) explained that other factors rather than genes (dry period and calving process) may be responsible for these results. Rogers *et al.* (1995) suggested that SCC in early and late lactation is not genetically the same trait.

Additive genetic and permanent environmental correlations:
Estimates for additive genetic and permanent environmental correlations are presented above and below the diagonal of Table 2, respectively, for daily milk yield in the first three parities. Additive genetic correlations among DIM tended to be high and positive between adjacent DIM and decreased as intervals between records increased. Negative correlations were found between some records through the lactation period (DIM $\geq$ 180 in the first parity, DIM=210 in the second parity and for 5, 30 and 60 DIM in the third parity). Genetic correlations were negative between the beginning and the end of lactation. Similar trend was found by Alnajjar (2001) for Holstein Friesian.

Figure 6. Estimates of additive genetic variance at selected days in milk (DIM) for log$_{10}$ somatic cell count in the first three parities
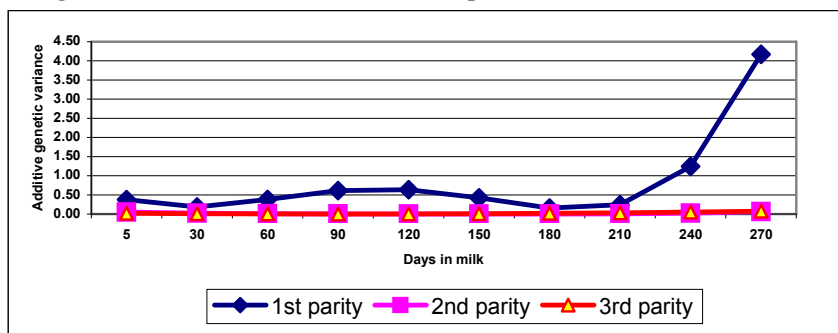

Figure 7. Estimates of permanent environmental variance at selected days in milk (DIM) for log$_{10}$ somatic cell count in the first three parities
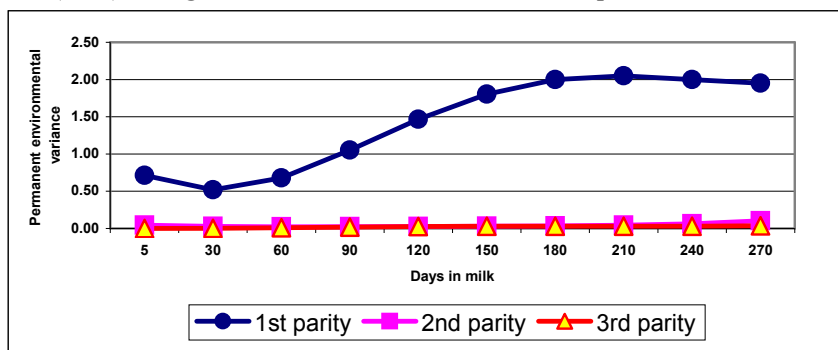

Figure 8. Estimates of residual variance at selected days in milk (DIM) for log$_{10}$ somatic cell count in the first three parities.
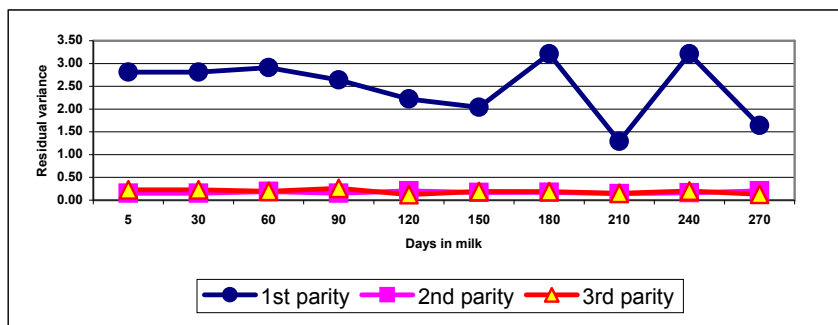
Table 2. Estimates of heritability (on the diagonal) additive genetic (above the diagonal) and permanent environmental correlations (below the diagonal) for daily milk yield at selected days in milk (DIM) in the first three parities.

