

COMPARISON BETWEEN EFFICIENCY OF PART- AND COMPLETE-LACTATION RECORD IN PROGENY TESTING FLECKVIEH BULLS

S.M. Zahed¹, M.H. Khalil² and A.M. Soliman³

1 Animal Production Research Institute, Ministry of Agriculture, Cairo, Egypt; 2 Department of Animal Production, Faculty of Agriculture at Moshtohor, Zagazig University, Banha Branch, Qalyoubia, Egypt; 3 Department of Animal Production, Faculty of Agriculture, Zagazig University, Zagazig, Egypt.

SUMMARY

Records of 100-day Fleckvieh lactation for yields of milk (M100), fat (F100), protein (P100), fat-plus-protein (FP100) and carrier (C100) were examined. Estimates of genetic and phenotypic variations and covariations were obtained for the first three lactations as well as for all lactations combined. A total of 26874 records representing 10466 cows sired by 650 bulls extracted from 50788 records were used.

The sire of the cow affected significantly ($P < 0.001$) all milk traits of the first three lactations. For all milk traits, the sire variance components (σ^2_s) expressed as percentage (V%) were moderate and ranged from 3.1% to 6.5% and decreased with the advance of lactation from 5.2-6.5% in the first lactation to 3.1-5.3% in the third lactation. Accordingly, moderate sire heritabilities (h^2_s) ranged from 0.20 to 0.26 in the first lactation, from 0.15 or 0.22 in the second lactation and from 0.13 to 0.21 in the third lactation. Heritability was high in the first lactation and decreased with advance of lactation. In each lactation, heritability estimates were lower for F100 than that for P100, whereas both M100 and C100 were in close agreement.

The cow within sire contributed significantly ($P < 0.001$) to variation of all milk traits. The percentage of variance component attributable to cow within sire for milk traits were high and ranged from 22.6% to 39.3%. Repeatability estimates for all milk traits were fairly moderate or slightly high ranging from 0.23 to 0.43.

Genetic (r_G) and phenotypic (r_P) correlations in the first three lactations between yield traits of 100-day were positive and high, ranging from 0.73 to 1.0. Genetic correlations between 100-day milk traits and the corresponding traits of 305-day in the first three lactations were high and positive (≥ 0.80). The estimates of r_P were also positive and ≥ 0.73 . All these estimates of r_G and r_P in the first lactation were greatly larger than those estimates of the second and third lactations.

Part-lactation yield traits of the daughters evaluated gave an efficient guide for the evaluation of Fleckvieh bulls. The relative efficiency of progeny test based on part-lactation record was as efficient as that based on complete-lactation record.

Keywords: Fleckvieh bulls, progeny test, lactation record

INTRODUCTION

Heifer yield is a good indicator of lifetime performance, but neglecting information of later lactations will lead to possible changes in the ranking of sires over lactations. In practice, assessing the value of later records for both sire and cow evaluation requires, in the first instance, knowledge of the genetic parameters concerned, i.e. heritabilities and genetic correlations. Meyer (1984) reported that first lactation yield is not only an efficient selection criterion for lifetime production since the performance in all lactations is determined more or less by the same genes, but including later lactations will improve the precision of sire evaluation only to a limited extent. Also, including later lactations will create more ties between sires, i.e. daughters of a sire will be compared with daughters of other sires which had no records in the first lactation, and consequently increase the accuracy of evaluation.

Phenotypic antagonistic relationship between reproductive interval traits and milk production may be the main cause for preferring the part-lactation (incomplete) records than complete ones in early selection programmes in dairy cattle. By selection on 100-day milk trait, the potential of bias in sire evaluation by selection of heifers will be reduced substantially (Wilmlink, 1987 & 1988). Soliman and Khalil (1991) found that the phenotypic correlations of days open with 100-day yield traits were smaller than that with 305-day yield traits. The same conclusion for both incomplete and complete milk yield traits have been reported by many investigators (Seykora and McDaniel, 1983; Strandberg and Danell, 1988).

The objectives of present study were (1) to estimate the sire and error variances and covariances for 100-day milk traits (milk, fat, protein, fat-plus-protein and carrier yield) of Fleckvieh records, (2) to estimate the genetic and phenotypic correlations among 100-day milk traits as well as between 100-day and 305-day milk traits and (3) to estimate the accuracy of selection based on progeny testing for 100-day lactation records as an alternative to the standard 305-day lactation records.

MATERIALS AND METHODS

Data

Data on performance of 100-day lactation of Fleckvieh cattle were obtained from Official Test Federation of Austrian Cattle Breeders (ZAR) in lower Austria. Detailed description of these data has been presented previously by Hartmann *et al.* (1992). Records were taken between 1977 and 1982. A total of 26874 lactation records representing 10466 cows sired by 650 bulls were used. All normal records of less than 305 days in length along with those reaching 305 days were included. Heifers were inseminated when they reached an average of 320 Kg body weight, while cows were inseminated during the first heat period 60 days post-partum. Artificial insemination technique was used, avoiding half-sib, full-sib and sire-daughter matings.

