ESTIMATION OF GENETIC PARAMETERS FOR MILK TRAITS OF FLECKVIEH RECORDS NOT SUBJECTED TO CULLING

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SUMMARY

Records of 305-day Fleckvieh lactation for yields of milk (MY), fat (FY), protein (PY), fat-plus-protein (FPY) and carrier (CY) were examined and estimates of genetic, phenotypic and environmental variations and covariations were obtained for the first three lactations as well as for combined all lactations. A total of 26874 records representing 10466 cows sired by 650 bulls extracted from 50788 records were used.

Means and standard deviations of milk traits increased with advancing of parity. Greater increase in yield traits was found from first to second lactation than from second to third lactation. Coefficients of variation (CV) for milk traits ranged from 12.9% to 17.2% in the first lactation, from 11.4% to 17.8% in the second lactation and from 14.3% to 15.5% in the third lactation. Estimates of CV% for FY was higher than that for PY.

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 component (σ^2_s) expressed as percentage (V%) decreased with advance of lactation from 6.7- 7.8% in the first lactation to 5.4-6.1% in the third lactation. The percentages of variance component attributable to the sire for all milk traits were

moderate and ranged from 5.4% to 7.8%. Moderate sire heritabilities (h^2_s) concurred with moderate estimates of sire variance components for yield traits. Estimates of h^2_s ranged from 0.27 to 0.31 in the first lactation, from 0.25 or 0.27 in the second lactation and from 0.22 to 0.24 in the third lactation. Heritability of the first lactation was high and decreased with advance of lactation. In each lactation, heritability estimates were lower for PY than that for FY, whereas both MY and CY 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 27.4% to 43.3%. Repeatability estimates for all milk traits were fairly moderate or slightly high ranging from 0.33 to 0.49.

Genetic correlations (r_G) in the first three lactations between yield traits were positive and high, ranging from 0.87 to 1.0. Phenotypic correlations (r_P) of milk traits were also positive and high ranging from 0.83 to 1.00. The same trend was also observed for environmental correlations (r_E). Estimates of r_P and r_E were higher than those corresponding estimates of r_G in the second and third lactations for yield traits. FPY had the highest correlations with all yield traits excluding CY which reached unity with MY.

INTRODUCTION

Heifer yield is a good indicator of lifetime performance (Hoque and Hodges, 1980), but neglecting information of later lactations will lead to possible changes in the ranking of sires over lactations. In Austria, Essl (1982 & 1984) concluded that selection of Fleckvieh, Braunvieh and Pinzgauer AI bulls should be based on records of the third lactation of their daughters. In addition, selection of bull dams should take place on the earliest lactation after the record of the third lactation is completed. 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 1st lactation, and consequently increase the accuracy of evaluation.

The objective of present study was to estimate the sire and error variances and covariances for milk traits (milk, fat, protein, fat-plus-protein and carrier yield) of Fleckvieh records.

MATERIALS AND METHODS

Data

Data on performance of 305-day lactation of Fleckvieh cattle were obtained from Official Test Federation of Austrian Cattle Breeders (ZAR) in lower Austria. Detailed descriptions of these data have been presented previously by Hartmann et al. (1992). Records were begun between 1977 and 1982. A total of 26874 lactation records representing 650 sires were used. All normal records of less than 305 day milk length along with those reaching 305 day were included.

Heifers were inseminated when they reached an average of 320 Kg body weight, while cows were inseminated during the 1st heat period after 60 days post-partum. AI technique was used, avoiding half-sib, full-sib and sire-daughter matings.