First parity

DIM	5	30	60	90	120	150	180	210	240	270
5	**0.038**	0.864	0.733	0.732	0.862	0.988	0.571	0.271	0.142	0.071
30	0.972	**0.048**	0.979	0.978	0.999	0.768	0.067	-0.263	-0.388	-0.453
60	0.931	0.991	**0.061**	0.999	0.976	0.618	-0.142	-0.458	-0.572	-0.628
90	0.877	0.966	0.992	**0.055**	0.977	0.622	-0.137	-0.454	-0.568	-0.625
120	0.791	0.914	0.961	0.988	**0.042**	0.783	0.090	-0.241	-0.368	-0.432
150	0.645	0.809	0.881	0.936	0.979	**0.032**	0.713	0.444	0.322	0.254
180	0.403	0.610	0.712	0.796	0.882	0.962	**0.056**	0.950	0.901	0.868
210	0.066	0.302	0.429	0.541	0.667	0.810	0.943	**0.230**	0.992	0.981
240	-0.265	-0.027	0.108	0.235	0.386	0.573	0.782	0.949	**0.283**	0.998
270	-0.528	-0.310	-0.179	-0.046	0.108	0.316	0.502	0.776	0.946	**0.384**

Second parity

DIM	5	30	60	90	120	150	180	210	240	270
5	**0.209**	0.867	0.541	0.290	0.113	-0.046	-0.252	-0.436	-0.315	-0.201
30	0.986	**0.219**	0.888	0.727	0.587	0.437	0.166	-0.376	-0.596	-0.591
60	0.965	0.995	**0.248**	0.961	0.891	0.786	0.527	-0.209	-0.698	-0.799
90	0.949	0.986	0.997	**0.243**	0.981	0.920	0.706	-0.057	-0.660	-0.819
120	0.934	0.974	0.989	0.997	**0.227**	0.977	0.817	0.090	-0.569	-0.768
150	0.913	0.952	0.971	0.984	0.995	**0.214**	0.919	0.286	-0.404	-0.642
180	0.875	0.910	0.931	0.950	0.970	0.990	**0.118**	0.639	-0.015	-0.297
210	0.805	0.831	0.852	0.879	0.912	0.949	0.983	**0.091**	0.758	0.543
240	0.683	0.695	0.716	0.749	0.796	0.853	0.917	0.974	**0.264**	0.959
270	0.504	0.499	0.517	0.556	0.614	0.691	0.784	0.883	0.967	**0.337**

Third parity

DIM	5	30	60	90	120	150	180	210	240	270
5	**0.488**	0.997	0.961	-0.741	-0.984	-0.866	-0.562	-0.104	0.266	0.493
30	0.956	**0.251**	0.980	-0.686	-0.993	-0.902	-0.625	-0.182	0.189	0.422
60	0.841	0.963	**0.035**	-0.528	-0.987	-0.996	-0.765	-0.372	-0.009	0.234
90	0.704	0.881	0.976	**0.002**	0.640	0.338	-0.098	-0.547	-0.805	-0.915
120	0.551	0.770	0.914	0.980	**0.030**	0.938	0.692	0.268	-0.101	-0.341
150	0.368	0.621	0.808	0.916	0.977	**0.078**	0.900	0.586	0.250	0.007
180	0.133	0.405	0.597	0.759	0.870	0.953	**0.108**	0.881	0.648	0.443
210	-0.166	0.112	0.365	0.553	0.706	0.839	0.950	**0.164**	0.931	0.814
240	-0.481	-0.237	0.014	0.220	0.406	0.588	0.774	0.933	**0.328**	0.970
270	-0.732	-0.556	-0.343	-0.146	0.047	0.254	0.490	0.739	0.931	**0.545**

Kettunen *et al.* (1998) found that genetic correlations between consecutive test days of DMY estimated by RR models were high and decreased as the interval between DIM increased. They added that correlations become negative when DIM were further than DIM= 200. They concluded that genetic parameters obtained from the RR models led to unexpectedly high estimates of heritability for DMY as well as negative genetic correlations between most of the distant records. Permanent environmental correlations were very high and positive between consecutive DIM for daily milk yield ranging from 0.943 to 0.991, 0.967 to 0.997 and 0.931 to 0.980 in the first three parities. Negative correlations were found when test days were further apart. This is in agreement with results of El-Saied (2004) for first lactation dairy cows.

Table 3. Estimates of heritability (on the diagonal), additive genetic (above the diagonal) and permanent environmental correlations (below the diagonal) for log$_{10}$ somatic cell count at selected days in milk (DIM) in the first three parities.

