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ESTIMATION OF GENETIC PARAMETERS FOR MILK YIELD IN THE FIRST THREE LACTATIONS OF HOLSTEIN COWS USING RANDOM REGRESSION MODEL

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SUMMARY

Data used in the study were collected from the Assiout private farm in Assiout Governorate in the south of Egypt. In total, a data set of 8473 test-day milk yield (TDMY) records for the first three lactations (3875, 2993 and 1605 records, respectively)of 414 cows daughters of more than 66 sires and 197 dams was available covering the period from 1998 till 2004. Data were classified according to the month of calving into four seasons, winter, spring, summer and autumn. The statistical model included year-season, the linear and quadratic regression orders on age, fixed regression, a random additive genetic effect for each animal, a random permanent environmental effect for each cow and a random residual effect. The Incomplete Gamma Function (IGF) was chosen to describe the shape of the lactation curve. This function was fitted for each lactation for each cow. DFREML software was used to estimate the components of (co)variance of TDMY in a Random Regression Model (RRM). Estimates of the additive genetic correlations between TDMYs ranged form -0.978 to 0.993, -0.730 to 0.992 and -0.086 to 0.991 for the three lactations, respectively. Estimates of heritability of TDMY increased from 0.030 for days in milk (DIM) 65 to 0.142 for DIM 185 then decreased to 0.035 for DIM 275 in the first lactation. Heritability increased from 0.154 for DIM 65 to 0.215 for DIM 155 then decreased to 0.180 for DIM 215 in the second lactation. Heritability decreased from 0.486 for DIM 5 to 0.409 for DIM 125 then increased to 0.696 for DIM 305 in the third lactation. Results indicated that IGF was suitable to describe the lactation curve of Holstein cattle in the first three lactations under the conditions of the present study.

Keywords: Random regression model, Incomplete Gamma Function, genetic parameters, Test-day milk yield, lactation curve, Holstein

INTRODUCTION

Many factors affect milk production of the cow from one test-day (TD) to the next. It is difficult to model for whole 305-day yields taking into account all such factors (Jamrozik *et al.*, 1996). A test-day model for genetic evaluation can account for these factors such as, day of the year (including weather conditions), management groups within a herd, and, for each cow, days in milk (DIM), pregnancy status and number of milkings daily (Meyer *et al.*, 1989 and Ptak & Schaeffer, 1993). Test-day

model (TDM) can, also, account for the effect of test date, number of records, interval between records and order of test-day records (Reents and Dopp, 1996). Moreover, models using longitudinal measurements would include information about the pattern of a lactation curve for a cow (Schaeffer and Dekkers, 1994).

Many models have been described for the analysis of test-day yields by several studies (Wood, 1967, Ali and Schaeffer, 1987 and Wilmink, 1987). Random regression model (RRM) has become a popular choice for the analysis of longitudinal data or repeated records. This analysis is challenging because it requires numerous parameters ((co)variances between random regression (RR) coefficients) and measurement of error variances (Meyer, 2002), in addition to the (co)variance structure of the test-day yields (Liu *et al.*, 2000).

The objective of this study was to estimate genetic parameters of test day milk yields (TDM's) in the first three lactations in single trait model with a small data set from a private Holstein dairy farm using random regression with the covariance function technique.

MATERIAL AND METHODS

Data

Data used in this study were collected from the Assiout private farm in Assiout Governorate in the south of Egypt. Most of records used in the study were taken from 210 Holstein heifers that had been imported from Germany in year 1998 as heifers-in-calf and F1 daughters. In total, a data set of 8473 test-day milk yield (TDMY) records of 415 Holstein cows daughters of more and than 66[1] sires 197 dams was available from 1998 till 2004. These data represent 892 lactations where test-day (TD) records were taken from day 5 until day 305. All records after 305 day were excluded. Data were classified according to the month of calving into four seasons, winter (from 21 December to 20 March), spring (from 21 March to 20 June), summer (from 21 June to 20 September) and autumn (from 21 September to 20 December). The average of TDMY in the three lactations was 11.43 kg with standard deviation 5.76 kg. Data structure is given in Table 1.

