GENETIC EVALUATION OF MILK YIELD IN HOLSTEIN-FRIESIAN RAISED IN EGYPT USING SINGLE- AND MULTI-TRAIT ANIMAL MODELS

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ABSTRACT

Single-trait (SAM) and multi-trait (MAM) animal model were compared using the data of 90-day (M90) and 305-days (M305) milk yield of 985 of Holstein-Friesian cows daughters of 104 sires and 985 dams in Egypt. Data included 985 first lactation records. Total number was 5642 for all lactations. Animal model in both single- and multi-trait contained season, year of calving, classes of age at calving and days open as fixed effects and animal and residual as random effects.

The variablity in predicted breeding value, PBV (i.e., range from maximum – minmum) was large for MAM in first lactation, however, the reverse trend was found in all lactations (i.e., ranges of PBV in SAM was larger than the estimates from MAM). Using MAM decreased the standard error of prediction (SEP) and consequently the accuracy (r_{TI}) increased . Closeness between r_{PM} and r_S of both SAM and MAM prove that any model may be effective in the evaluation of sires, dams and cows.

Using records of all lactation reduced SEP in both SAM and MAM procedures than those of first lactation only. Incrasing accuracy with all lactations was markedly pronounced when compared with the first lactation. Increasing information from all lactations has a direct effect toward increasing the accuracy (r_{TI}) of the all lactaion than using only first lactation. Disclosness between correlations (r_{PM} & r_S) of PBV and ranks in first and all lactations, indicate that the sires, dams and cows were reranked when using first lactation and all lactation records.

Part-lactation yields (M90) in both first and all lactation records proved to be a good parameter in estimating sire genetic values without complications and would also afford an opportunity for a faster return for sires. Reduction in sires, dams and cows SEP by using M90 compared with M305 using either SAM or MAM provided a considerable potential for rapid genetic progress through sire selection, (i.e. there is a considerable potiential for improving milk production through selection of bull or bull-dam's of Holstein population).

Keywords: Holstein cattle, milk yield, breeding values, animal models, accuracy.

INTRODUCTION

Simultanous sire and cow evaluation would reduce the number of assumptions that have been needed and increases the accuracy of evaluation for sires and cows (Westell and Van Vleck, 1987). Animal model is currently considered the best statistical mehtod to predict animal's breeding value (PBV); all available information from relatives is ustilized and the fixed effects are estimated simultaneously with BVs. The animal model allows comparison of the bulls, dams and cows based on BVs and comparison of

cows across herds. This is important in choosing bull dams and in estimating breeding values of young bulls entering progeny testing.

The accuracy (r_{TI}) of the genetic evaluation is defined as the correlation between true and the estimated breeding value (PBV). Van Vleck *et al.* (1989) found that genetic progress is proportional to the correlation between actual and predicted genetic value. The ratio of the actual to the theoretically approximated multiple correlation coefficient (r_{TI}) might be an appropriate measure of efficiency of the evaluation procedures.

Genetic improvement of dairy animals is based on 305-day lactations, and changing to a system of genetic evaluations using only test day yields or part-lactation yields may be resisted (Ptak and Schaeffer, 1993). Early selection of sires based on part-lactation yields helps in reducing the generation interval which consequently would increase the genetic gain for milk yield in dairy cattle. In most cattle breeding schemes sires are selected on the basis of breeding values estimated from complete-lactation yields of their daughters. However, the part-lactation yields have been reported to be highly correlated with the complete-lactation yields (Kumar *et al.*, 1992 and Zahed *et al.*, 1997).

The objectives of the present study were: (1) to compare breeding values (PBV) for sires, dams and cows predicted by single-trait animal model with those predicted by multi-trait animal model for initial milk yield (90-day milk yield, M90) and 305-day milk yield (M305) in the first and all lactations of Holstein-Friesian cattle raised in a commercial farm in Egypt, (2) to demonstrate the closeness between the two models of evaluation, (3) to compare breeding values predicted from records of the first lactation with those predicted from records of all lactations using product-moment and rank correlations, and (4) to compare genetic evaluation using part- vs completed lactation records as a guide for early selection.