First parity

DIM	5	30	60	90	120	150	180	210	240	270
5	**0.097**	0.598	-0.123	-0.395	-0.547	-0.707	-0.957	-0.394	0.074	0.238
30	0.874	**0.052**	0.746	0.534	0.381	0.181	-0.358	-0.960	-0.774	-0.663
60	0.522	0.880	**0.096**	0.965	0.905	0.796	0.355	-0.828	-0.989	-0.990
90	0.285	0.729	0.970	**0.142**	0.992	0.942	0.619	-0.629	-0.920	-0.972
120	0.181	0.651	0.938	0.995	**0.147**	0.985	0.743	-0.490	-0.843	-0.921
150	0.155	0.631	0.928	0.992	0.999	**0.099**	0.884	-0.261	-0.685	-0.798
180	0.184	0.653	0.938	0.995	0.999	0.999	**0.045**	0.608	0.163	-0.615
210	0.262	0.712	0.962	0.999	0.996	0.994	0.997	**0.068**	0.982	0.936
240	0.385	0.797	0.988	0.992	0.975	0.970	0.978	0.992	**0.193**	.999
270	0.568	0.903	0.994	0.946	0.908	0.899	0.912	0.943	0.984	**0.537**

Second parity

DIM	5	30	60	90	120	150	180	210	240	270
5	**0.210**	0.988	0.890	0.493	-0.234	-0.870	-0.435	0.236	0.450	0.552
30	0.945	**0.115**	0.949	0.620	-0.082	-0.785	-0.568	0.084	0.308	0.418
60	0.731	0.909	**0.034**	0.836	0.236	-0.551	-0.797	-0.233	-0.007	0.111
90	0.451	0.706	0.935	**0.014**	0.731	-0.002	-0.996	-0.729	-0.555	-0.453
120	0.230	0.509	0.811	0.963	**0.005**	0.681	-0.771	-0.999	-0.973	-0.939
150	0.085	0.354	0.675	0.877	0.971	**0.003**	-0.059	-0.680	-0.828	-0.889
180	0.005	0.230	0.525	0.742	0.878	0.965	**0.003**	0.772	0.608	-0.509
210	-0.019	0.132	0.355	0.551	0.708	0.846	0.958	**0.029**	0.974	0.940
240	0.001	0.062	0.185	0.331	0.487	0.656	0.826	0.956	**0.089**	0.993
270	0.042	0.021	0.045	0.132	0.270	0.451	0.659	0.850	0.968	**0.167**

Third parity

DIM	5	30	60	90	120	150	180	210	240	270
5	**0.075**	0.996	0.954	-0.392	-0.995	-0.994	-0.975	-0.950	-0.918	-0.879
30	0.153	**0.036**	0.978	-0.305	-0.983	-0.999	-0.991	-0.974	-0.951	-0.919
60	-0.233	0.925	**0.010**	-0.098	-0.922	-0.978	-0.994	-0.998	-0.993	-0.980
90	-0.381	0.855	0.988	**0.001**	0.474	0.302	0.191	0.096	0.008	0.080
120	-0.492	0.785	0.961	0.992	**0.017**	0.983	0.954	0.921	0.883	0.838
150	-0.603	0.696	0.916	0.967	0.994	**0.038**	0.993	0.977	0.955	0.925
180	-0.729	0.565	0.835	0.911	0.956	0.986	**0.079**	0.995	0.983	0.962
210	-0.774	0.506	0.795	0.880	0.932	0.972	0.998	**0.151**	0.996	0.980
240	-0.976	0.057	0.431	0.566	0.663	0.757	0.856	0.952	**0.180**	0.994
270	-0.981	-0.329	-0.053	0.208	0.326	0.449	0.594	0.762	0.924	**0.314**

Additive genetic correlations between all adjacent LSCC were high and decreased as records are further apart. Some negative correlations were found between records in the three parities. Genetic correlations between early and late DIM tended to be higher in second parity when compared to the first parity. This is in close agreement with results reported by Haile-Mariam *et al.* (2001) for SCC using random regression. The third parity had different genetic correlations between the beginning (DIM=5) and the end (DIM=270) with high and negative (-0.879) estimate. Ødegård *et al.* (2003) pointed out that moderate to high genetic correlations were found between SCS in the beginning and the end of lactation (0.38-0.71) while genetic correlation among adjacent DIM were near unity.