Management

Animals were kept in open yards. Each twenty five cows were joined with a bull for mating. Cows were fed corn silage in summer and alfalfa in winter. Concentrates were provided at a daily rate of 5.5 kg/dry cow, 7.5 kg for freshening non-milked cow and 4 kg for maintenance requirement and 1 kg for each 2 kg milk produced for milking cows. Cows were machine-milked twice a day and the amount of milk was automatically recorded.

Statistical analysis

Model. The model for the three studied lactations in matrix notation was assumed as follows:

$$\mathbf{Y= Xb +Za +Wp + e,} \qquad (1)$$

where,

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[1] some of the animals had unknown sires

Y: the TDMY vector; **b:** the fixed effect of year-season, the fixed regression coefficients of TDMY on DIM and the fixed regression coefficients of TDMY on age vector; **a:** the random regression coefficients vector; **p:** the random permanent environmental effects vector of cows; **X**, **Z**, and **W:** the covariables and incidence matrices; and **e**: the random residual effects vector.

Random effects (a, p and e) are assumed to be normally distributed with mean 0 and variance V as follows

$$\begin{bmatrix} a \\ p \\ e \end{bmatrix} \sim (0, V) \qquad (2)$$

where,

$$V = \text{Var}\begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & I P & J \\ 0 & 0 & R \end{bmatrix} \quad (3)$$

And, $G = \text{Var}(\alpha_{j0} \quad \alpha_{j1} \quad \alpha_{j2})$`, according to Jamrozik *et al.* (1997)

where,

G: the matrix of additive genetic covariance between RR coefficients, assumed to be homogenous for all animals, while the α_{jm}**:** random regression coefficients (m), of TDMY on DIM; **P:** the covariance matrix of the permanent environmental effect; **I:** is the identity matrix; **A:** the matrix of additive genetic numerator relationship between the animals; ⊗ : the Kronecker product function (direct product) (Searle, 1966); and **R:** a diagonal matrix with elements that depend on DIM.

Table 1. Structure of the raw data in the first three lactations

	Lactation		
	First	Second	Third
Number of TD[1] milk records	3875	2993	1605
Number of cows	414	283	188
Number of dams	197	136	89
Number of known sires	66	58	50
Number of year-seasons	24	23	19
Average age of cows at calving, mo	29	42	57
Mean of TDMY[2], kg	10.41	12.41	11.48
Phenotypic range of TDMY, kg	0.2-34	0.2-40	0.2-33
Standard deviation of TDMY, kg	5.1	6	6.2
Coefficient of variation of TDMY %	48.15	48.36	52.31

[1]Test-day (TD), [2]Test-day milk yield (TDMY)

where, R is estimated for each group of DIM, where each lactation is divided into ten periods within each of them the residual variance matrix is constant for all DIM. So that R has 10 different values on the diagonal. Residual variance was assumed to be constant for each subclass (k) within lactation. The covariance between residuals in

TD records on different DIM records was assumed zero in the single trait models for both within and between cows.

Fitting the curve. Orders of Legendere, Ali and Schaeffer function and Incomplete Gamma function were tried to describe the lactation curve. Among these functions the only one that met the conditions of the present data and gave full results was the Incomplete Gamma function (IGF) which was fitted for each lactation for each cow. According to Wood (1967) this function is:

$$Y_t = a_0 t^{a1} \exp^{a2t}, \quad (4)$$

Where,

Y_t: TDMY at time t; exp: refers to the natural exponential function; a_0: the initial MY; a_1: the ascent to peak; a_2: the descent from peak; and a_0, a_1 and a_2 are constants for a given lactation

So, the linear function of the three covariates that describe TDMY at t time is:

$$\ln Y_t = \ln a_0 + a_1 \ln t + a_2 t \quad (5)$$

This submodel, i.e. Wood's function is to illustrate the main features of RR coefficients of TDMY at t time with the three parameters (a_0, a_1 and a_2) to be estimated. Now the submodel can be detailed for fitting the lactation curve as