MATERIALS AND METHODS

Animals

Holstein-Friesian cows and bulls of the present study were imported from USA to Egypt since 1982 and raised in El-Salhia commercial herd, Ismailia Governorate (East south of Nile Delta). The data covered nine consecutive years (1983-1991). All the imported females were imported as pregnant heifers. A total of 5642 complete lactation records for 985 cows produced from 104 bulls and 985 dams were used. Lactation records were grouped into age subclasses of 3-month intervals.

Management and feeding

Heifers and cows were inseminated artificially using frozen semen imported from USA. Heifers were bred when reached 16-18 months of age (about 350-375 kg) and cows were served during the first heat period following the 45th day post-partum. Pregnancy was diagnosed by rectal palpation 60 days after the last service. Calves were given colostrum four days after birth and housed in calf-boxes where they were bucket fed on milk

and/or milk replacer until weaning at 90 kg weight for male calves and 100 kg weight for females. After weaning and up to six months of age, calves of the same age were housed in group pens provided with yards for exercise. At six-month of age, male calves were separated from females and housed in open sheds up to their sexual maturity.

Cows were machine milked twice daily. Cows were usually milked until two months before the expected calving date. Then if they did not go dry, they were dried off gradually by milking them once a day until complete drying off. Cows were kept under similar systems of feeding and management. All year round, all cows were supplied with concentrates and corn silage. During winter and spring months (from December to May), animals were supplied with Egyptian clover (*Trifolium alexandrium*), while during summer and autumn months (from June to the end of November), beets, maize and green Sorghum (*Sorghum Vulgar*) were available. Also, rice straw was available all the year round. Concentrate feed was supplied to cows according to their live weight, production and pregnancy status. Free clean water and minerals mixture were available all the time.

Models of analysis

Productive traits studied were 90-day milk yield (M90) and 305-day milk yield (M305). Data were used to estimate variance components by using LSMLMW (Harvey, 1990). Heritabilities from sire (h^2_s) were estimated (Table 1) by a linear mixed model including the effects of year of calving, season of calving, age of cow at calving (classes of three-month intervals) and days open (60 days for 1st class and increased by 30 days for successive classes) as fixed effects and sire and error as random effects.

Table (1): Etimates of means, standard deviation (SD), additive genetic (σ^2_a), and error variance (σ^2_e) estimated from mixed model for 90-day (M90) and 305-day (M305) milk yield of first and all lactations in Holstein-Friesian cattle.

Trait	Mean	SD	σ^2_a	σ^2_e	h^2
First lactation					
M90	1615.4	420.9	11788	112233	0.10+0.7
M305	4099.4	1073.8	69592	725787	0.09+0.7
All lactation					
M90	2055.6	554.3	40900	175116	0.19+0.4
M305	5159.5	1412.7	255960	1128131	0.18+0.4

Sires, dams and cows were genetically evaluated using Animal model (Boldman *et al.*, 1995). Heritabilities obtained by the sire model (Table 1) were used in calculating the guessed values for the estimation of variance components (i.e. σ^2_a and σ^2_e) by the animal model. The breeding values of cows with own records and their parents without records (sires and dams) were predicted. The evaluated animals in the first and all lactations were 985 cows, fathered by 104 sires and mothered by 985 dams. The animal models (in matrix notation) used were:

$$y= Xb + Za + e$$

Where: y was the observation vector; b was the vector of fixed effects, a was the vector of random animal effect (direct additve effect); and e was the vector of random residual effects. The X and Z matrices consisted of ones and zeros, relating to fixed and random effects, respectively. Variance-covariance matrix of random effects was as follows:

$$Var \begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} A\sigma^2_a & 0 \\ 0 & I_n\sigma^2_e \end{bmatrix}$$

Where: A= the numerator relationship matrix and I_n = the identity matrix with order of number of records. The mixed model equations were written as follows:

$$\begin{bmatrix} X'X & X'Z_a \\ Z'_aX & Z'Z_a+\lambda A^{-1} \end{bmatrix} \begin{bmatrix} \beta \\ a \end{bmatrix} = \begin{bmatrix} X'y \\ Z'_a y \end{bmatrix}$$

Where $\lambda = \sigma^2_e/\sigma^2_a$, σ^2_a = the additive variance of the animal and σ^2_e = the variance of the residual effects and A^{-1}= the inverse of numerator-relationship matrix of animal accounted for additive genetic relationships between them. Expectations of variances were $E(\sigma^2_a)$ = σ^2_G, and $E(\sigma^2_e)$= σ^2_ϵ, where σ^2_G is the genetic variance and σ^2_ϵ is the variance of environmental effect on milk yield traits.