Milk traits of 100-day lactation included yields of milk (M100), fat (F100), protein (P100), fat-plus-protein (FP100) and carrier (C100 = $M100 - (F100 + P100)$). The corresponding traits at 305 day lactations involved yields of milk (M305), fat (F305), protein (P305), fat-plus-protein (FP305) and carrier (C305). The data set comprised only cows that have information on their first lactation and subsequent later ones. However, those cows having information on later lactations with no first lactation

information were eliminated. To avoid bias due to differences among sires in the average values of herd, each record was expressed as deviation from its herd average, i.e. herd effect was eliminated. Consequently, any herd that contained only one record didn't contribute to the present study. Also, if the cow was changed from a herd to another, her records were eliminated. Each sire was represented in at least two different herds.

Statistical Models

Herd-adjusted data of the first three lactations were analysed for each lactation separately using the least-square maximum likelihood mean weighted (LSMLMW) computer program of Harvey (Harvey, 1990). In matrix notation, the model adopted was:

$$\begin{array}{ccccc} X'X & X'Z & a & X'Y \\ & & & = & \\ Z'X & Z'Z & s & Z'Y & \dots\dots\dots \end{array} \quad \text{(Model 1)}$$

where: a = represents all the fixed effects of year-season (16 subclasses), age at calving (subclasses classified monthly from <24 months to 61 months), and days open (subclasses starting from <45 days as a first class and intervals of 30 days thereafter), X represents its corresponding matrix, s represents the random effect of sire and Z represents its corresponding matrix. Heritabilities for each lactation (h^2_s) were calculated as: $h^2_s = 4\sigma^2_s / (\sigma^2_s + \sigma^2_e)$. Standard errors of h^2 estimates were computed according to Harvey (1990).

Data of all lactations were analysed using the following mixed model in matrix notation:

$$\begin{array}{ccccc} X'X & X'Z_1 & X'Z_2 & a & X'Y \\ Z_1'X & Z_1'Z_1 & Z_1'Z_2 & s & Z_1'Y \\ Z_2'X & Z_2'Z_1 & Z_2'Z_2 & c & Z_2'Y \end{array} \quad \dots\dots\dots \text{(Model 2)}$$

where a represents all fixed effects of year-season (16 subclasses), age at calving (three-month interval starting from <24 months till 77 months) and days open (subclstarting from <45 days as a first class and interval of 30 days thereafter), s and c represent the random effects (sire and cow) and Z_1 Z_2 represents their corresponding matrices. Heritability across all lactations (h^2_s) were calculated as: $h^2_s = 4\sigma^2_s / (\sigma^2_s + \sigma^2_{c:s} + \sigma^2_e)$.

Repeatability estimates (t) for milk traits were calculated across all lactations as:

$$t = (\sigma^2_s + \sigma^2_{c:s}) / (\sigma^2_s + \sigma^2_{c:s} + \sigma^2_e).$$

Standard errors of h^2 and t estimates were computed according to Harvey (1990).

The accuracy of sire selection on the basis of part records were computed by using the heritabilities and genetic correlations of part and complete lactation records. Relative efficiency of progeny testing was estimated as the ratio (expressed in percentage) between the accuracy of progeny test based on part-lactation and that based on complete-lactation records. Rate of progress in the genetic merit for complete lactations when selecting for sires on the basis of part records of their daughters was calculated relative to using whole records is $(r_{gp gc})(h_p/h_c)$, where $r_{gp gc}$ = the genetic correlation between whole and part records and h_p & h_c = the

square root of heritability of part and complete records, respectively (Van Vleck and Henderson, 1961).

RESULTS AND DISCUSSION

Means and variations

Means, phenotypic standard deviations (SD), coefficients of variation (CV%) and determination (R^2) of part-lactation yields of milk (M100), fat (F100), protein (P100), fat-plus-protein (FP100) and carrier (C100) in the first three lactations (model 1) and across all lactations (model 2) are given in Table 1. Means and phenotypic standard deviations of milk traits increased with advancing parity. Greater increase in yield

Table 1. Means, standard deviations (SD), percentages of variation (CV%) and coefficients of determination (R^2) of 100-day (part-lactation) milk traits of the first three lactations and all lactations in Fleckvieh cattle.

Traits ⁺	Mean, kg	SD	CV%	R^2
First lactation				
M100	1554	238.8	14.6	51.0
F100	63	10.4	14.8	50.8
P100	53	8.4	14.6	51.0
FP100	116	17.5	14.4	50.8
C100	1439	223.9	14.6	51.0
Second lactation				
M100	1866	285.3	14.5	51.7
F100	74	11.0	14.5	51.3
P100	59	9.1	14.8	51.4
FP100	133	19.1	13.8	51.4
C100	1733	269.0	14.6	51.7
Third lactation				
M100	2032	288.6	13.6	51.2
F100	80	10.5	12.8	50.9
P100	63	9.1	14.1	50.7
FP100	144	18.3	12.4	50.8
C100	1887	273.1	13.8	51.2
All lactations				
M100	1808	340.5	11.3	71.5
F100	71	13.3	12.1	68.7
P100	67	11.4	10.9	67.8
FP100	127	23.5	11.4	70.1
C100	1681	316.6	11.4	64.2

⁺ M100= 100-day milk yield, F100= 100-day fat yield, P100= 100-day protein yield, FP100= 100-day fat and protein yield, C100= 100-day carrier yield.

traits was found from first to second lactation than from second to third lactation. The present estimates generally fall within the range of those estimates obtained from

Fleckvieh cattle in most Austrian studies (e.g. Soliman *et al.*, 1990; Soliman and Khalil, 1993).