$\text{Ln } Y_{ijkl} = [\ln \mu_0 + \mu_1 \times (\ln c) + \mu_2 \times (c)] + [\ln a_{0j} + a_{1j} \times (\ln c) + a_{2j} \times (c)]$
$+ [\ln p_{0j} + p_{1j} \times (\ln c) + p_{2j} \times (c)] + [\ln e_{0j} + e_{1j} \times (\ln c) + e_{2j} \times (c)] + \varepsilon_{ijkl}$,

where the first part in this equation represents the fixed regression; the second part represents RR of the animal additive genetic effects; the third part represents RR of the cow permanent environmental effects; the fourth part represents residual regression of a DIM ; and the fifth part represents error term.

Procedure of analysis. DFREML software package (Meyer, 1998a) was used to estimate the components of variance and covariance. Starting value was obtained from the results of Alnajjar (2001).

RESULTS AND DISCUSSION

Additive genetic and permanent environmental (co)variance estimates for coefficients of IGF

Estimates of additive genetic and permanent environmental (co)variances for coefficients a's of IGF in the first three lactations are presented in Table 2. Additive genetic variances for the natural logarithm of the initial milk yield ($\ln a_0$) were 0.0233, 0.3363 and 0.3914 for the three lactations, respectively. Additive genetic variances for the rate of ascent to peak (a_1) of lactation were 0.0136, 0.0518 and 0.2420 for the three lactations, respectively. Additive genetic variances for the rate of descent from peak (a_2) of lactation were 0.0211, 0.00001 and 0.0001 for the three lactations, respectively.

The additive genetic variance for a_0 and a_1 increased with advance in lactation. The additive genetic variance for a_2 decreased sharply from first lactation to second lactation but increased slightly from second lactation to third lactation. In the first lactation, the additive genetic covariance between the coefficients, with the highest magnitude, was that negative between a_0 and a_2, i.e. the higher the initial yield the slower the descent. In the second and third lactations, the additive genetic covariance

between the coefficients with the highest magnitude was that negative between a_0 and a_1, i.e. the higher the initial yield the slower the ascent. Permanent environmental variances for the natural logarithm of the initial milk yield (ln ep_0) were 0.2327, 1.2699 and 1.1622 for the three lactations, respectively. Permanent environmental variances for the rate of ascent to peak (ep_1) of lactation were 0.0813, 0.1502 and 0.4578 for the three lactations, respectively. Permanent environmental variances for the rate of descent from peak (ep_2) of lactation were 0.0229, 0.00003 and 0.0001 for the three lactations, respectively. The permanent environmental variance for ep_0 increased from first lactation to second lactation but decreased from second lactation to third lactation. The permanent environmental variance for ep_1 increased with advance in lactation. The permanent environmental variance for ep_2 decreased from first lactation to second lactation but increased from second lactation to third lactation. The covariance estimates of permanent environmental were very low for the three lactations.

Table 2. Estimates of additive genetic and permanent environmental (co) variances in the first three lactations for coefficients (a's) of IGF, kg

	Additive genetic				Permanent environmental		
	ln a_0[1]	a_1[2]	a_2[3]		ln ep_0[4]	ep_1[5]	ep_2[6]
First lactation							
ln a_0	0.0233			ln ep_0	0.2327		
a_1	0.0074	0.0136		ep_1	0.0133	0.0813	
a_2	-0.0218	-0.0065	0.0211	ep_2	0.0094	0.0166	0.0229
Second lactation							
ln a_0	0.3363			ln ep_0	1.2699		
a_1	-0.1310	0.0518		ep_1	-0.4100	0.1502	
a_2	0.0015	-0.0006	0.00001	ep_2	0.0046	-0.0019	0.00003
Third lactation							
ln a_0	0.3914			ln ep_0	1.1622		
a_1	-0.1268	0.2420		ep_1	-0.5552	0.4578	
a_2	-0.0002	-0.0036	0.0001	ep_2	0.0035	-0.0050	0.0001

[1] ln a_0: natural logarithmic of estimate of additive genetic effect of the initial milk yield
[2] a_1 : estimate of additive genetic effect of the ascent to peak
[3] a_2 : estimate of additive genetic effect of from peak
[4] ln ep_0: natural logarithmic of the permanent environmental effect of the initial milk yields
[5] ep_1 : the permanent environmental effect of the ascent to peak
[6] ep_2: the permanent environmental effect of the descent from peak.