Standard error of prediction (SEP) and accuracy estimates (r_{TI}) obtained by single-trait (SAM) and multi-trait (MAM) animal model were the criteria by which the models were compared to determine which were optimal, SEP or Var (u – u) accuracy because the "best" evaluation method has been defined as the one which in the class of linear unbiased predictors has minimum SEP (Henderson, 1975) and accuracy (r_{TI}) because it is defined as the correlation between estimated and true breeding values.

The product-moment correlation (r_{PM}) among PBV as well as Spearman rank correlation (r_S) among ranks of PBV in the two methods and the two data sets of lactations were calculated (SAS, 1989).

RESULTS AND DISSCUSSION

Predicted Breeding Values (PBV)

Estimates of predicted breeding values (PBV) for sires without records were obtained by single- (SAM) and multi-trait (MAM) animal model (Table 2). The etimates for M90 in the first lactation ranged from –23 to 13 kg and from –164 to 129 kg for SAM and MAM, respectively. The respective estimates for M305 in the first lactation ranged from –75 to 52 kg and – 417

876

to 328 kg (Table 2). The PBV estimates for all lactation ranged from – 458 to 378 kg vs –338 to 300 kg for M90 using SAM and MAM, repectively. The estimates for M305 were – 1151 to 930 kg vs – 852 to 743 kg in the same sequence (Table 2). It is clear from these estimates that the variablity in PBV (i.e. range from maximum – minmum) was large   for MAM in the first lactation, however, the reverse trend was found in all lactations, i.e. ranges of PBV in SAM was larger than the estimates from MAM. This was also true for PBV of dams and cows (Table 2).

Table (2): Minimum and maximum predicted breeding values (PBV) for sire, dam, and cow, standard error of prediction (SEP) and accuracy of prediction (r_{TI}) estimated by single and multi-trait animal models for milk yield traits of Holstein Friesian cattle.

Evaluation and Trait[*]	Single-trait animal model (SAM)						Multi-trait animal model (MAM)					
	Minimum[++]			Maximum			Minimum			Maximum		
	PBV	SEP	r_{TI}	PBV	SEP	r_{TI}	PBV	SEP	r_{TI}	PBV	SEP	r_{TI}
Sires without records												
M190	-23	110	0.10	13	248	0.41	-164	67	0.36	129	174	0.82
M1305	-75	281	0.12	52	626	0.39	-417	169	0.34	328	497	0.80
MA90	- 458	87	0.62	378	195	0.70	-338	34	0.42	300	36	0.94
MA305	-1151	220	0.59	930	497	0.65	-852	97	0.38	743	438	0.90
Dams without records												
M190	-5	271	0.04	9	290	0.09	-97	180	0.25	36	193	0.28
M1305	-19	732	0.01	26	863	0.06	-247	454	0.21	106	486	0.24
MA90	- 468	200	0.70	456	204	0.73	-263	30	0.83	283	135	0.88
MA305	-1207	509	0.68	1125	520	0.71	- 663	99	0.82	708	345	0.86
Cows with records												
M190	-18	173	0.15	17	187	0.32	-192	103	0.47	255	185	0.56
M1305	-60	441	0.13	51	475	0.26	- 489	263	0.44	649	496	0.55
MA90	-725	111	0.72	714	164	0.78	- 467	35	0.82	496	36	0.85
MA305	-1841	279	0.70	1791	412	0.75	-1172	103	0.80	1249	105	0.83

[*] M190= 90-day milk yield in first lactation, M1305= 305-day milk yield in first lactation , MA90= 90-day milk yield in all lactations, and MA305 = 305-day milk yield in all lactations.