For the first three and all lactations, estimates of coefficients of variation (CV%) for yield traits ranged from 10.9% to 14.8% (Table 1). Austrian studies (e.g. Soliman and Khalil, 1989; Soliman *et al.*, 1990; Soliman and Khalil, 1993) reported higher variation for part-lactation yield traits than for complete-lactation traits. The CV% for F100 in the first and second lactations was nearly the same as that for P100. The CV% for F100 was found to be larger than that for P100 as cited in many other studies (e.g. Soliman and Khalil, 1989; Soliman *et al.*, 1990; Soliman and Khalil, 1993). A reverse trend was found in the third lactation. Comparing these results with those obtained for 305-day yield traits (Zahed, 1994), the variability in 100-day part-lactation records was less (10.9%-14.8%) than that in 305-day records (11.4%-15.6%). This may be due to the fact that 100-day lactation records are not greatly affected by pregnancy and consequently it had no effect on lactation (Van Arendonk *et al.*, 1989). Meyer (1985) concluded that high CV% indicated that there was short-term environmental variation affecting dairy performance.

Sire variance components and heritability estimates in each lactation

The sire of the cow affected significantly ($P < 0.001$) all part-lactation milk traits of the first three lactations (Table 2). Most of the studies evidenced this trend (e.g. Soliman *et al.*, 1990; Soliman and Khalil, 1991; Soliman and Khalil, 1993).

Estimates (σ^2) and percentages (V%) of variance components due to sire and remainder and heritability estimates (h^2_s) for milk traits in the first three lactations are presented in Table 3. Sire variance component (σ^2_s) expressed as percentage (V%) decreased from the first to the third lactation, while the residual variance component (σ^2_e) takes the reverse direction (Table 3). The same trend was reported by many other workers (e.g. Meyer 1984; Soliman *et al.*, 1990; Soliman and Khalil, 1993). Boldman and Freeman (1990) reported that the sire variance component is increased with the increase of production level.

The percentages of variance component attributable to the sire for all part-lactation milk traits were moderate and ranged from 3.1% to 6.5% (Table 3). This range was in agreement with the results obtained by Soliman and Khalil (1993) on the same breed (1.3% to 6.7%). Also, it was lower than that of 7.1% to 12.9% reported by Soliman *et al.*, (1990) on Pinzgauer cattle.

The moderate variance component due to sire suggests that there is an opportunity for selection in this population (Soliman *et al.*, 1990; Soliman and Khalil, 1993). Moderate sire variance component estimates lead to moderate heritabilities (Table 3). This indicates that selection on incomplete records can be an acceptable alternative to select animals on their completed records (305-day lactation). These estimates of yield traits agreed with those previously reported (Wilmink, 1987 & 1988; Soliman *et al.*, 1990; Soliman and Khalil, 1993); most estimates ranged between 0.13 to 0.26. The present estimates were larger than those reported by Meyer (1985) on Australian cattle (0.13-0.18) and those reported by Soliman and Khalil (1993) on Fleckvieh cattle (0.05-0.27), while they were lower than those estimates reported in other studies (e.g. Van Arendonk *et al.* 1989; Soliman *et al.* 1990). The lower estimates

reported by Meyer (1985) could therefore, in part, be attributable to the comparatively low level of production in Australia.

Table 2. F-ratios of least-squares ANOVA for 100-day (part-lactation) milk traits of the first three lactations in Fleckvieh cattle (model 1).

Source of variation	df	M100	F100	P100	FP100	C100
First lactation						
Sire	646	2.2***	1.8***	2.0***	1.9***	2.3***
Year-season	13	16.0***	8.1***	19.2***	12.2***	15.4***
Age at calving	14	12.3***	12.3***	11.3***	12.0***	12.2***
Days open	5	9.4***	8.2***	1.4ns	3.1*	9.3***
Remainder df	10207					
Remainder mean squares		50595	90.1	60.2	279.1	44271
Second lactation						
Sire	646	1.9***	1.6***	1.8***	1.7***	1.9***
Year-season	11	24.4***	10.8***	22.4***	15.3***	23.8***
Age at calving	16	18.4***	17.1***	15.1***	17.8***	18.6***
Days open	5	16.6***	13.1***	9.5***	12.0***	16.5***
Remainder df	10202					
Remainder mean squares		73126	115.3	76.6	336.4	64834
Third lactation						
Sire	397	1.7***	1.4***	1.5***	1.5***	1.7***
Year-season	7	10.9***	7.6***	6.7***	6.2***	11.3***
Age at calving	12	6.1***	5.5***	4.7***	5.2***	6.0***
Days open	5	8.9***	7.2***	5.2***	6.4***	8.9***
Remainder df	4685					
Remainder mean squares		76310	105.1	78.6	317.0	68230