In general, results showed that the correlations between adjacent TD records within a given lactation were higher than those between records, which are further apart. This is in agreement with results from other studies (Haile-Mariam *et al.* 2001;

Negussie *et al.* 2002 and Mrode and Swanson 2003). Miller *et al.* (1991) suggested that SCC after first calving is largely influenced by differences in temporary factors. However, late in first lactation and in later parities, SCC was high due to responses to infection, which result in more stable elevation of SCC. The large temporary environmental effects estimates for residual variance in early lactation supports this interpretation (Haile-Mariam *et al.,* 2001). Again, Kettunen *et al.* (1998) concluded that estimation of genetic parameters using RR models led to unexpected high estimates of heritabilities as well as negative genetic correlations between the most distant tests.

Permanent environmental correlations between adjacent LSCC tended to be high ranging from 0.874 to 0.999, 0.909 to 0.971 and 0.153 to 0.998 in the first three parities, respectively, and decreased as the interval between records increased (Table 3). Permanent environmental correlations were high and positive except for correlations of (DIM=5) and with the rest of records in the 3rd parity which were negative. In general, permanent environmental correlations within the first parity were positive and more uniform throughout the lactation than those in 2nd and 3rd parities. Similar trend was observed by Haile-Mariam *et al.* (2001) and El-Saied (2004) for dairy cows.

Phenotypic correlations:

Table 4 presents estimates of phenotypic correlations at selected DIM for DMY (above the diagonal) and LSCC (below the diagonal) in the first three parities. Phenotypic correlations between all adjacent (DIM) for daily milk ranged 0.119 to 0.706, 0.318 to 0.611 and 0.389 to 0.743 in the first three parities, respectively. Negative phenotypic correlations were found for DIM=5 with DIM= 240 and 270 in the 1st parity and with DIM=150, 180 and 210 in the 3rd parity (Table 4). In general, phenotypic correlations tended to increase between adjacent records and decreased as the interval between DIM increased and become negative toward the end of trajectory (DIM=270) following the same pattern of genetic correlation but tended to be lower than the corresponding genetic correlation. Similar trend was found by Alnajjar *et al.* (2001), El-Saied (2004) and Mayeres *et al.* (2004) for dairy cows.

Estimates of phenotypic correlations at selected DIM in the three parities for LSCC were similar in pattern to the genetic correlations (Table 4). Phenotypic correlations between adjacent TD records within lactation tended to increase with DIM ranging from 0.039 to 0.704 in the three parities and decreased as DIM are further apart. Phenotypic correlation between adjacent TD records within lactation were generally higher in 1st parity than in parities 2 and 3. The within parity phenotypic correlation were lower than the corresponding genetic correlations and this is due to the fact that permanent environmental effects in different DIM were less correlated than additive genetic effects (Mrode and Swanson 2003).

Table 4. Estimates of phenotypic correlations for daily milk yield (above the diagonal) and $\log_{10}$ somatic cell count (below the diagonal) at selected days in milk (DIM) in the first three parities.

First parity

DIM	5	30	60	90	120	150	180	210	240	270
5		0.119	0.141	0.147	0.150	0.138	0.081	0.036	-0.210	-0.063
30	0.186		0.263	0.283	0.249	0.272	0.157	0.060	-0.053	-0.141
60	0.080	0.190		0.371	0.392	0.372	0.227	0.114	-0.404	-0.156
90	0.139	0.182	0.324		0.475	0.310	0.205	0.017		-0.118
120	-0.203	0.177	0.347	0.453		0.553	0.403	0.334	0.129	-0.010
150	-0.026	0.168	0.341	0.453	0.508		0.403	0.477	0.247	0.148
180	-0.004	0.171	0.332	0.446	0.515	0.494		0.670	0.524	0.446
210	0.053	0.147	0.244	0.327	0.397	0.414	0.589		0.565	0.554
240	0.102	0.091	0.097	0.126	0.177	0.225	0.394	0.422		0.706
270	0.176	0.061	-0.020	-0.038	0.005	0.092	0.289	0.417	0.704	