The sire breeding values predicted from first lactation were smaller than those predicted from all lactations (Table 2). This was true for both M90 and M305. The same observation was notified for both dam PBV and cow PBV. On the contarary, Szkotnicki et al. (1978) found that cows breeding values (PBV) calculated from first lactation were greater than that calculated from all lactations. Also, Hintz et al. (1978) reported that the difference in Brown Swiss cow transimitting ability for milk yield was larger (245 kg.) when first lactation was only used than those for all lactations (116 kg).

The range in sire PBV was greater for complete lactation (M305) than for partial lactation (M90) in both first and all lactations (Table 2). It ranged from 36 to 836 kg for M90 in SAM model compared with 127 to 2081 kg for M305 in the same model. The corresponding estimates for MAM model were 293 to 638 kg for M90 compared with 745 to 1595 kg for M305 (Table 2). The same trend was observed for range of PBV for dams and cows. Variability in sire transmiting ability was larger (2371 kg) for M305 than the corresponding estimate (442) for 100-day milk yield (Khalil et al., 1995 and Zahed et al., 1998)

Standard Errors of Predictors (SEP)

Standard error of predictor (SEP) is more indicative of accuracy or reliability of sire evaluation (Ufford *et al.*, 1979). The SEP estimates of first lactation ranged from 110 to 248 kg and from 67 to 174 kg for M90 applying SAM and MAM; from 281 to 626 kg and from 169 to 497 kg for M305 with the same sequence (Table 2). Also, the SEP of all lactation ranged from 87 to 195 kg and from 34 to 36 kg for M90 and from 220 to 497 kg and from 97 to 438 kg for M305 using SAM and MAM, respectively (Table 2). It was clear that using MAM decreased the SEP and consequently the accuracy increased than when SAM was used. The same trend was observed for SEP of dams and cows. Pollak *et al.* (1984), in a simulation study, concluded that applying multi-trait methodology increased the accuracy of prediction for the trait and in some cases eliminated bias due to selection.

When using either SAM or MAM, estimates of SEP for sires were reduced when using all lactations compared with those of the first lactation only, consequently, the accuracy was increased in sires, dams and cows evaluation (Table 2). Records from later lactations provided more complete information on lifetime performance than those from the first lacation (Wiggans *et al.*, 1988). Aboubakar *et al.*, (1986) reported that first lactation records were evidenced to be a key factor in estimating sire genetic values without many complications and also would afford an opportunity for a faster return for sires. Nath and Sharma (1998) found that standard error and standard deviation of the breeding values predicted for buffalo cows were larger (5.3 and 64.8 kg) when using the first and second lactations than those when using only the first lactation (4.2 and 51.7 kg). The same author concluded that in spite of low accuracy for breeding value predicted from first lactation, this method had low standard error as well as the rank correlation of it with predicted breeding value using the first and second lactations. The first method (using only first lactation) is, moreover, advantageous in comparison with the second method (using the first and second lactations) as it can be used for ranking animals after the completion of their first lactation 305-day milk yield. Thus, the first lactation in cow evaluation could reduce the generation interval which in turn could result in higher genetic gain.

Comparing estimates of SEP when using part-lactation (M90) vs complete lactation (M305) in sire evaluation within each mehtod of evaluation, we found that SEP estimates were lower when using M90 than those when using M305 in both SAM and MAM (Table 2). The estimates of SEP when using SAM ranged from 87 to 248 kg vs 220 to 626 kg in both first and all lactations. The estimates of SEP when using MAM ranged from 34 to 174 kg vs 97 to 497 kg in the same sequence (Table 2). The same trend was observed in dams and cows SEP (Table 2). Part-lactation yields (M90) were evidenced to be a good measure in estimating sire genetic values without many complications and also would afford an opportunity for a faster return for sires. Reduction in sires, dams and cows SEP found in the present study from using M90 compared with M305 using either SAM or MAM provided a considerable potential for rapid genetic progress through sire selection (i.e. there is a considerable potiential for improvement of milk production through selection of bull or bull-dam's within the Holstein population).

