RANDOM REGRESSION TEST DAY MODEL FOR ESTIMATION OF GENETIC PARAMETERS FOR MILK YIELD AND PROTEIN PERCENTAGE OF PRIMIPAROUS FRIESIAN COWS IN EGYPT

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SUMMARY

Both fixed and random linear and quadratic regressions were used to model test day records that are measured over the trajectory from DIM = 5 to 320-d of primiparous Friesian cows. The (co)variance components were estimated with a single trait animal model with REML algorithm for each of daily milk yield and protein percentage using the computer package DF-REML (Version 3β) of Meyer (1998a) for a total of 1226 records. Records were taken from Sakha Animal Production Research Station belonging to Animal Production Research Institute (Sakha, Kafr El-Shaiekh Governorate, Egypt between 1997 and 2000).

Heritabilities for milk yield and protein percentage were higher for early lactation (< 35 DIM) and gradually decreased as DIM advanced. Genetic correlations through DIM were generally high and tended to decrease as the interval throughout the lactation increased for both traits. Permanent environmental and phenotypic correlations had the same trend. Varied heritability estimates for milk yield and protein percentage along with DIM and the wide range of genetic correlation estimates between records could suggest that yield pattern in first lactation Friesian cows are genetically different.

Keywords: random regression, test day model, genetic parameters, primiparous Friesian cows

Abbreviation key: RRM = random regression model, TD = test day, TDM = test day model, DIM = days in milk, DF-REML = derivative-free restricted maximum likelihood, DMY = daily milk yield.

INTRODUCTION

Genetic improvement of milk yield traits has always started from an analysis of standardized 305-d lactation records. These records are generated from a set of TD records taken at approximately monthly intervals throughout the lactation period. TD records are subject to many non-genetic factors (herd, year and season of calving, age or parity number, region, DIM, number of milkings per day, etc). Averaging these TD records on one measure per lactation for each animal make it difficult for an

appropriate modeling of standardized traits. Moreover, incomplete lactations are still needed to be projected correctly.

Ptak and Schaeffer (1993) suggested a repeatability TDM that accounts for the shape of the lactation curve assuming the fixed herd-test date effect. This would permit better removing of more sources of variation through more precise modeling of individual TD yields in comparison with traditional 305-d models, avoid the use of extension factors, offer more flexible system of evaluation and allow an increased number of daughters to be included in sire evaluation since TDM allows a cow to be evaluated based on any number of TD records during a lactation.

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) incorporated random regression coefficients in animal model for genetic evaluations of cows using TD records, which would account for individual differences between cows in lactation curves. RRM has two sets of regressions on function of DIM. The first is fixed and common to all cows of particular fixed effects and the second is random and associated with random animal effects. Meyer (1998b) clarified that a better way of dealing with traits that are measured over a trajectory is to fit a set of random coefficients of time for each individual to allow for individual variation in the course of the trajectory. 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 possible. In short, 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.

The objective of this study was to estimate (co)variance structure of the additive genetic and permanent environmental effects for daily milk yield and protein percentage taken at approximately monthly intervals throughout the lactation period of primiparous Friesian cows with the RRM.

MATERIAL AND METHODS

Animals and management:
Data were provided by Sakha Animal Production Research Station, Kafr El-Shaikh Governorate, located North of the Nile Delta and belonging to Animal Production Research Institute (APRI), Ministry of Agriculture and Land Reclamation, Egypt. Animals were housed in semi-roofed yards. Feeding allowances were calculated according to NRC (1981). Roughage (Berseem hay and bean straw) to concentrate ratio was 40:60. The ration was offered twice daily at 8 a.m. and 3 p.m. and clean water was available all times. Cows were inseminated artificially with frozen semen of selected sires according to the breeding plan designed by the Cattle Breeding Research Department, APRI. Heifers were first conceived at the

approximate age of 16 months. Heifers with chronic reproductive disorders are annually discarded from the herd. Cows were machine-milked twice a day and milking interval was almost 12-h.

Data:

A total of 1226 TD milk yield and protein percentage records were collected at monthly intervals over the period from January 1997 to October 2000 from 75 Friesian cows sired by 13 sires. Only TD records from first lactation between 5 and 320 DIM were included in the statistical analysis. Records after the 10th TD record were discarded. Average TD records per animal in data file was 8.2. Protein percentage was measured alternatively following an a.m.-p.m. recording scheme by automated method of infrared absorption spectrophotometry (Milk-o-Scan; Foss Electric, Hillerød, Denmark) at the Dairy Services Unit, which belongs to the Animal Production Research Institute, Sakha, Kafr El-Shaiekh Governorate, Egypt.