Milk traits of 305-day lactation included yields of milk (MY), fat (FY), protein (PY), fat-plus-protin (FPY) and carrier (CY= MY -(FY+PY)). The data set comprised only cows that have information on their first lactation and subsequent later ones. However, those cows having information of 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 a deviation from the average of the herd which belong to it, i.e. herd effect was eliminated. Consequently, any herd that contains

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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

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

$$Y_{iklmn} = \mu + S_i + YS_k + A_l + D_m + e_{iklmn} \quad \text{(model 1)}$$

where: Y_{iklmn} = 2X-305 milk record expressed as a deviation from the herd average, μ = the overall mean, S_i = the random effect of ith sire, YS_k = the fixed effect of kth year-season combination (K=16), A_l = the fixed effect of lth age at calving (subclasses classified monthly from <24 month to 61 month), D_m = the fixed effect of mth days open (subclasses starting from <45 days as a first class and intervals of 30 days thereafter) and e_{iklmn} = the random error (0, σ^2_e). Estimates of variance and covariance components were calculated using LSMLMW program (Harvey, 1990) depending on method 3 of Henderson for such estimation (Henderson, 1984). Paternal half-sib analysis of variance was utilized to obtain estimates of h^2_s for each lactation as: $h^2_s = 4\sigma^2_s/(\sigma^2_s+\sigma^2_e)$. Estimates of genetic ($r_G$) and phenotypic ($r_P$) correlations between any two milk traits were also calculated. The respective standard errors of the genetic correlations were approximated according to Harvey (1990) as described by the formula of Swiger et al. (1964).

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

$$Y_{ijklmn} = \mu + S_i + C_{ij} + Y_{Sk} + A_l + D_m + e_{ijklmn} \quad \text{(model 2)}$$

where all terms as in model (1) except C_{ij} = the random effect of jth cow nested within the random effect of ith sire and A_l = the fixed effect of age at calving (in terms of three-month interval starting from <24 month, till 77 month). Heritabilities across all lactations (h^2_s) were calculated as: $h^2_s = 4\sigma^2_s/(\sigma^2_s + \sigma^2_c + \sigma^2_e)$. 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).

RESULTS AND DISCUSSION

Means and variations

Means, phenotypic standard deviations (SD), coefficients of variation (CV%) and determination (R2) of yields of milk (MY), fat (FY), protein (PY), fat-plus-protein (FPY) and carrier (CY) in the first three lactations and across all lactations are given in Table 1. As expected, means and phenotypic standard deviations of milk traits increased with advancing parity. Greater increase in 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). Results given in Table 1 indicate that estimates of standard deviation for each trait tend to increase with the increase of the mean of the trait in each lactation (a scale effect).

For the first three lactations and all lactations, estimates of CV for yield traits ranged from 11.0% to 17.8% (Table 1). Similarly, the Austrian studies (e.g. Soliman and Khalil, 1989; Soliman et al., 1990; Soliman and Khalil, 1993) reported higher variation for yield traits. The CV% for FY was higher than that for PY, which was in agreement with findings of many other studies (e.g. Soliman and Khalil, 1989; Soliman et al., 1990; Ashmawy and Khalil, 1990; Soliman and Khalil, 1993). Meyer (1985) concluded that high CV indicate that there was short-term environmental variation affecting dairy performance. In Australian cattle, the high CV could be explained by misidentification of some sires in Australian milk recording system (Meyer, 1985) which may have a reduction effect on the variance between sires. The latter author added that the high CV clearly demonstrates a substantially higher residual variance in this population (21% in Australian cattle vs 14% in British cattle). Sire variance components and heritability estimates in each lactation.

The sire of the cow affected significantly (P<0.001) all milk traits of the first three lactations (Table 2). Most of the studies evidenced this trend

(e.g. Berger et al., 1981; White et al., 1981; Soliman and Khalil, 1989; Soliman et al., 1990; Ashmawy and Khalil 1990; Soliman and Khalil; 1993).