Variances of ln a_0 and ep_0 are lower than those reported by Alnajjar (2001) in the three lactations. Low variance could be due to lesser pedigree information. The much lower additive genetic variances of the lactation curve a_0, a_1 and a_2 relative to their permanent environmental variances indicate that in this set of data the environment plays, by far, the dominant influence on the lactation curve.

Additive genetic and permanent environmental eigenvalues

The three eigenvalues for the additive genetic and permanent environmental covariances for TDMY in the first three lactations are presented in Table 3. The first eigenvalues for the additive genetic effects accounted for 80.99%, 99.83% and 73.22% of the total additive genetic variance in the three lactations, respectively. The first eigenvalues for the permanent environmental effects accounted for 69.58%, 98.87 and 90.58% of the total permanent environmental variance in the three lactations, respectively. The estimates of the first eigenvalue in the three lactations indicated that most genetic variation is expressed in the beginning of lactation. Genetic eigenvalues estimated in this study are small as compared to the environmental indicating that changing the shape of lactation curve is more likely to be through environment than genetics. Pool and Meuwissen (2000) used 4 and 5 eigenvalues for the additive and permanent environmental effects. They noted that eginvalues for permanent environment were lower than those of the additive ones. The first retained three additive genetic eigenvectors (factors) absorbed the genetic variances in the coefficients a's of IGF. Each factor has an egeinvalue that corresponds to the amount of additive genetic variance explained by that factor from the total additive genetic variance, each a combination of the observed test-day milk yields. These three derived traits could be named as the initial milk yield, the rate of ascent to peak and the rate of descent from peak.

Table 3. Eigenvalues for the additive genetic and permanent environmental covariances for TDMY in the three lactations

	Eigenvalues		Proportion of total variance (%)		Cumulative proportion of total variance (%)	
	additive	permanent	additive	permanent	additive	permanent
First lactation						
Factor 1[1]	0.046953	0.234380	80.99046	69.58113	80.99	69.58
Factor 2[1]	0.010678	0.084122	18.41941	24.97368	99.41	94.55
Factor 3[1]	0.000342	0.018342	0.590129	5.445188	100.00	100.00
Second Lactation						
Factor 1	0.387445	1.403990	99.82830	98.865647	99.83	98.86
Factor 2	0.000665	0.016105	0.171293	1.134090	99.99	99.99
Factor 3	0.000002	0.000004	0.000408	0.000263	100.00	100.00
Third lactation						
Factor 1	0.463853	1.467570	73.22117	90.58309	73.22	90.58
Factor 2	0.169620	0.152566	26.77524	9.416859	99.99	99.99
Factor 3	0.000023	0.000001	0.003586	0.000047	100.00	100.00

[1] Factors 1, 2 and 3: highest three roots of the additive matrix whose values > zero

Additive genetic correlations and heritability of TDMYs

Estimates of genetic correlations between TDMYs, ranged from -0.978 to 0.993, -0.730 to 0.992 and -0.086 to 0.991 for the three lactations (Table 4 and Fig. 1, 2 and 3), respectively. In the first and second pariteies, the estimates of genetic correlations were lower than those estimated by Van der Werf *et al.* (1998), Veerkamp and

Thompson (1999) and Alnajjar (2001). Some of these estimates were negative. Liu *et al.* (2000) reported that using the biological lactation curves resulted in negative genetic correlations between the beginning and the end of lactation. Mean of genetic correlations between TDMYs were 0.149, 0.568 and 0.732 for the three lactations, respectively, i.e. increased from one lactation to the next. Alnajjar (2001) showed an opposite trend.