Statistical Model:

Data were analyzed by REML with a derivative-free algorithm using the computer package (DF-REML, Version 3β) developed by Meyer (1998a) with the following animal model:

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

Where:

Y_{ijkl} = record l on DMY or protein percentage made on DIM of the first lactation in TD subclass i for the jth 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 320-d,

TD_i = fixed effect of test date i (34 levels between January 1997 and October 2000),

P_j = random effect of permanent environment associated with all TD yields of the jth cow.

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

β_{km} and a_{jm} = fixed and random regression coefficients, respectively, of TD milk yield or protein percentage on DIM where m = the number of covariates describing the lactation curve with 4 covariates appeared as: $X_1 = DIM/c$, $X_2 = (DIM/c)^2$, $X_3 =$ ln (c/DIM) and $X_4 = (ln(c/DIM))^2$ where DIM is days in milk and c is a constant set to 305. These coefficients were used to fit the covariance structure for additive genetic and permanent environmental effects.

The previous model is similar to models frequently found in the literature (Ali and Schaeffer, 1987; Ptak and Schaeffer, 1993; Schaeffer and Dekkers, 1994; Swalve 1994, 1995; Jamrozik and Schaeffer, 1997; Jamrozik *et al.*, 1997b; Kettunen *et al.*, 1998; Ptak and Zarnecki, 1998) for Friesian and other dairy breeds with high values for R square reaching 0.975 and small means of absolute errors reaching 0.878. More on goodness of fit was investigated and discussed by Jamrozik *et al.*, 1997a and Strabel *et al.* (2003). All known relationships among individuals were considered in the animal model.

RESULTS AND DISCUSSION

Phenotypic average of daily milk yield and protein percentage (±SD) was 11.73 (3.85) and 2.70 (0.45), respectively. Table 1 presents estimates for heritabilities (h^2) and proportion of permanent environmental effect (c^2) for DMY and protein percentage for selected DIM of primiparous Friesian cows. Heritability estimates ranged from 0.10 to 0.52 for DMY and from 0.01 to 0.31 for protein percentage being highest for early lactation (DIM=5), then gradually decreased up to (DIM=125) and increased therafter to the end of lactation. Jamrozik and Schaeffer (1997) and Negussie *et al.* (2002) obtained similar results. Differences in heritability estimates along with DIM may suggest that parts of the lactation curve are genetically different. However, Kettunen *et al.* (1998) noted that the mathematical characteristics of random regression sub-models could result in an over projection of genetic variances in the edges of defined lactation trajectory.

Table 1. Estimates for heritabilities (h^2) and proportion of permanent environmental effect (c^2) for daily milk yield (DMY) and protein percentage (Protein %) for selected DIM of primiparous Friesian cows maintained in Egypt

DIM	DMY		Protein %	
	h^2	c^2	h^2	c^2
5	0.52	0.09	0.31	0.14
35	0.42	0.01	0.12	0.18
65	0.29	0.01	0.03	0.22
95	0.16	0.03	0.01	0.21
125	0.10	0.06	0.01	0.16
155	0.11	0.07	0.01	0.10
185	0.16	0.06	0.02	0.05
215	0.19	0.05	0.02	0.02
245	0.19	0.04	0.02	0.01
275	0.13	0.04	0.04	0.01
305	0.13	0.05	0.07	0.01

The overall mean of heritability was 0.25 and 0.06 for DMY and protein percentage, respectively. Estimates, in general, are comparable with estimates reported in the literature (Jamrozik and Schaeffer, 1997).

Estimates of proportion of permanent environmental effect (c^2) were low for both traits along with DIM and tended to decrease as DIM advanced averaging 0.05 and 0.10 for DMY and protein percentage, respectively. Misztal *et al.* (2000) and Alnajjar (2001) found high values of (c^2) at end of lactation.