Table 1. Means, standard deviations (SD), percentages of variation (CV%) and coefficients of deter-mination (R^2) of milk traits in the first three lactations and across all lactations of Fleckvieh records

Trait	Mean	SD	CV%	R^2 of model
First lactation				
MY	3803	608.4	14.8	0.523
FY	155	25.9	15.6	0.518
PY	155	21.5	12.9	0.519
FPY	279	45.2	15.0	0.520
CY	3486	554.9	14.8	0.523
Second lactation				
MY	4351	719.6	15.2	0.527
FY	191	31.1	16.1	0.523
PY	172	23.6	11.4	0.524
FPY	324	53.5	15.2	0.525
CY	3981	652.4	15.1	0.527
Third lactation				
MY	4731	729.6	14.3	0.523
FY	194	32.2	15.6	0.519
PY	154	23.6	14.3	0.520
FPY	350	54.4	14.5	0.520
CY	4381	679.5	14.4	0.523
All lactations				
MY	4254	783.5	11.0	0.663
FY	174	33.9	12.1	0.651
PY	168	28.7	11.5	0.669
FPY	314	58.67	11.5	0.661
CY	3949	729.3	10.8	0.590

Estimates (σ^2) and percentages (V%) of variance component 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), i.e. with advance of lactation the sire genetic variance decreases along with an increase in the nongenetic variance. The same trend was reported by many other workers (e.g. Tong et al., 1979; Karras and Schlote, 1982; Pape et al., 1983; Romberg et al., 1983; Meyer 1984; Soliman et al., 1990; Soliman and Khalil, 1993). In contrast, Meyer (1985) on Australian cattle, found that both sire and residual components increased proportionally by about 20% from the first to the second lactation for MY and FY. This suggests a scale effect associated with the increase of production from the first to the second lactation. However, Boldman and Freeman (1990) reported that the sire variance component is increased with increasing production level.

Table 2. F-ratios of least-squares ANOVA for milk traits in the first three lactations of Fleckvieh records

Source of variation	df	MY	FY	PY	FPY	CY
First lactation						
Sire	646	2.3***	2.4***	2.2***	2.4***	2.3***
Year-season	13	17.8***	11.7***	19.7***	16.3***	17.9***
Age at calving	14	11.6***	11.6***	11.7***	12.8***	11.8***
Days open	5	104.6***	81.9***	61.5***	78.7***	103.8***
Remainder df	10207					
Remainder mean square		314912	578	401	1749	359277
Second lactation						
Sire	646	2.1***	2.1***	2.2***	2.2***	2.1***
Year-season	11	22.8***	16.9***	20.5***	19.0***	22.7***
Age at calving	16	16.8***	16.3***	15.2***	16.6***	17.0***
Days open	5	98.8***	84.0***	92.4***	92.1***	99.2***
Remainder df	10202					
Remainder mean square		439366	831	472	2429	502333
Third lactation						
Sire	397	1.8***	1.7***	1.7***	1.7***	1.8***
Year-season	7	16.7***	13.7***	12.2***	13.4***	16.8***
Age at calving	12	5.2***	4.4***	4.4***	4.5***	5.2***
Days open	5	43.2***	35.1***	42.7***	40.4***	42.9***
Remainder df	4685					
Remainder mean square		459523	913	486	2588	398452

***= P<0.001.

The percentages of variance component attributable to the sire for all milk traits were moderate and ranged from 5.4% to 7.8% (Table 3). This range was lower than that of 11.1% to 13.6% reported by Soliman and Khalil (1989) on Braunvieh cattle and also lower than that of

7.5% to 10.7% reported by Soliman et al. (1990) on Pinzgauer cattle. However, the moderate variance component due to sire suggests that there is a considerable opportunity for selection in this population (McDowell et al., 1976; Aboubakar et al., 1987).