Estimates of heritability of TDMY (Table 4 and Fig. 4) increased from 0.030 for DIM 65 to 0.142 for DIM 185 then, decreased to 0.035 for DIM 275 in the first lactation. Heritability increased from 0.154 for DIM 65 to 0.215 for DIM 155 then decreased to 0.180 for DIM 215 in the second lactation. Heritability decreased from 0.486 for DIM 5 to 0.409 for DIM 125 then increased to 0.696 for DIM 305 in the third lactation. Estimates were generally low for all DIM in the first and second lactations. Low hertability observed here could be due to the relatively low production as Strabel and Misztal (1999) noticed that lower production, as the case in the present study, usually leads to lower heritability estimates. Veerkamp and Goddard (1998) reported heritability average around 0.13 for a herd with an average TDMY around 18 kg which is greater than that obtained in the present study. Low heritability could also be due to the small number of selected sires. The pattern of estimates of heritability agrees with that reported by Jamrozik *et al.* (1998) and Strabel and Misztal (1999) and Rekaya *et al.* (1999), high estimates at the beginning (0.118 and 0.090 at DIM 5 for the first and second lactation, respectively) followed by a decrease in following stage, and rising estimates toward the end of lactation. Generally, heritability estimates increased from the first to the second lactation and considerably increased in the third lactation.

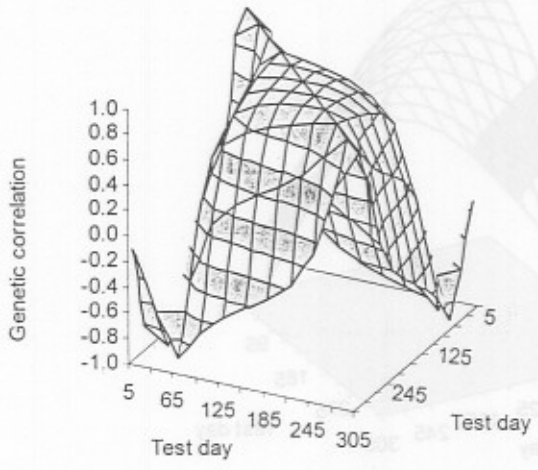

Fig. 1. Genetic correlations between TDMYs in the first lactation

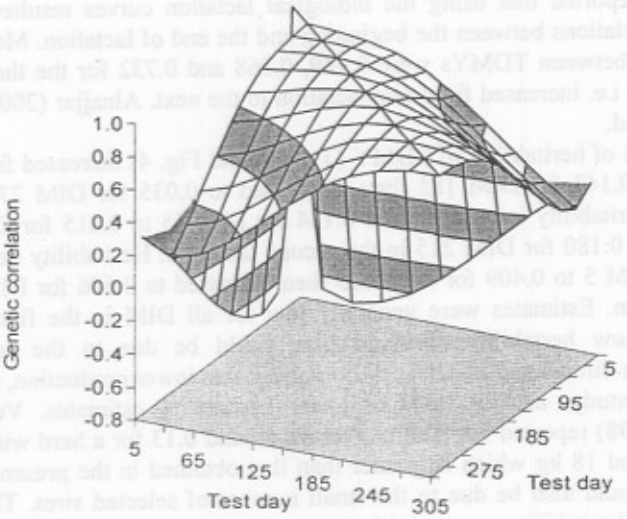

Fig. 2. Genetic correlations between TDMYs in the second lactation.

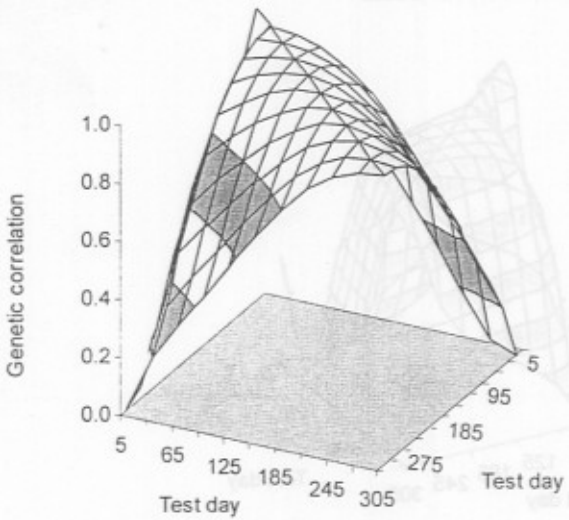

Fig. 3. Genetic correlations between TDMYs in the third lactation.