Tables 2 and 3 present estimates of genetic (above diagonal) and permanent environmental (below diagonal) correlations at selected DIM for DMY and protein percentage for first lactation of Friesian cows. Genetic correlations among DMY records were all positive and tended to be high between adjacent DIM and gradually decreased as intervals between records increased up to DIM = 215 and increased thereafter to the end of lactation period. A similar trend was noticed for protein percentage; however, some negative correlations were found between records through the lactation period (Table 3). Kettunen *et al.* (1998) noted that the mathematical characteristics of random regression sub-models could result in an over projection of genetic variances in the edges of defined lactation trajectory.

Table 2. Estimates of genetic (above diagonal) and permanent environmental (below diagonal) correlations at selected DIM for daily milk yield in primiparous Friesian cows maintained in Egypt

DIM	5	35	65	95	125	155	185	215	245	275	305
5		0.9936	0.9914	0.9992	0.8995	0.5869	0.3684	0.3154	0.3990	0.6883	0.9965
35	0.9983		0.9998	0.9903	0.8453	0.4925	0.2618	0.2068	0.2935	0.5968	0.9984
65	-0.9855	-0.9737		0.9879	0.8438	0.4778	0.2454	0.1901	0.2770	0.5827	0.9978
95	-0.9989	-0.9943	0.9968		0.9349	0.6079	0.3923	0.3394	0.4219	0.7008	0.9929
125	-0.9998	-0.9968	0.9887	0.9996		0.7784	0.7366	0.6969	0.7578	0.9316	0.8624
155	-0.9999	-0.9980	0.9861	0.9990	0.9999		0.9718	0.9568	0.9903	0.9894	0.5121
185	-0.9999	-0.9985	0.9845	0.9985	0.9996	0.9999		0.9986	0.9991	0.9283	0.2922
215	-0.9997	-0.9981	0.9849	0.9982	0.9994	0.9998	0.9999		0.9960	0.9083	0.2429
245	-0.9990	-0.9957	0.9942	0.9993	0.9994	0.9993	0.9992	0.9997		0.9440	0.3342
275	-0.9944	-0.9873	0.9955	0.9977	0.9963	0.9951	0.9945	0.9957	0.9985		0.6416
305	-0.9820	-0.9699	0.9979	0.9895	0.9857	0.9831	0.9818	0.9830	0.9883	0.9964	

Table 3. Estimates of genetic (above diagonal) and permanent environmental (below diagonal) correlations at selected DIM of protein percentage of primiparous Friesian cows maintained in Egypt

DIM	5	35	65	95	125	155	185	215	245	275	305
5		0.9990	0.9858	0.5842	-0.8066	-0.9006	-0.8954	-0.8360	-0.7150	-0.6016	-0.5671
35	0.8677		0.9923	0.6192	-0.7802	-0.8808	-0.8748	-0.8119	-0.6879	-0.5745	-0.5420
65	0.7013	0.9625		0.7113	-0.6973	-0.8158	-0.8096	-0.7410	-0.6146	-0.5062	-0.4812
95	0.5969	0.9145	0.9895		0.0077	-0.1715	-0.1735	0.0379	-0.0159	0.0194	-0.0106
125	0.5401	0.8795	0.9726	0.9938		0.9825	0.9757	0.9502	0.8601	0.7421	0.6757
155	0.5175	0.8550	0.9528	0.9822	0.9949		0.9963	0.9646	0.8678	0.7508	0.6932
185	0.5286	0.8369	0.9248	0.9546	0.9739	0.9915		0.9838	0.9075	0.8056	0.7540
215	0.5983	0.8426	0.8979	0.9154	0.9337	0.9599	0.9869		0.9699	0.9012	0.8605
245	0.7763	0.9497	0.9411	0.9097	0.8850	0.8671	0.8554	0.8719		0.9808	0.9584
275	0.3327	0.5020	0.5127	0.4726	0.4082	0.3165	0.2046	0.1333	0.5717		0.9954
305	0.1615	0.4016	0.4609	0.4458	0.3924	0.3007	0.1767	0.0739	0.4610	0.9778	

Table 4. Estimates of phenotypic correlations for selected DIM of daily milk yield (above diagonal) and protein percentage (below diagonal) of primiparous Friesian cows maintained in Egypt