Table 3. Estimates of variance component due to sire (σ^2_s) and remainder (σ^2_e), and sire heritability estimates (h^2) for milk traits in the first three lactations of Fleckveih records

Trait	Sire		Remainder			
	σ^2_s	V%	σ^2_e	V%	h^2	SE
First lactation						
MY	24310	7.2	314913	92.8	0.29	.027
FY	49	7.8	578	92.2	0.31	.028
PY	29	6.7	401	93.3	0.27	.026
FPY	147	7.8	1750	92.2	0.31	.028
CY	27953	7.2	359278	92.8	0.29	.027
Second lactation						
MY	29100	6.2	439366	93.8	0.25	.025
FY	59	6.6	831	93.4	0.26	.026
PY	34	6.7	473	93.3	0.27	.026
FPY	179	6.9	2429	93.1	0.27	.026
CY	33391	6.2	502334	93.8	0.25	.025
Third lactation						
MY	29412	6.0	459524	94.0	0.24	.037
FY	52	5.4	914	94.6	0.22	.036
PY	28	5.5	487	94.5	0.22	.036
FPY	153	5.6	2588	94.4	0.22	.036
CY	25801	6.1	398453	93.9	0.24	.037

Moderate sire heritabilities concurring with moderate sire variance component estimates were obtained (Table 3). However, heritability estimates of yield traits agreed with those previously published (Soliman and Khalil, 1993); most estimates ranged between 0.2 to 0.3. The present estimates were larger than those reported by Meyer (1985) (0.1-0.2) on Australian cattle, while they were lower than those estimates reported in Austrian studies (e.g. Soliman and Khalil 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. Boldman and Freeman (1990) reported that estimates of each variance component (genetic, permanent and

remainder) increased with the increasing production level. Method of eliminating the herd effect may be one of the reasons for the variability in estimated heritabilities (Danell, 1982). However, there are several factors influencing the level of estimated heritability. Among these are:

(1) The selection of sires, which is the reason why only unimproved sires were included in different genetic studies (Pedersen, 1980; Danell, 1982).

(2) Culling of cows can be expected to influence variation, both between and within progeny. Thus, the heritability estimates may therefore be biased downwards (Danell, 1982).

(3) Days in milk and changing of restriction imposed on records of cows could be effective (Schutz et al., 1990),

(4) Expression of genetic difference may be greater in regions where cows are provided with a better environment for performance (Schutz et al., 1990).

(5) Heritabilities could be biased upward by use of bulls from different population, i.e. importing semen from other countries (Santus et al., 1993).

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 (Tong et al., 1979; Karras and Schlote, 1982; Pape et al., 1983; Romberg et al., 1983; Alps and Averdunk, 1984; Meyer, 1984; Swalve and Van Vleck, 1986; Reinhardt et al., 1987; Soliman et al., 1990; Soliman and Khalil, 1993). Multiple possible explanations for the decline of h^2 with advance of lactation could be summarized as:

(1) This may be due in part to an increase in error variance in later lactations (Table 2) since additional sources of variation such as days open (i.e. calving interval) have more influence on later lactations than on the first lactation (Tong et al., 1979).

(2) Maternal effects, which have smaller effects in succeeding lactations, may be one of the causes for higher heritability in first lactation (Van Vleck and Bradford, 1966).

(3) A fairly large increase in the non-additive genetic variance and a decrease in the genetic variance from the first to subsequent lactations could be another

cause (Tong et al., 1979; Meyer, 1984; Soliman and Khalil, 1993).

(4) If all genes have equal effects, the first lactation is controlled by more pairs of genes than the second lactation or if the same number of genes control both lactations, they have larger effects in the first lactation (Soliman and Khalil, 1993).

(5) The presence of constant genetic effects and an increase in the environmental effects in the second lactation will lead to lower estimates of heritability of the second lactation. Other environmental factors, such as variation in length of dry period, calving interval and mastitis which could not be fully accounted for by the model, would logically seem to add more variation in the second and later lactations (Tong et al., 1979).

Heritabilities across lactations and repeatabilit estimates

The cow contributed significantly (P<0.001) to the variation of all milk traits (Table 4). This is in full agreement with findings of most available literature (e.g. Camoens et al., 1976; Soliman and Khalil, 1989; Soliman et al., 1990; Soliman and Khalil, 1993).