Second parity

DIM	5	30	60	90	120	150	180	210	240	270
5		0.318	0.279	0.223	0.189	0.177	0.139	0.099	0.062	0.016
30	0.303		0.447	0.413	0.386	0.384	0.304	0.191	0.062	-0.058
60	0.175	0.170		0.534	0.523	0.536	0.431	0.270	0.076	-0.104
90	0.069	0.121	0.128		0.554	0.581	0.478	0.312	0.108	-0.093
120	0.025	0.063	0.092	0.126		0.611	0.520	0.363	0.168	-0.481
150	-0.007	0.038	0.080	0.125	0.132		0.603	0.463	0.287	0.042
180	-0.001	0.024	0.061	0.104	0.120	0.155		0.504	0.408	0.184
210	0.015	0.029	0.048	0.082	0.104	0.153	0.196		0.539	0.359
240	0.062	0.043	0.030	0.042	0.063	0.117	0.182	0.281		0.577
270	0.113	0.062	0.016	0.004	0.021	0.074	0.155	0.281	0.379	

Third parity

DIM	5	30	60	90	120	150	180	210	240	270
5		0.613	0.364	0.198	0.056	-0.040	-0.086	-0.077	-0.030	0.048
30	0.053		0.431	0.329	0.216	0.143	0.060	0.003	-0.029	-0.038
60	0.022	0.039		0.389	0.337	0.310	0.214	0.101	0.004	-0.091
90	-0.009	0.021	0.055		0.445	0.460	0.358	0.214	0.066	-0.092
120	-0.050	0.009	0.075	0.106		0.530	0.447	0.305	0.153	-0.025
150	-0.069	-0.011	0.053	0.091	0.174		0.572	0.443	0.301	0.114
180	-0.093	-0.032	0.038	0.085	0.178	0.184		0.510	0.439	0.307
210	-0.124	-0.058	-0.017	0.764	0.180	0.200	0.260		0.555	0.510
240	-0.129	-0.075	-0.011	0.047	0.139	0.168	0.217	0.279		0.743
270	-0.162	-0.111	-0.050	0.020	0.115	0.165	0.257	0.232	0.311	

CONCLUSION

Heritability estimates for DMY within each parity were high at the edges and low in middle of the lactation trajectory. The literature explained that relatively smooth genetic and permanent environmental variances with two-parity model suggested the large swings of heritabilities could be artifacts of single-trait RRM. This study was focused only on single-trait analysis for each of DMY and LSCC, however, further work should consider a multiple-trait model for TD milk yield traits.

Heritabilities for LSCC were low in early lactation and tended to increase as DIM advanced. This result may suggest that SCC in early and late lactation are not genetically the same trait. LSCC in First parity had different trend for additive genetic, permanent environmental and residual variance than those for second and

third parities which were very close. This result may suggest that LSCC in first parity is not genetically the same as in later parities. Heritability of LSCC estimated from this study fall within the range frequently reported for dairy cows and therefore genetic and environmental reduction of SCC for dairy buffaloes could be achieved using practices similar to those for dairy cows.

REFERENCES

Ali, A. K. A., and G. E. Shook, 1980. An optimum transformation for somatic cell concentration in milk. J. Dairy Sci. 63:487-490.

Alnajjar, K. A.., 2001. A Study on Animal Genetic Evaluation in Dairy Cattle, Ph.D. Thesis, Faculty of Agriculture, Ain Shams University, Egypt.

De Ross, A. P. W., A. G. F. Harbers, and G. De Jong, 2003. Genetic parameters of test-day somatic cell score estimated with a random regression model. Proceedings of the Interbull Technical workshop, Rome, Italy, August 28-30, Bulletin no 31, 79-101.

El-Saeid, U. M., 2004. Random regression estimation of genetic parameters for milk yield and protein test day model for percentage of primiparous Frisian cows in Egypt. Egyptian J. Anim. Prod.41 (1): 1-10.

Haile-Mariam, M., M. E. Goddard, and P.J. Bowman, 2001. Estimates of genetic parameters for daily somatic cell count of Australian daily cattle. J. Dairy Sci. 84:1255-1264.

Jamrozik, J., and L. R. Schaeffer, 1997. Estimates of genetic parameters for a test day model with random regressions for yield traits of first lactation Holsteins. J. Dairy Sci. 80:762-770.

Jamrozik, J., L. R. Schaeffer and J. C. M. Dekkers, 1997. Genetic evaluation of dairy cattle using test day yields and random regression model. J. Dairy Sci. 80:1217-1226.