***= $P < 0.001$, *= $P < 0.05$, ns= non-significant.

In general, sire heritabilities for milk traits were found to be large in the first lactation and decreased slightly thereafter with succeeding second and third lactations (Table 3). Most of the previous studies evidenced this trend (e.g. Meyer, 1984; Swalve and Van Vleck, 1986; Van Arendonk *et al.*, 1989; Soliman *et al.*, 1990; Soliman and Khalil, 1993). Boldman and Freeman (1990) reported that estimates of each variance component (genetic, permanent and remainder) increased with the increase of production level. Decreasing heritabilities with advance of lactation may indicate that non-additive genetic differences became more important in later lactations than the first one. Heritabilities for part-lactation yield traits in the present study were found to be smaller (0.15-0.26) than those obtained for the same breed by Zahed (1994) for 305-day milk traits (0.22-0.31). Similar trend was observed by Van Arendonk *et al.*, (1989), Soliman *et al.* (1990) and Soliman and Khalil (1993).

Table 3. Estimates of variance components due to sire (σ_s^2) and remainder (σ_e^2) and heritability estimates ($h_s^2 + SE$) of 100-day (part-lactation) milk traits of the first three lactations in Fleckvieh cattle (model 1).

	Sire		Remainder		h^2_s	SE
Trait	σ^2_s	V%	σ^2_e	V%		
First lactation						
M100	3457.5	6.4	50595.1	93.6	.26	.026
F100	5.5	5.7	90.2	94.3	.21	.024
P100	3.4	5.3	60.2	94.7	.20	.023
FP100	15.3	5.2	279.1	94.8	.21	.024
C100	3082.2	6.5	44271.2	93.5	.26	.026
Second lactation						
M100	4126.9	5.3	73127.0	94.7	.22	.024
F100	4.3	3.5	115.3	96.5	.15	.021
P100	3.4	4.2	76.6	95.8	.18	.022
FP100	14.8	4.2	336.4	95.8	.17	.022
C100	3773.4	5.5	64834.0	94.5	.21	.024
Third lactation						
M100	4225.7	5.2	76311.0	94.8	.21	.036
F100	3.3	3.1	105.1	96.9	.13	.031
P100	3.0	3.6	78.6	96.4	.15	.032
FP100	12.2	3.7	317.0	96.3	.15	.032
C100	3839.9	5.3	68230.0	94.7	.21	.036

Heritabilities across lactations

The cow contributed significantly ($P < 0.001$) to the variation in all milk traits (Table 4). This is in full agreement with findings in most available literature (e.g. Soliman and Khalil, 1989; Soliman *et al.*, 1990; Soliman and Khalil, 1993). The percentages of variance component (V%) attributable to cow effect for milk traits were high and ranged from 22.6% to 39.3% (Table 5). This range was similar to that of 27.1 to 44.8% obtained by Soliman and Khalil (1993) on Fleckvieh cattle while it was lower than that of 52.4% to 60.1% reported by Soliman and Khalil (1989) on Braunvieh cattle. The differences in estimates reported by different workers could be attributed to differences in the models and the structure of the sample used. Across all lactations, large estimates of V% attributable to sire and cow indicate that genetic improvement of milk traits could be achieved through sire and cow selection. In particular for Fleckvieh and Pinzgauer cattle, large magnitude of the cow estimates might indicate a sizable potential for cow in selection programmes and/or in changes of the herds management to improve yield traits (Soliman *et al.*, 1990; Soliman and Khalil, 1993).

Estimates of h^2 from the first lactation are higher than those estimates from all lactations (Tables 3&5). This notation is typically found by Tong *et al.*, (1979). This trend appears to depend on the sample examined.

Repeatability estimates

Fairly moderate or slightly high repeatability estimates (t) for all milk traits were obtained as showed in Table 5. The estimates ranged from 0.23 to 0.43. This range seems in full agreement with that range of 0.29 to 0.41 reported by and Khalil (1993) for milk, fat, protein and fat+protein yields of Fleckvieh cattle. Repeatabilities in Table 5 also indicate that M100 and C100 are more repeatable than that of F100 and P100. Soliman and Khalil (1993) reported the same trend. More caution must be taken when considering the P100 as a selection criterion since it has the lowest repeatability estimate (0.23). Lower repeatability estimate for protein relative to other milk traits was also reported by Tong *et al.*, (1979) and Soliman and Khalil (1993). This result also indicates that an increase in accuracy could be achieved in characterization of the performance of the cow for P100 by having several records rather than just one.

Table 4. F-ratios of least-squares ANOVA for 100-day (part-lactation) milk traits across all lactations in Fleckvieh cattle (model 2).

Source of variation	df	M100	F100	P100	FP100	C100
Sire	649	2.4***	2.1***	2.2***	2.2***	2.4***
Cow:sire	10239	2.7***	2.1***	1.7***	2.2***	2.6***
Year-season	15	16.4***	10.2***	31.3***	16.0***	17.2***
Age at calving	18	217.7***	229.3***	869.8***	249.6***	363.8***
Days open	5	2.8**	1.17ns	12.2***	0.7ns	1.7ns
Remainder df	18284					
Remainder mean squares		41712	73.3	53.8	210.5	36954

***= $P < 0.001$, **= $P < 0.01$, ns= non-significant.

Table 5. Estimates (σ^2) and percentages (V%) of variance compo-nent due to sire (σ^2_s), cows (σ^2_c) and remainder (σ^2_e) and estimates of repeatability (t) and heritability (h^2_s) for 100-day (part - lactation) milk traits across all lactations in Fleckvieh cattle (model 2).