Accuracy (r_{TI})

The accuracy (r_{TI}) of genetic evaluation is defined as the correlation between the true and estimated breeding value, however, the squared term of the correlation, called repeatabiltiy or reliability (r^2) (Uimari and Mantysaari, 1993). Incrasing accuray was pronounced when MAM was used compared with SAM. Estimates of r_{TI} for sires ranged from 0.10 to 0.70 for M90 and 0.12 to 0.65 for M305 in the first lactation using SAM compared with 0.36 to 0.94 and 0.34 to 0.90 when using MAM (Table 2). The same trend was observed for dams and cows r_{TI} estimates of the first and all lactations (Table 2). Sorensen (1988) reported that the accuracy (correlations between true and predicted breeding values) was the highest when using reduced animal model, while the lowest correlation was recoded when using selection index (0.773 vs 0.745). Mrode (1996) reported that the main advantage of multi-variate BLUP is that it increases the accuracy of evaluation.

The accuracies (r_{TI}) recorded by SAM procedure for breeding values were relatively low and ranged from 0.10 to 0.41 for first lactation compared with 0.59 to 0.70 for all lactations, while the respective accuracies recorded by MAM ranged from 0.34 to 0.82 for first lactation vs 0.38 to 0.94 for all lactations (Table 2). Records additional to the first lacatation would be expected to contribute significanly in more accuracy, but computing costs may also be increased significantly (Ufford et al., 1979). Nath and Sharma (1998) found that accuracies of breeding values for buffalo cows estimated from records of the first lactation only were lower than those estimated from the first and second lactations (0.559 vs 0.760).

Accuracy estimates for M90 and M305 in first lactation were nearly the same and ranged form 0.10 to 0.41 and from 0.12 to 0.39 using SAM (Table 2). The same closeness between accuracy estimates of M90 and M305 was observed in all lactationa (0.62 to 0.70 for M90 and 0.59 to 0.65 for M305). The same trend was found in MAM model (Table 2). Also, closeness of dams and cows accuracy estimates were observed (Table 2).

The findings of the present study (smaller SEP of M90 and closeness between r_{TI} estimates of M90 and M305), considerd M90 yields to be more effective than M305 as a criterion for early selection of both bull, bull-dam's and cows.

Product moment (r_{PM}) and Spearman rank correlation (r_S)

The correlations among predicted breeding value were calculated by using prodcut moment (Pearson) correlation (r_{PM}), while the correlation among ranks of these estimates were calculated by Spearman (r_S) rank correlation (Tables 3&4&5).

The correlations among PBV for sires of the same trait estimatd by two animal models of evaluation (SAM & MAM) were large and close to unity being 0.952 and 0.951 for M90, M305 in the first lactation and 0.985 and 0.984 for M90 and M305 in all lactations (Table 3). The same trend was found among PBV for dams (0.990, 0.991, 0.993, 0.990) and PBV for cows (0.920, 0.919, 0.986, 0.980). The rank correlation between ranks of sire PBV for the same trait in the two models of evaluation was large and close to unity (Table 3). The range in rank correlations among ranks of PBV were very

Table (6). Percentage of sires in common between different methods of evaluation in top ten sires list.

Trait*	Single-trait (SAM)				Multi-trait (MAM)			
	First lactation		All lactation		First lactation		All lactation	
	M190	M1305	MA90	MA305	M190	M1305	MA90	MA305
Single-trait model								
M190		90	20	10	90	90	10	10
M1305			10	10	90	90	0	0
MA90				100	10	10	90	90
MA305					10	10	90	90
Multi-trait model								
M190						100	0	0
M1305							0	0
MA90								100
MA305								

* The abbreviations as described before.

Percent of sires in common between first and all lactations of the same trait were very low (10-20% between M90 in the first and all lactations and for M305 in the first and M305 in all lactations using SAM procedure; while it was zero percent when using MAM procedure (Table 6). This indicate that ranking of sires according to first lactation will diffenitily differ from the ranking according to all lactations performance. Reents *et al.* (1995) reported that lowest percentage of sires in common was showed between repeated single-trait animal model (using combined first three lactations) and single-trait animal model using only first lactation which ranged from 25 to 44%.

Table (6) shows percent of sires in common between methods of evaluation in first and all lactations. Ninty percent of sires are common in both M90 and M305 evaluation in first lactation either using SAM or MAM and the same percent was found in both M90 and M305 in all lactations. This reveals that ranking of sires according to M90 was accurate as ranking using M305. The evaluation of sires using M90 is moreover advantagous in comparison to evaluation using M305 as it can be used for ranking sires after the completion of their daughters first 90-day milk yield. Thus, the evaluation using M90 yield could reduce the generation interval which in turn results in higher genetic gain.