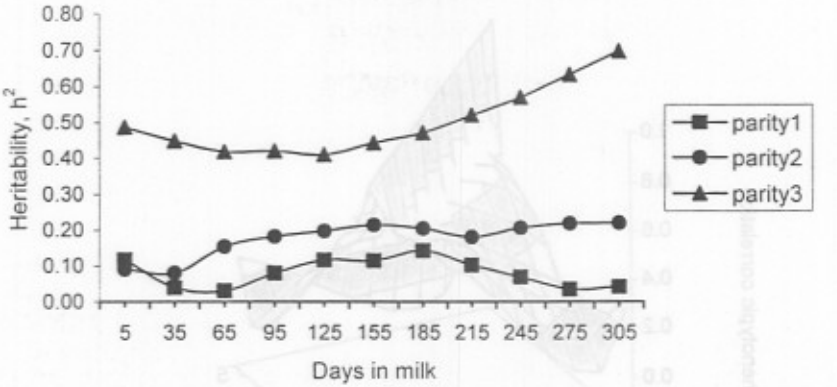

Fig. 4. Estimates of heritability for TDMYs in the first three lactations

Phenotypic correlations between TDMYs

Estimates of the phenotypic correlations ranged from 0.067 to 0.681, -0.110 to 0.788 and -0.112 to 0.958 for the three lactations (Table 4 and Fig. 5, 6 and 7), respectively. Phenotypic correlations between adjacent TDMY were relatively high, ranging from 0.430 to 0.681, 0.081 to 0.788 and 0.737 to 0.957 for the three lactations, respectively, with the exception of DIM 5 with DIM 35 in the second lactation. As the interval between days increased, the estimates of phenotypic correlations generally decreased but with some irregularity involving the estimates of phenotypic correlations for DIM 5 with the others. White *et al.* (1999) showed that phenotypic correlations declined from 0.76 between adjacent lactation stages to 0.4 between initial and day 255 for the first lactation.