Trait	Sire		Cow		Remainder		t^+	h^2^+
	σ^2_s	V%	σ^2_c	V%	σ^2_e	V%		
M100	3567	4.9	26250.7	36.6	41712	58.5	.41	.20
F100	4.0	3.6	31.5	28.9	73.3	67.5	.32	.15
P100	3.0	4.0	16.6	22.6	53.8	73.4	.23	.14
FP100	13.2	4.1	100.1	30.9	210.5	65.0	.34	.16
C100	3238	4.8	26956.5	39.3	36954	59.3	.43	.21

+ Standard errors of heritabilities ranged from 0.015 to 0.019, while for repeatabilities were from 0.007 to 0.008.

Comparing estimates of repeatability for 100-day in the present study with those of 305-day yield traits (Zahed, 1994), we find that estimates for M100 and C100 were somewhat similar to those estimates of corresponding traits of 305-day lactation (M305 and C305), while those for F100, P100 and FP100 were greatly lower than the correspondings in 305-day yield traits. Also, Shelke *et al.*, (1992) found that repeatability of milk traits of part-lactation of Red Kandhari and Jersey x Red Kandhari cows ranged from 0.30 to 0.47. These estimates indicate that selection based on early records can be fairly reliable in selection programmes. The low estimates for yields of fat, protein and fat+protein in the present study may reveal that early selection of cows for these traits may not be more accurate as if it is practiced on complete record (305-day). The negative genetic correlations between milk yield traits and days open across parities (Hansen *et al.*, 1983) may be a cause of the present reduction of repeatabilities of milk yield traits.

Correlations

(i) Genetic correlations (r_G)

Genetic correlations (r_G) among 100-day (part-lactation) milk traits in the first three lactations were positive and high (Table 6). Reviewed estimates of r_G among yield traits of Fleckvieh cattle (Soliman and Khalil, 1993) were, in general, similar where they were positive and high (estimates ranged from 0.76 to 1.00). These high correlations were also evidenced for Braunvieh (Soliman and Khalil, 1989) and Friesian cattle (Meyer, 1985).

The estimates of r_G in the first lactation ranged from 0.87 to 1.00 between M100 and other yield traits; from 0.87 to 0.98 between F100 and others, from 0.87 to 0.96 between P100 and others; from 0.92 to 0.98 between FP100 and others and from 0.88 to 1.00 between C100 and others (Table 6). In the second and third lactations, the same trend prevailed but with a decreasing magnitude. M100 was strongly genetically associated with C100 (Table 6).

Estimates of r_G between M100 and P100 in each lactation were slightly lower than those correlations between M100 and F100 (Table 6). The same trend was noticed between C100 and P100 and C100 and F100. M100 was more associated with P100 than with F100 as indicated in several studies (e.g. Meyer, 1985; Soliman and Khalil, 1993). The estimates of r_G between M100 and each of F100 and P100 indicate that the progress made in increasing P100 is expected to be the same as that achieved for F100. The cost of producing one unit of fat requires twice as much feed energy as the production of an equal weight of protein (Dommerholt *et al.*, 1978), and it seems desirable, from the economic and human health view points to pay more attention to select for milk with more protein than for more milk with more fat. All estimates of r_G among 100-day milk traits and their correspondings milk traits of 305-days lactation were high ranging from 0.94 to 0.96 in the first lactation, from 0.81 to 0.88 in the second lactation and from 0.80 to 0.86 in the third lactation (Table 6). These findings are in agreement with other investigations (Ferris *et al.*, 1985; Wilmink, 1988; Soliman and Khalil, 1989; Soliman *et al.*, 1990; Soliman and Khalil, 1993). Also, Jain *et al.*, (1991) found that genetic correlations of 305-day milk yield with cumulative monthly milk yield of two, three and four months milk yield were close to one. These mainly part-whole genetic relationships indicate that milk, fat and protein

yields in 100-day of lactation could be used as a good indicator for the same traits in 305-days of lactation, and selection based on 100-day production record would be expected to give similar improvement in lactation yield traits as selection based on lactation yield of complete record itself.

(ii) Phenotypic correlations (r_p)

Phenotypic correlations of M100 and other part-lactation yield traits were high, ranging from 0.74 to 1.00 (Table 6). The same trend was observed for C100 with other part-lactation yield traits. Phenotypic correlations of M100 and P100 in second and third parities were higher than those of M100 and F100 (Table 6). These findings are in agreement with other investigations (e.g. Tong *et al.*, 1979; Meyer, 1985; Schutz *et al.*, 1990; Soliman *et al.*, 1990 and Soliman and Khalil, 1993). However, high r_p 's obtained here for Fleckvieh cattle gives, in practice, a considerable advantage in management and culling policy for such breed of dairy cattle.