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التقييم الوراثى لمحصول اللبن فى ماشية الهولشــتين-فريزيــان المربــاه فــى جمهورية مصر العربية باستخدام نماذج الحيوان الفردية والمتعددة

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تمت مقارنة نموذج الحيوان فردى الصفة ومتعدد الصفات باســـتخدام بيانـــات ٩٠- (M90) و ٣٠٥-يوم (M305) لــ ٩٨٥ بقرة هولشتين-فريزيان ناتجة من ١٠٤ أب ، ٩٨٥ أم مرباه فى مصر. كانت بيانات الموسم الأول ٩٨٥ سجل إنتاجى، بينما كانت لكل المواسم مجتمعة ٥٦٤٢ ســـجلا إنتاجيـــا. إشـــتمل نموذج الحيوان سواء الفردى أو المتعدد على موسم وسنة الولادة ، العمر عند الولادة وكذلـك فـتـرة الأيـام المفتوحة كتأثيرات ثابتة، بينما تضمن الحيوان والخطأ المتبقى كتأثيرات عشوائية.

كانت الإختلافات فى القيم التربوية المتنبأ بها (PBV) كبيرة فى نموذج الحيوان متعدد الصفـــات عند استخدام سجلات الموسم الأول بينما كان العكس عند استخدام سجلات كل المواسم مجتمعـة (أى كـانت الإختلافات كبيرة فى النموذج الفردى عن النموذج متعدد الصفات فى حالة الســجلات مجتمعة). انخفـض الخطأ القياسى للقيم التربوية المتنبأ بها (SEP) عند تطبيق نموذج الحيـوان المتعـدد بالمقارنـة بـالنموذج الفردى، وبالتالى زادت الدقة عند استخدام النموذج المتعدد عنه عند استخدام النموذج الفردى. التقـارب الشـديد بين معاملات الإرتباط (بيرسون ، وسبيرمان) بين النموذجين (الفـــردى والمتعـدد) يؤكـد كفـاءة أى مـن النموذجين فى التقييم الوراثى للطلائق والأمهات والأبقار.

استخدام سجلا ت كل المواسم مجتمعة فى التقييم الوراثى يقلل بدرجة كبيرة من الخطـأ القياسـى للقيم التربوية المتنبأ بها سواء استخدم نموذج الحيوان الفردى أو المتعدد بالمقارنة باستخدام سجلات الموسـم الأول فقط. كذلك كانت الزيادة فى الدقة (rij) من استخدام كل المواسم مجتمعة واضحة بالمقارنـة باسـتخدام سجلات الموسم الأول فقط. وهذا يؤكد أن ترتيب الطلائق والأمهات والأبقار سيختلف اختلافا كبيـرا عنـد تقيمها باستخدام الموسم الأول فقط عنه عن استخدام كل السجلات، حيث كانت معاملات الإرتباط بيـن القـيم التربوية المتنبأ بها بإستخدام السجل الأول وتلك الناتجة من السجلات مجتمعة ضعيفة جدا.

يمكن الإعتماد على المحصول الجزئى للبن (انتاج الــ ٩٠ يوم الأولى من موسم الحليب ، M90) فى التقييم الوراثى لحيوانات الهولشتين-فريزيان بدون أى تعقيدات كما يتيح فرصة العائد السريع من استخدام الطلائق. انخفاض الخطأ القياسى للقيم التربوية المتنبأ بها لكل من الطلائق والأمهات والأبقار عند اسـتخدام محصول اللبن الجزئى بالمقارنة بمحصول الــ٣٠٥-يوم فى كل من النموذجين (الفردى والمتعدد) يؤكد علـى تحقيق تحسين وراثى سريع من انتخاب الآباء ، وهذا يعنى إمكانية التحسين الوراثى فى انتاج اللبن من خـلال الإنتخاب المبكر على اساس انتاج اللبن الجزئى فى عشيرة الهولشتين-فريزيان فى مصر.