DIM	5	35	65	95	125	155	185	215	245	275	305
5		0.4994	0.3665	0.2354	0.1297	0.0614	0.0312	0.0336	0.0634	0.1186	0.1886
35	0.3335		0.3432	0.2385	0.1445	0.0706	0.0392	0.0337	0.0592	0.1183	0.2058
65	0.2112	0.2462		0.2229	0.1548	0.0999	0.0666	0.0577	0.0758	0.1253	0.2029
95	0.1156	0.1858	0.2137		0.1604	0.1298	0.1087	0.1014	0.1109	0.1398	0.1829
125	0.0493	0.1308	0.1738	0.1826		0.1591	0.1555	0.1535	0.1547	0.1580	0.1530
155	0.0063	0.0823	0.1312	0.1434	0.1334		0.1968	0.2016	0.1965	0.1751	0.1213
185	-0.0190	0.0412	0.0804	0.0974	0.0979	0.0860		0.2333	0.2247	0.1868	0.0985
215	-0.0326	0.0096	0.0396	0.0552	0.0595	0.0556	0.0464		0.2368	0.1924	0.0896
245	-0.0409	-0.0095	0.0143	0.0279	0.0334	0.0335	0.0305	0.0275		0.1904	0.1025
275	-0.0511	-0.0139	0.0127	0.0264	0.0305	0.0290	0.0259	0.0260	0.0342		0.1405
305	-0.0682	-0.0028	0.0399	0.0579	0.0583	0.0485	0.0373	0.0339	0.0483	0.0889	

For both traits, permanent environmental correlations were high and positive between records unless correlations between each of DIM = 5 and DIM = 35 with the rest of records which were high and negative. The trend of both types of correlations is in agreement with results in the literature (Negussie *et al.*, 2002).

Single trait model applied in this study could allow for a detailed work describing genetic and environmental relationship between different traits in the same parity or across parities. Further work in the future should consider a multiple-trait animal model for TD milk yield traits. TD model from later lactations can also be added to multiple trait model as separate trait.

Table 4 presents estimates of phenotypic correlations for selected DIM of DMY (above diagonal) and protein percentage (below diagonal) for first lactation of Friesian cows. Most of the values were positive and tended to be high between adjacent records and decreased when the interval between records increased, following the same pattern of genetic correlations.

CONCLUSION

Different heritability estimates for daily milk yield (from 0.10 to 0.52) and protein percentage (from 0.01 to 0.31) along with DIM and the wide range of genetic correlation estimates between records (from 0.19 to 0.99 for milk) and (from 0.90 to 0.99 for protein) could suggest that yield pattern in first lactation Friesian cows are genetically different. This study was focused only on single-trait analysis for each of DMY and protein percentage, however, further work should consider a multiple-trait model for TD milk yield traits. TD records from later lactations can also be added to multiple-trait model as separate traits.

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إستخدام نمـوذج يوم الاختبار من خلال الانحدار العشوائي في تقدير المقاييس الوراثية لانتاج اللبن و نسبة البروتين للموسم الأول لأبقار الفريزيان فى مصر

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استخدم الانحدار الثابت و العشوائي الخطى و التربيعي في تحليل بيانات يوم الاختبار خلال منحنى الحليب (من اليوم الخامس و حتى اليوم رقم ٣٢٠) لبيانات الموسم الأول لأبقار الفريزيان فى محطة سخا بوزارة الزراعة فى مصر فى السنوات ١٩٩٧-٢٠٠٠. قدرت مكونات التباين و التباين المشترك باستخدام نمـوذج حـيوان لصـفة منفردة باستخدام طريقة (REML) لعدد ١٢٢٦ سجل لانتاج اللبن اليومي و نسبة البروتين باستخدام برنامج ((DF-REML, Version 3β of Meyer (1998a).

ارتفعـت تقديـرات العمق الوراثي لصفتى انتاج اللبن و نسبة البروتين في المرحلة المبكرة من موسم الحليـب (أقـل مـن ٣٥ يوم) و انخفضت تدريجياً بتقدم موسم الحليب. ارتفعت تقديرات معاملات الارتباط الوراثيـة لكلتا الصفتين للسجلات المتقاربة زمنياً و اتجهت للانخفاض مع زيادة الفترة بين السجلات خلال موسم الحليب. و كـان لكل من معاملات الارتباط المظهرية و البيئية الدائمة نفس الاتجاه. قد تشير القيم المتفاوتة لكل من العمق الوراثي لانتاج اللبن و نسبة البروتين و كذلك المدى الواسع للارتباطات الوراثية بين السجلات لكلتا الصفتين إلى الاختلاف الوراثي لنمط إنتاجهما للفريزيان في الموسم الأول.