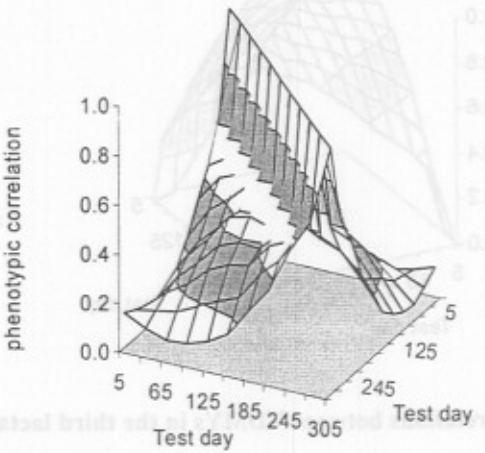

Fig. 5. Phenotypic correlations between TDMYs in the first lactation

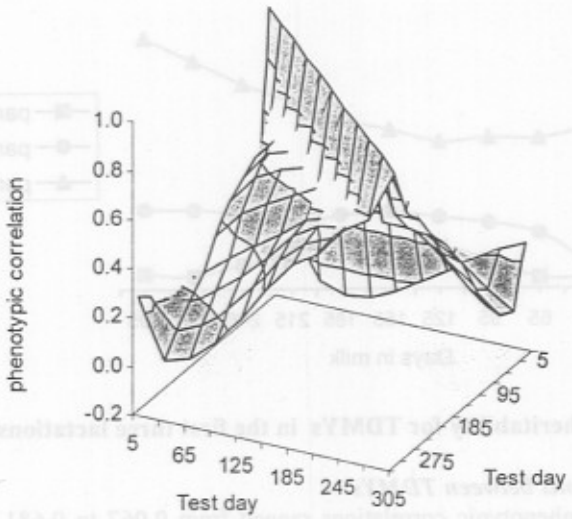

Fig. 6. Phenotypic correlations between TDMYs in the second lactation

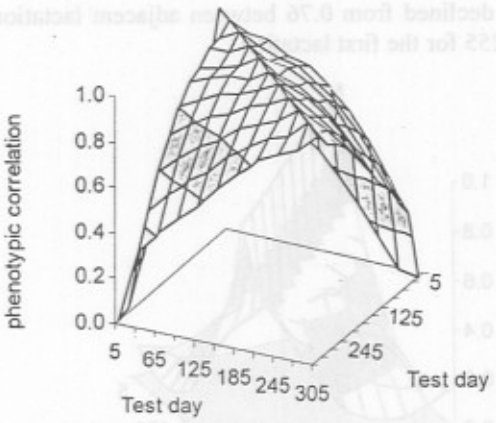

Fig. 7. Phenotypic correlations between TDMYs in the third lactation

Table 4. Estimates of genetic correlations (below the diagonal), heritability (on the diagonal and bold) and phenotypic correlations (above the diagonal) for TDMY in the first three lactations

DIM	5	35	65	95	125	155	185	215	245	275	305
First lactation											
5	**0.118**	0.593	0.44	0.34	0.224	0.138	0.11	0.087	0.096	0.116	0.141
35	0.854	**0.039**	0.492	0.445	0.351	0.261	0.243	0.192	0.167	0.131	0.097
65	-0.073	0.456	**0.030**	0.478	0.417	0.338	0.334	0.269	0.222	0.145	0.067
95	-0.572	-0.062	0.860	**0.080**	0.494	0.421	0.434	0.359	0.299	0.19	0.074
125	-0.732	-0.271	0.733	0.977	**0.117**	0.43	0.458	0.391	0.338	0.227	0.103
155	-0.813	-0.394	0.638	0.942	0.991	**0.115**	0.434	0.386	0.353	0.261	0.15
185	-0.874	-0.498	0.543	0.895	0.969	0.993	**0.142**	0.465	0.455	0.375	0.265
215	-0.933	-0.619	0.411	0.816	0.919	0.963	0.988	**0.102**	0.49	0.451	0.374
245	-0.978	-0.792	0.156	0.631	0.778	0.853	0.909	0.962	**0.069**	0.585	0.548
275	-0.816	-0.947	-0.417	0.078	0.279	0.400	0.505	0.632	0.819	**0.035**	0.681
305	-0.138	-0.606	-0.924	-0.685	-0.529	-0.417	-0.307	-0.157	0.117	0.666	**0.042**
Second lactation											
5	**0.090**	0.081	-0.075	-0.11	-0.094	-0.049	0.017	0.082	0.154	0.216	0.263
35	-0.676	**0.080**	0.557	0.537	0.5	0.45	0.357	0.25	0.177	0.098	0.027
65	-0.730	0.989	**0.154**	0.654	0.624	0.573	0.463	0.332	0.244	0.146	0.055
95	-0.687	0.969	0.992	**0.182**	0.657	0.624	0.528	0.403	0.327	0.235	0.146
125	-0.601	0.927	0.960	0.988	**0.198**	0.659	0.587	0.479	0.426	0.349	0.269
155	-0.476	0.852	0.893	0.943	0.983	**0.215**	0.642	0.559	0.535	0.48	0.414
185	-0.320	0.742	0.789	0.860	0.929	0.981	**0.205**	0.59	0.601	0.575	0.531
215	-0.151	0.603	0.655	0.744	0.839	0.924	0.981	**0.180**	0.618	0.62	0.598
245	0.013	0.454	0.508	0.611	0.727	0.839	0.929	0.983	**0.206**	0.721	0.717
275	0.157	0.312	0.366	0.477	0.609	0.742	0.859	0.942	0.987	**0.218**	0.788
305	0.275	0.186	0.239	0.356	0.497	0.646	0.782	0.889	0.957	0.991	**0.220**
Third lactation											
5	**0.486**	0.737	0.653	0.597	0.523	0.458	0.366	0.26	0.139	0.013	-0.112
35	0.877	**0.448**	0.958	0.948	0.902	0.875	0.806	0.719	0.598	0.463	0.319
65	0.815	0.991	**0.418**	0.957	0.923	0.909	0.854	0.781	0.673	0.55	0.414
95	0.751	0.965	0.991	**0.419**	0.946	0.944	0.901	0.84	0.743	0.63	0.502
125	0.671	0.918	0.963	0.990	**0.409**	0.944	0.915	0.869	0.788	0.689	0.575
155	0.571	0.845	0.908	0.955	0.988	**0.441**	0.954	0.924	0.858	0.773	0.671
185	0.450	0.744	0.825	0.892	0.947	0.986	**0.469**	0.947	0.901	0.836	0.751
215	0.313	0.618	0.715	0.800	0.878	0.942	0.985	**0.518**	0.935	0.893	0.83
245	0.171	0.478	0.588	0.688	0.784	0.872	0.942	0.986	**0.569**	0.922	0.884
275	0.035	0.335	0.454	0.566	0.677	0.784	0.877	0.947	0.988	**0.632**	0.921
305	-0.086	0.201	0.325	0.445	0.568	0.689	0.801	0.893	0.956	0.990	**0.696**