Phenotypic correlations of 100-day milk traits with their corresponding traits of 305-days of lactation were positive and high and ranged from 0.83 to 0.87 in the first lactation, from 0.76 to 0.84 in the second lactation, from 0.73 to 0.83 in the third lactation and from 0.77 to 0.85 in all lactations (Table 6). The present results agree well with those findings of Soliman *et al.*, (1990) on Pinzgauer cattle and Soliman and Khalil (1993) on Fleckvieh cattle. Shelke *et al.*, (1992) found that the phenotypic correlations between various part-lactation yields and total-lactation yields of Red Kandhari and Jersey x Red Kandhari cows were positive and highly significant. These estimates suggest that part-lactation yield traits are affected by at least some of the same physiological pathways involved in the 305-day lactations. Also, the early records of part-lactation can be used with high degree of accuracy for predicting yield of complete lactation (Zaman *et al.*, 1990 and Shelke *et al.*, 1992).

Accuracy and relative efficiency of progeny test

The accuracy of progeny testing based on part and complete lactation records was compared using variable number of daughters per bull (5 to 100). Results given in Table 7 show that with the increase of number of daughters, the accuracy of progeny test of the bull increased but at a decreasing rate. The same trend was reported by Jain *et al.*, (1991). Coefficients obtained here revealed also that for a given number of daughters the progeny test based on part-lactation was as accurate as that based on 305-day yield of the daughters. In agreement with these results, Jain *et al.*, (1991) found that the progeny test based on third monthly milk yield or cumulative monthly milk yield of three or four months of the daughters were more accurate than based on 305-day milk yield.

Results given in Table 7 also reveal that selection based on part-lactation yield of the daughters was as efficient as selection based on complete-lactation yield. The relative efficiency of part-lactation record expressed in percentage ranged from 87% to 100%. For F100, P100 and FP100 and depending on the number of daughters, the relative efficiency increasing from 87-89% for five daughters to 97-98% for 100 daughters. For M100 or C100, increasing number of daughters per bull was not reflected in a great improvement of relative efficiency (96% for 5 daughters to 100% for 100 daughters). Jain *et al.*, (1991) reported that selection based on three or four months yield of the daughters was slightly more efficient than that based on complete

Table 6. Estimates of genetic (rG)+ and phenotypic (rP)++ correlation between milk traits of 100-day part-lactation and the corresponding estimates of 305-day milk traits of the first three lactations and across all lactations in Fleckvieh cattle.

Traits	F100	P100	FP100	C100	M305	F305	P305	FP305	C305
First lactation									
M100	0.91 (0.84)	0.87 (0.78)	0.92 (0.86)	1.00 (1.00)	0.94 (0.87)	0.84 (0.78)	0.84 (0.71)	0.86 (0.79)	0.94 (0.87)
F100		0.87 (0.74)	0.98 (0.93)	0.92 (0.85)	0.88 (0.72)	0.94 (0.84)	0.86 (0.65)	0.92 (0.79)	0.88 (0.73)
P100			0.96 (0.91)	0.88 (0.80)	0.86 (0.66)	0.86 (0.66)	0.96 (0.85)	0.92 (0.78)	0.87 (0.68)
FP100				0.93 (0.88)	0.89 (0.73)	0.93 (0.80)	0.92 (0.78)	0.94 (0.83)	0.90 (0.75)
C100					0.94 (0.87)	0.85 (0.79)	0.85 (0.72)	0.87 (0.80)	0.94 (-0.87)
Second lactation									
M100	0.87 (0.80)	0.86 (0.87)	0.88 (0.87)	1.00 (1.00)	0.85 (0.83)	0.65 (0.71)	0.68 (0.73)	0.67 (0.74)	0.84 (0.83)
F100		0.92 (0.80)	0.98 (0.95)	0.88 (0.82)	0.78 (0.67)	0.81 (0.76)	0.77 (0.65)	0.80 (0.73)	0.78 (0.68)
P100			0.98 (0.92)	0.87 (0.88)	0.83 (0.72)	0.82 (0.70)	0.88 (0.80)	0.85 (0.76)	0.84 (0.73)
FP100				0.90 (0.88)	0.81 (0.72)	0.83 (0.76)	0.83 (0.75)	0.84 (0.77)	0.82 (0.73)
C100					0.85 (0.83)	0.66 (0.72)	0.69 (0.74)	0.68 (0.75)	-0.84 (0.83)
Third lactation									
M100	0.91 (0.75)	0.82 (0.86)	0.88 (0.85)	1.00 (1.00)	0.85 (0.83)	0.67 (0.71)	0.69 (0.74)	0.69 (0.74)	0.86 (0.83)
F100		0.97 (0.75)	0.99 (0.93)	0.90 (0.73)	0.77 (0.63)	0.80 (0.73)	0.82 (0.62)	0.82 (0.70)	0.76 (0.62)
P100			1.00 (0.91)	0.80 (0.85)	0.72 (0.71)	0.77 (0.69)	0.85 (0.80)	0.81 (0.75)	0.71 (0.70)
FP100				0.86 (0.83)	0.76 (0.71)	0.80 (0.75)	0.86 (0.74)	0.83 (0.77)	0.75 (0.70)
C100					0.85 (0.83)	0.66 (0.70)	0.67 (0.73)	0.67 (0.73)	0.86 (0.83)
All lactations									
M100	0.88 (0.80)	0.86 (0.79)	0.89 (0.86)	0.99 (0.98)	0.88 (0.84)	0.71 (0.73)	0.74 (0.68)	0.74 (0.76)	0.88 (0.82)
F100		0.92 (0.72)	0.98 (0.94)	0.88 (0.80)	0.81 (0.68)	0.86 (0.77)	0.82 (0.60)	0.86 (0.74)	0.81 (0.67)
P100			0.97 (0.86)	0.87 (0.84)	0.83 (0.66)	0.83 (0.64)	0.91 (0.84)	0.87 (0.72)	0.84 (0.71)
FP100				0.89 (0.85)	0.83 (0.72)	0.86 (0.77)	0.87 (0.71)	0.88 (0.79)	0.83 (0.71)
C100					0.89 (0.83)	0.72 (0.73)	0.75 (0.73)	0.74 (0.75)	0.88 (0.85)