Jensen, J., J. Jamrozik and L. R. Schaeffer, 2001. Modelling production in all lactations in dairy cattle using random regression test day models. Book of Abstract of the 52nd Annual meeting of the European, Budapest, 2001. 26-29 August 2001, P2.

Kettunen, A. E. A. Mäntysaari I. Strandén J. Pösö and M. Lidauer, 1998. Estimation of genetic parameters for first lactation test day milk production using random regression models. Proc. 6th WCGALP. January 11-16. Armidale, New South Wales, Australia, Vol. 23:307-310.

Kirkpatrick, M. and N. Heckman, 1989. A quantitative genetic model for growth, shape, reaction norms, and other infinite dimensional characters. J. Math. Biol. 27:429-450.

Kirkpatrick, M. D., Lofsvold and M. Bulmer, 1990. Analysis of the inhertance, selection and evolution of growth trajectories. Genetics. 124: 979-993.

Kumar, R., and P.N. Bhat, 1979. Lactation curve in Indian buffaloes. Indian J. Dairy Sci. 32:156-160.

Mansour, H., I. A. Soliman and G. A. Abd El-Haafiz, 1993. Factors affecting lactation curve of buffalo in upper Egypt. Proceeding of the international Symp.

on prospects of buffalo production in the Mediterranean and middle East. Cairo, Egypt Nov., 9-12 1992. EAAP publications. 62:234-237.

Mayeres, P., J. Stoll J. Bormann, R. Reents and N. Gengler, 2004. Prediction of daily milk, fat, and protein production by a random regression test-day model. J. Dairy Sci. 87: 1925-1933.

Meyer, K., 1998. DF-REML program, version 3-β http: agbu. une. edu. au/~Kmeyer/ dfreml.html.

Miller, R. H., M. J. Paape and L. A. Fulton. 1991. Variation in milk somatic cells of heifers at first calving. J. Dairy Sci. 74:3782-3790.

Mrode, R. A. and G. J. T. Swanson. 2003. Estimation of genetic parameters for somatic cell count in the first three lactations using random regression. Livest. Prod. Sci. 79: 239-247.

Negussie, E., M. Koivula and E. A. Mantysaari. 2002. Random regression test-day model for genetic evaluation of Finnish dairy cattle for somatic cell count (SCC). 53rd Annual EAAP meeting, Cairo, Egypt (September, 1-4 2002).

Ødegård, J., J. Jensen G. Klemetsdal P. Madsen and B. Heringstad, 2003. Genetic analysis of Somatic cell score in Norwegian Cattle using random regression test-day models. J. Dairy Sci. 86:4103-4114.

Ptak, E. and L. R. Schaeffer, 1993. Use of test day yields for genetic evaluation of dairy sires and cows. Livest. Prod. Sci., 34:23-34.

Reents, R., J. Jamrozik L. R. Schaeffer and J. C. M. Dekkers, 1995. Estimation of genetic parameters for test day records of somatic cell score. J. Dairy Sci. 78: 2847-2856.

Rekaya, R., M. J. Carabano and M. A. Toro, 1999. Use of test day yields for the genetic evaluation of production traits in Holstein-Friesian cattle. Livest. Prod. Sci. 57:203-217.

Robert-Granie, C., Maza E. Rupp R and Foulley J. L, 2002. Proceedings of the 7th World Congress on Genetic Applied to Livestock Production, Session 16, and Communication No. 1605.

Rogers, G. W., G. L. Hargrove and J. B. Cooper, 1995. Correlations among somatic cell scores of milk within and across lactations and linear type traits of Jerseys. J. Dairy Sci. 78:914-920.

Sadek, R. R., Mahasin M. Mohamed M. A. M. Ibrahim and Hoda M. A. Abdel-Lattef, 1998. Estimation of lactation curve parameters in Egyptian buffaloes. Egyptian J. Anim. Prod. 35 (1): 1-27.

Samak, M. A., G. A. Hassan A. Hassan and N. Yassen, 1988.The lactation curve and performance of the Egyptian buffalo. Alex. Sci. Exch. 9:83-96.

Schaeffer, L. R. and J. C. M. Dekkers, 1994. Random regression in animal models for test day production in dairy cattle. Proc. 5th WCGALP. Canada, Guelph, Vol. 18:443-446.