Table 4. F-ratios of least-squares ANOVA for milk traits across all lactations of Fleckvieh records

Source of variation	df	MY	FY	PY	FPY	CY
Sire	649	2.6***	2.6***	2.6***	2.7***	2.5***
Cows within sire	10239	3.3***	3.0***	2.1***	2.9***	3.2***
Year-season	15	21.3***	16.8***	28.5***	17.9***	21.3***
Age at calving	18	107.6***	115.8***	900.5***	135.1***	241.8***
Days open	5	121.7***	84.8***	39.2***	96.8***	81.3***
Remainder df	18284					
Remainder mean square		217634	444	374	1313	239833

***= P<0.001.

The percentages of variance component (V%) attributable to cow-within sire for milk traits were high and ranged from 27.4% to 43.3% (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, 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 (Camoens et al., 1976; Soliman and
Khalil, 1993).

Fairly moderate or slightly high repeatability
estimates (t) for all milk traits were obtained as
showed in Table 5. The estimates ranged from 0.33 to
0.49. This range seems in full agreement with that range
of 0.40 to 0.47 reported by Soliman and Khalil (1993)
for milk, fat and protein yields of Fleckvieh cattle
while it was lower than that of 0.69-0.74 reported by
Soliman and Khalil (1989) on Braunvieh cattle.

Table 5. Estimates (σ^2) andpercentages (V%) ofvariance
component due to sire (σ^2_s), cows within sire
($\sigma^2_{c:s}$) and remainder (σ^2_e) and estimates of
repeatability (t) and heritability (h^2) for
milk traits in all lactations of records

Trait	Sire		Cows within sire		Remainder		t	h^2
	σ^2_a	V%	$\sigma^2_{c:s}$	V%	σ^2_c	V%		
MY	24937	3.8	185198	43.3	217635	50.9	0.49	0.23
FY	48	6.0	325	39.8	445	54.2	0.46	0.24
PY	28	5.1	152	27.4	374	67.5	0.33	0.20
FPY	146	6.1	938	39.1	1313	54.8	0.45	0.25
CY	26434	5.7	197684	42.6	239833	51.7	0.48	0.23

+ Standard errors of heritabilities ranged from 0.018
  to 0.021, while for repeatabilities were 0.01.

Estimates of repeatability (t) in Table 5, indicate
that MY and CY are more repeatable than that of FY and
PY. Camoens et al. (1976) reported that MY is slightly
more repeatable than FY. Also, Welper and Freeman (1992)
and Soliman and Khalil (1993) evidenced the same trend.
More caution must be paid when considering the PY as a
selection objective since it has the lowest
repeatability estimate (0.33). Lower repeatability

estimate for protein relative to other milk traits was also reported by Tong et al. (1977) and Soliman and Khalil (1993). This result indicates that an increase in accuracy could be achieved in characterization of the performance of the cow for PY trait by having several records rather than just one.

Across all lactations, repeatability estimates were higher than those corresponding estimates of h^2 (Table 5). The repeatabilities for milk traits were twice as large as the corresponding h^2 estimated across all lactations. This is because relationship between consecutive lactations generally increases as the cow get older, i.e. repeatability of consecutive records of the same cow tends to increase, while the h^2 estimates tend to decrease with the advance of lactation (Sorensen et al., 1987; Soliman and Khalil, 1989; Soliman et al., 1990; Soliman and Khalil, 1993). Selection based on culling policies, which was commonly applied by dairy cattle breeders in the second and succeeding lactations, may be responsible for decreasing additive genetic variance (Soliman and Khalil, 1993).

Furthermore, 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) and Berger et al. (1981). This trend appears to depend on the sample examined.