+ Standard errors for the genetic correlations ranged from 0.000 to 0.073. ++ Estimates of phenotypic correlation are presented between parentheses.

lactation yield. In similar studies, Van Vleck and Henderson (1961) reported a maximum of 92% relative selection efficiency, when Holstein-Friesian bulls were evaluated on the basis of the third month yield of their daughters.

Genetic progress

Table 8 presents the relative progress in milk traits that could be possibly obtained by selection on the basis of part-lactation relative to complete lactation records. For diffmilk traits, the part-lactation record would attain 77% to 89% as much progress as complete-lactation record. Jain *et al.*, (1991) found that the expected annual genetic

Table 7. Accuracy and relative efficiency (RE, %) of progeny testing of Fleckvieh bulls based on part lactation (100-day) and complete lactation (305-day) records using different numbers of daughters per bull.

Criterion of bull selection	Number of daughters per bull					
	5	10	20	25	50	100
Milk yield						
100-day	0.51	0.64	0.76	0.80	0.88	0.94
305-day	0.53	0.66	0.78	0.81	0.89	0.94
RE(%)	97	98	99	99	100	96
Fat yield						
100-day	0.47	0.60	0.73	0.76	0.86	0.92
305-day	0.54	0.68	0.79	0.82	0.90	0.95
RE(%)	87	88	93	93	96	97
Proteinyield						
100-day	0.46	0.59	0.72	0.75	0.85	0.92
305-day	0.52	0.65	0.77	0.80	0.89	0.94
RE(%)	89	91	94	94	96	98
Fat+Protein yield						
100-day	0.47	0.60	0.73	0.76	0.86	0.92
305-day	0.54	0.68	0.79	0.82	0.90	0.95
RE(%)	87	88	93	93	96	97
Carrier yield						
100-day	0.51	0.64	0.76	0.80	0.88	0.94
305-day	0.53	0.66	0.78	0.81	0.89	0.94
RE(%)	96	97	98	99	99	100

gains through the use of progeny-tested Holstein-Friesian bulls selected on the basis of three or four month yields seemed to be the best criterion of bull selection in comparison to complete-lactation yield. These results also showed that an improvement in lactation milk yield could be achieved through indirect selection based on part-lactation yield of the daughters. The progeny testing of bulls on the basis of complete-lactation yield would be expected to give lower genetic gains because the lactation yield is influenced relatively more by the temporary environmental variation especially during the early and late stages of lactation and thus affecting the accuracy and efficiency of progeny testing. Jain *et al.*, (1991)

mentioned that the progeny testing and selection of bulls on third-month yield of the daughters will lead to more effective and faster annual genetic gain in the lactation yield of the herd at the rate of 2.7% to 3.7% of the herd average (herd average= 2900 kg) depending on the number of daughters used for progeny testing of bulls.

Table 8. Genetic progress using part-lactation relative to 305-day lactation records

Trait	Milk	Fat	Protein	Fat+Protein	Carrier
Genetic progress	0.89	0.77	0.83	0.77	0.89

CONCLUSION AND GENERAL CONSIDERATIONS

Yields of part-lactation (100-day) of the first lactation in the present study had the highest heritability estimates and it gave higher accuracy in estimating the breeding value of the sire than subsequent lactations (Soliman and Khalil, 1993). Therefore, the first lactation seems adequate for proving sires, but the information on the second and third records would help considerably in estimating the breeding values of the cows. The practical consequence of the present study as well as reviewed ones is that, through the first 100-day production of the first lactation record, progeny test may be used as an initial decision to select the bull that should be brought into general AI service, while the final decision is to wait some assessment of complete-lactation records. However, several studies (e.g. Soliman and Khalil, 1993) showed that sires can be ranked on records of their daughters' performance in the first 100-day of the first lactation with little loss in accuracy and no apparent harmful effects on longevity or future production of the daughters, especially because the correlations between first and later lactations were positive and high (Maijala and Hanna, 1974; Strandberg, 1985).

Since overproduction of fat is the main problem in the current markets in Europe and USA, the desired breeding goal would be changed to increase the protein percentage, while holding fat percentage constant (Young *et al.*, 1986). Also, from the economic point of view, production of fat requires twice as much feed energy as the production of an equal weight of protein (Dommerholt *et al.*, 1978). Consequently, the attention has been changed in USA and Europe toward the selection for more protein than fat. Heritability estimates obtained in this study in each lactation for Fleckvieh cattle were lower for PY than that for FY yield. Because of the genetic correlations of P100 and F100 are close to unity (0.92, 0.96 and 0.96 in the first, second and third lactations, respectively), very slow progress would be made toward the proposed goal.