Strabel, T. and I. Misztal, 1999. Genetic parameters for first and second lactation milk yields of Polish Black and white cattle with random regression test-day models. J. Dairy Sci. 82: 2805-2810.

Swalve, H. H., 1995. The effect of test day models on the estimation of genetic parameters and breeding values for dairy yield traits. J. Dairy Sci. 78:929-938.

Swalve, H. H., 1998. Use of test day records for genetic evaluation. Proc. 6th World Congr. Genet. Livest. Prod. Armidale. January 11-16, 1998. New South Wales Australia. 23:295-302.

Van der Werf, J. H. J., M. E. Goddard and K. Meyer, 1998. The use of covariance functions and random regressions for genetic evaluation of milk production based on test day records. J. Dairy Sci. 81: 3300-3308.

Wood, P.D.P., 1967. Algebraic model of the lactation curve in cattle. Nature, London 216:164-165.

Yadav, B. S., F. H. Khan and M. C. Yadav, 1995. Lactation curve in Murrah buffaloes. Indian J. Dairy Sci. 48:570.

تقدير المعايير الوراثية لصفتى إنتاج اللبن اليومي و تعداد الخلايا الجسدية ليوم الاختبار فى المواسم الثلاثة الأولى للجاموس المصري باستخدام الانحدار العشوائي

منال محمد البرمونى[1]، على عطيه نجم[2]، كوثر عبد المنعم مراد[1]، محمد عبد العزيز محمد إبراهيم[2]، أسامة محمد السعيد[1]

١ – معهد بحوث الإنتاج الحيواني، وزارة الزراعة و استصلاح الأراضي، الدقى، جيزه، مصر، ٢ – قسم الإنتاج الحيواني كلية الزراعة، جامعة القاهرة، جيزه، مصر

استخدم كل من الانحدار الثابت و العشوائي في نمذجة بيانات يوم الاختبار خلال منحنى الحليب للمواسم الثلاثة الأولى للجاموس المصري. قدرت مكونات التباين و التغاير باستخدام نموذج الحيوان لصفة منفردة باستخدام طريقة (REML) لعدد ٣١٨٩ سجلا لإنتاج اللبن اليومي و تعداد الخلايا الجسدية. سجلت البيانات بين عامى ١٩٩٩ و ٢٠٠٤ فى أربع قطعان بحثية تابعة لمعهد بحوث الإنتاج الحيواني – مصر. استهدف العمل دراسة النمط الوراثي و البيئي الدائم و المتبقي لصفتي إنتاج اللبن اليومى و تعداد الخلايا الجسدية خلال منحنى الحليب من اليوم الخامس و حتى اليوم رقم ٣٠٠ فى الثلاثة مواسم الأولى للجاموس المصري.

أظهرت النتائج اتساع مدى تقديرات العمق الوراثي لكلتا الصفتين داخل كل موسم و اتجاهها للزيادة عند طرفى منحنى الحليب و بلغ متوسط تلك التقديرات لتعداد الخلايا الجسدية ٠.١٥ و ٠.٠٧ و ٠.٠٩ للمواسم الثلاثة الأولى على الترتيب.

انخفضت تقديرات التباينات البيئية الدائمة نسبياً عند بداية منحنى الحليب و اتجهت للزيادة نحو نهاية المسار بينما انخفضت تقديرات التباين المتبقي عند حافتي المسار للموسم الثالث بعكس الموسمين الأول والثاني لصفة إنتاج اللبن اليومي .

إختلفت تقديرات التباينات الوراثية و البيئية الدائمة و المتبقي لصفة تعداد الخلايا الجسدية فى الموسم الأول حيث كانت مرتفعة بوضوح بالمقارنة بالموسمين الثاني و الثالث التى اتجهت للإنخفاض فيهما.

هذا قد يُشير إلى الإختلاف الوراثي لنمط تعداد الخلايا الجسدية للموسم الأول عن باقى المواسم.

ارتفعت تقديرات كل من الارتباطات الوراثية للسجلات المتقاربة على طول مسار منحنى الحليب لصفتى إنتاج اللبن اليومي و تعداد الخلايا الجسدية و اتجهت للتناقص كلما ازدادت الفترة بين السجلات. و كان لكل من الارتباطات البيئية الدائمة والمظهرية نفس الاتجاه.