Correlations
   (i) Genetic correlation (r_G)

Genetic correlations (r_G) in the first three lactations between milk traits were positive and high (Table 6). Similarly, reviewed estimates (Soliman and Khalil, 1993) of r_G among yield traits of Fleckvieh cattle were, in general, positive and significantly higher estimates ranged from 0.84 to 0.99. These high correlations were evidenced for Braunvieh and Friesian cattle (Peterson et al., 1982; Meyer, 1985; Soliman and Khalil, 1989; Ashmay and Khalil, 1990; Welper and Freeman, 1992; Santus et al., 1993).

The estimates of r_G in the first lactation ranged from 0.90 to 1.00 between MY and other yield traits; from 0.90 to 0.99 between FY and others, from 0.91 to 0.97 between PY and others; from 0.92 to 0.97 between FPY and others and from 0.91 to 1.00 between CY and others (Table 6). In the second and third lactations, the same

Table 6. Estimates of genetic (r_G), phenotypic (r_P) and environmental (r_E) correlation for milk traits in the first three lactations and across all lactations of Fleckvieh records

Traits correlated	First lactation			Second lactation			Third lacation			All lactations		
	r_G ± SE	r_P	r_E	r_G±SE	r_P	r_E	r_G+SE	r_P	r_E	r_G+SE	r_P	r_E
MY &FY	.90+.013	.90	.89	.88+.016	.89	.90	.88+.027	.88	.88	.88+.012	.89	.89
PY	.91+.016	.83	.80	.91+.013	.92	.92	.88+.025	.92	.93	.90+.012	.83	.81
FPY	.92+.011	.91	.90	.90+.013	.93	.93	.89+.023	.92	.93	.90+.010	.92	.93
CY	1.00+.000	1.00	1.00	1.00+.000	1.00	1.00	1.00+.000	1.00	1.00	.99+.001	.98	.98
FY &PY	.92+.015	.81	.76	.96+.008	.90	.88	.96+.016	.89	.88	.94+.008	.81	.78
FPY	.99+.003	.96	.95	.99+.002	.98	.98	.99+.003	.98	.98	.99+.001	.98	.97
CY	.91+.012	.91	.90	.90+.015	.90	.90	.86+.030	.87	.87	.88+.012	.88	.88
PY &FPY	.97+.005	.94	.93	.99+.003	.97	.96	.99+.005	.96	.96	.98+.004	.89	.87
CY	.92+.014	.84	.81	.92+.011	.93	.93	.86+.028	.91	.92	.91+.010	.88	.87
FPY&CY	.93+.009	.92	.92	.92+.011	.94	.94	.87+.026	.91	.92	.90+.010	.91	.91

trend was observed but with a decreasing magnitude.

Estimates of r_G between MY and PY in each lactation were slightly higher than those correlations between MY and FY (Table 6). The same trend was noticed between CY and PY and CY and FY. MY was more associated with PY than with FY as indicated in several studies (e.g. Hargrove et al., 1981; Miller et al., 1981; Peterson et al., 1982; Monardes and Hayes, 1985; Meyer, 1985; deJager and Kennedy, 1987; Sorensen et al., 1987; Soliman and Khalil, 1993). The estimates of r_G between MY and both FY and PY indicate that the progress involved in increasing PY is expected to be the same as that achieved for FY, although the estimates of r_G between FY or PY with MY are nearly the same. Although the cost of producing an unit of fat requires twice as much feed energy as the production of an equal weight of protein (Dommerholt et al., 1978), it seems necessary, from the economical view point and from that of human health, to pay more attention to select for milk with more protein than for more milk with more fat.

MY was strongly genetically associated with CY (Table 6), i.e. part-whole relationship was evidenced. Anunity estimate of r_G among MY and CY was also reported by deJager and Kennedy (1987) for Friesian cattle.