DIM : day in milk; TDMY: test day milk yield

CONCLUSIONS

It was concluded that the IGF was suitable to describe the lactation curve in Holstein cattle under the conditions of this study. Low variance of coefficients of IGF could be due to incomplete pedigree information. The lactation curve of the present animals could be improved by improving management rather than genetics.

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تقدير المعالم الوراثية لإنتاج اللبن في أول ثلاثة مواسم لأبقار الهولشتين باستخدام نموذج الإنحدار العشوائى

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تم جمع البيانات المستخدمة في هذه الدراسة من مزرعة أسيوط الخاصة بمحافظة أسيوط جنوب مصر. تتكون البيانات من8473 سجل اختبار إنتاج لبن يومي للثلاثة مواسم الأولى (3875 و 2993 و 1605 سجلاً على التوالى) لـ 414 بقرة هولستين بنات أكثر من 66 طلوقة و 197 أم خلال الفترة من 1998 إلى 2004. قسمت البيانات تبعاً لشهر الولادة إلى أربعة فصول : شتاء وربيع وصيف وخريف. احتوى النموذج الإحصائي على تأثير سنة الولادة وفصل الولادة والانحدار الخطى والتربيعي للعمر والانحدار الثابت والتأثير العشوائي الوراثي التجمعي والتأثير العشوائي البيني الدائم لكل بقرة . استخدمت دالة جاما غير الكاملة (IGF) لتوصيف منحنى الحليب لكل موسم لكل بقرة . استخدم برنامج DFREML (Meyer,1998 a) لتحليل البيانات وتقدير مكونات التباين والتغاير لإنتاج اللبن يوم الاختبار (TDMY) عن طريق معادلة الإنحدار العشوائي .

تراوحت تقديرات معامل الارتباط الوراثى التجمعى من -0.978 إلى 0.993 و من -0.730 إلى 0.992 و من -0.086 إلى 0.991 للثلاثة مواسم الأولى على التوالى. ارتفعت قيمة المكافئ الوراثى من 0.03 لإختبار اليوم 65 من الحليب إلى 0.14 لليوم 185 ثم انخفضت إلى 0.035 لليوم 275 فى الموسم الأول كما ارتفعت قيمة المكافئ الوراثى من 0.154 لإختبار اليوم 65 من الحليب إلى 0.215 لليوم 155 ثم انخفضت إلى 0.180 لليوم 215 فى الموسم الثانى ، بينما انخفضت قيمة المكافئ الوراثى من 0.486 لليوم الخامس إلى 0.409 لليوم 125 ثم ارتفعت إلى 0.696 لليوم 305 فى الموسم الثالث. أوضحت النتائج أن دالة جاما غير الكاملة (IGF) مناسبة لتوصيف منحنى الحليب لأبقار الهولشتين تحت ظروف الدراسة.