Fairly moderate or high repeatabilities obtained in the present study lead to indicate that records beyond the first lactation add little information in predicting the producing ability of the cow (Soliman and Khalil, 1993). Consequently, culling policies of cows for yield traits based on single record, would be efficient from a genetic viewpoint, and assessment of several records are not required before selecting cows for these traits.

High and positive genetic and phenotypic correlations attained here for 100-day milk traits will lead to conclude that high gain would come from direct selection for composite trait of FP100. Consequently, these correlations are sufficiently high to state that an initial decision can be made on the basis to select for FP100 of the first 100-day production through progeny test of a bull that should be brought back into general AI service. The final decision should be at least based on the first 305-day lactation to select cows and bulls for breeding purposes (Soliman and Khalil, 1993). Since correlations of C100 with F100, P100 and FP100 were at least the same as those correlations of M100 with the same traits, procedures wishing to take advantage of component pricing schemes (when additional fluid carrier is not needed) should perhaps depend on selection for composite trait of FP100. High estimates of genetic and phenotypic correlation between 100-day and 305-day yield traits are of interest for early selection programmes. By selection on these 100-day yield traits, a potential bias in sire evaluation will be reduced substantially. Also by reduction in generation interval, an increase in selection gain and a decrease in costs of progeny test will be gained through using the part-lactation production as an alternative for the standard complete records.

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مقارنة كفاءة استخدام جزء من السجل والسجل الكامل في اختبار النسل لطلاق ماشية الفلاك في

سميح محمد زاهد^١ ، ماهر حسب النبي خليل^٢ و أشرف محمد سليمان^٣

١ معهد بحوث الإنتاج الحيواني، الدقى ، الجيزة، مصر، ٢ قسم الإنتاج الحيوانى - كلية الزراعة بمشترى، جامعة الزقازيق، بنها، مصر، ٣ قسم الإنتاج الحيوانى، كلية الزراعة، جامعة الزقازيق، مصر

استخدمت في هذه الدراسة سجلات إدرار ١٠٠ يوم لتقدير التباينات والتغايرات الوراثية والمظهرية لصفات محصول اللبن، والدهن والبروتين وذلك للثلاث مواسم الأولى بالإضافة إلى كل المواسم مجتمعة. استخدمت بيانات ٢٦٨٧٤ سجل إدرار تمثل ١٠٤٦٦ بقرة لعدد ٦٥٠ طلوقة تم إستخلاصهم من ٥٠٧٨٨ سجل. ويمكن تلخيص النتائج المتحصل عليها فيما يلى:

١- كان لأب البقرة تأثيرا عالى المعنوية على جميع صفات اللبن للثلاث مواسم الأولى. تراوحت قيم نسبة التباين الأبوى لجميع صفات اللبن ٥,٢ - ٦,٥ ٪ فى الموسم الأول والتي إخذت فى الإنخفاض بتقدم مواسم الحليب لتصبح ٣,١ - ٥,٣ ٪ فى الموسم الثالث. كانت قيم المكافئ الوراثى متوسطة حيث تراوحت بين ٠,٢٠ - ٠,٢٦ فى الموسم الأول، ٠,١٥ - ٠,٢٢ فى الموسم الثانى و ٠,١٣ - ٠,٢١ فى الموسم الثالث. كانت قيم المكافئ الوراثى منخفضة لمحصول الدهن أكثر من محصول البروتين لمواسم الإدرار الثلاثة الأولى بينما كانت قيم المكافئ الوراثى لمحصول اللبن ومحصول اللبن الخالى من الدهن والبروتين متقاربة مع بعضها.

٢- أظهرت البقرة داخل الأب تأثير عالى المعنوية على جميع صفات اللبن. كانت نسبة التباين الوراثى الراجع للبقرة مرتفعة حيث تراوحت بين ٢٢,٦ - ٣٩,٣ ٪. كانت قيم المعاملات التكرارية لجميع صفات اللبن متوسطة إلى عالية حيث تراوحت بين ٠,٢٣ - ٠,٤٢.

٣- كانت معاملات الارتباط الوراثى والمظهري فى الثلاث مواسم الأولى بين صفات اللبن موجبة وعالية حيث تراوحت بين ٠,٧٣ - ٠,١٠. إتضح كذلك أن معاملات الارتباط الوراثى بين صفات اللبن لل ١٠٠ يوم و ٣٠٥ يوم فى الثلاث مواسم الأولى موجبة وعالية (أكبر من ٠,٨٠). كذلك كانت قيم معاملات الارتباط المظهري (أكبر من ٠,٧٣). كما كانت قيم معاملات الارتباط الوراثى والمظهري فى الموسم الأول أعلى بكثير من مثيلاتها فى الموسمين الثانى والثالث.

٤- أعطى استخدام جزء من السجل (١٠٠ يوم) مؤشرا جيدا لتقييم الطلائق. كانت الكفاءة النسبية لإختبار النسل باستخدام جزء من السجل متقاربة لكفاءة استخدام السجل الكامل (٣٠٥ يوم).