(ii) Phenotypic correlation (r_p)

Phenotypic correlations of MY and other yield traits were high, ranging from 0.83 to 1.00 (Table 6). The same trend was observed for CY with other yield traits. In the first three lactations and across all lactations, phenotypic correlations among traits including protein were relatively low. Phenotypic correlations of MY and PY in second and third parities were higher than those of MY and FY (Table 6). These findings are in agreement with other investigations (e.g. Tong et al., 1977; Hargrove et al., 1981; Miller et al., 1981; Peterson et al., 1982; Meyer, 1985; deJager and Kennedy, 1987; Sorensen et al., 1987; Soliman and Khalil, 1989; Ashmawy and Khalil, 1990; Schutz et al., 1990; Soliman et al., 1990; Welper and Freeman, 1992; Soliman and Khalil, 1993).

Comparing estimates of r_G with their corresponding estimates of r_p (Table 6), it seems that seven estimates out of ten of r_G were larger than estimates of r_p in the first lactation, while in the second or third lactation

three estimates of r_G out of ten were larger than their corresponding estimates of r_P. The same findings were reported by Soliman and Khalil (1993) for Fleckvieh cattle. In most available literature, r_P estimates were larger than their corresponding estimates of r_G in the same investigation (e.g. Hargrove et al., 1981; Hudson and Van Vleck, 1982; deJager and Kennedy, 1987; Sorensen et al., 1987; Ashmawy and Khalil, 1990). The high r_P's obtained in the present study gives, in practice, a considerable advantage in management and culling policy for such breed of dairy cattle.

(iii) Environmental correlation (r_E)

Environmental correlations among milk traits are presented in Table 6. These estimates were positive and high in magnitude, ranging from 0.76 to 1.00, 0.88 to 1.00 and 0.87 to 1.00 in the first, second and third lactations, respectively. Comparable estimates were reported by Soliman and Khalil (1993) for milk, fat and protein yield traits on the same breed. Estimates of r_E increased from the first to second lactation and decreased thereafter (Table 6). Soliman and Khalil (1993) on the same breed found that the estimates of r_E increased with the advance of lactation in most cases for MY, FY and PY. Non-genetic effects, such as nutrition, not only increase yield but make the individualization of superior genotypes more difficult to appear (Santus et al., 1993). A sizable portion of the environmental variation seems to be due to variation in record length (Meyer, 1985).

Estimates of r_E between milk and protein are higher than those of milk and fat in the second and third lactations, while the reverse was found in the first lactation (Table 6). This may indicate that FY is more affected by environment than PY with advance of lactation. This may be partly due to high yielders increased more in fat with age or because animals with a high fat content increased more in yield with age (Barker, 1966). Estimates of r_E between FPY with FY are larger than the correlations of FPY with PY (Table 6).

Estimates of correlations show that r_P and r_E were higher than the corresponding estimates of r_G in the second and third lactations for yield traits (Table 6). The same findings were reported by Soliman and Khalil (1993). These results indicate that these relationships

were influenced by additional environmental factors in lactations after the first one.

The r_P were nearly equal in sign and magnitude with the r_E (Table 6). This was in agreement with the conclusion of Weller et al. (1985) for Holstein cattle. The close estimates of both r_G and r_E may indicate that yield traits affected by genetic and environmental sources of variation through different physiological mechanisms (Falconer, 1989). This conclusion may lead to state that, in partly, any improvement in environent (management, feeding, housing ... etc) may have a reflection on the genetic progress achieved through selection programmes.

CONCLUSION AND GENERAL CONSIDERATIONS

First lactation of the present study had the highest heritability estimates and it gives more 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 in 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 lactation, 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 mature lactations. However, several studies (i.e. Soliman and Khalil, 1993) have shown that sires can be ranked on the daughter's first lactation records 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 and Strandberg, 1985). Since overproduction of fat is the main problem in current markets in Eroupe and USA, the desired breeding goal would be changed to increase the protein percentage, while holding fat percentage constant (Young et al., 1986; Welper and Freeman, 1992). 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. Unfortunatly, heritability estimates obtained here in each lactation for Fleckvieh cattle were lower for PY than that for FY yield. In practice, selection for yield traits may be the most economically rewarding, considering current payment systems, while selection for percentages would result in large sacrifice in genetic gains of yield traits. Because of the genetic correlations of PY and FY 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 (Welper and Freeman, 1992).

Fairly moderate to high repeatabilities obtained here may indicate that records beyond the first lactation add little information in predicting the producing ability of the cow (Karras and Scholte, 1982; Pape et al., 1983; Reinhardt et al., 1987; 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, phenotypic and environmental correlations attained here for 305-day milk traits will lead to conclude that high gain would come from direct selection for composite trait of FPY. Consequently, these correlations are sufficiently high to state that an initial decision can be made on the basis to select for FPY of the first lactation 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 the cows ,and bulls for breeding (Soliman and Khalil, 1993). The greater relationship of MY and PY than MY and FY suggested that correlated responses to single-trait selection for MY ought to be greater for PY than for FY. Since correlations of CY with FY, PY and FPY were higher than those correlations of MY 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 FPY.

High estimates of environmental correlations among milk traits are of interest for herd management purposes. Such environmental associations among yield traits are relatively important within a given herd

(Soliman and Khalil, 1993). These high estimates of correlation emphasize the large environment influences the cow record, which must be considered in the selection program to achieve more genetic progress along the time.

ACKNOWLEDGEMENTS

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تقدير المقاييس الوراثية لصفات إنتاج اللبن من سجلات الفلاكفى الغير خاضعة للإستبعاد

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استخدمت سجلات ادرار ٣٠٥ يوم لتقديـر التباينـات والتغايرات الوراثية والمظهرية والبيئية لصفات محصول اللبن ، محصول الدهن والبروتين وذلك للثلاث مواسم ادرار الأولى وكذلك لكل المواسم مجتمعة واقتصرت البيانـات المستخدمة فى التحليل على تلك البيانات الخاصة بالأبقار التى لها معلومـات فى موسم الأدرار الأول والمواسم التالية له .استخدم بناءا على ذلك ٢٦٨٧٤ سجل إدرار مستخلصة من ٥٠٧٨٨ سجل. كـان عدد السجلات فى الثلاث مواسم إدرار الأولى على التوالى هـى ١٠٨٨٦، ١٠٨٨١ , ٥١٠٧ لبنـات أنصاف أشقه تمثل ٦٤٧، ٦٤٧، ٣٩٧ أب بنفس الترتيب . ويمكن تلخيص النتائج المتحصل عليها من تلك الدراسة فيما يلى:

١- ازدادت المتوسطات والانحرافات القياسية لصفـات اللبن بتقدم ترتيـب موسم الادرار وكانت الزيادة فى صفات محصول اللبن فى الموسم الثانى عن الموسم الأول أكبرمن زيادتها فى الموسم الثالث عن الثانى.

٢- تراوحت معاملات الاختلافات فى صفات اللبن بين ١٢,٩ الى ١٧,٢٪ فى موسم الادرار الأول وبين ١١,٤ الى ١٧,٨٪ فى موسـم الادرار الثانى. وكانت معاملات الإختلاف لمحصول الدهن أكبر مـن نظيراتها لمحصول البروتين.

٣- كان لأب البقرة تأثيرا معنويا عاليا على جميـع صفات اللبن. هـذا وقد إنخفضت نسبة التباين الأبوى لجميع صفات اللبن بتقدم موسم الإدرار مـن الأول (٦,٧-٧,٨٪) إلى الثالث (٥,٤-٦,١٪). كانت قيم المكافىء الوراثى لصفات اللبن متوسطة حيث تراوحت القيم بين ٠,٢٢ إلى ٠,٣١ إلا أنها تنـاقصت بتقدم موسم الإدرار مـن الأول إلى الثالث. كـانت قيم المكافىء الوراثى لمحصول البروتين لمواسم الإدرار الثلاثة الأولى أقل من مثيلاتها لمحصول الدهن بينما كانت قيم المكافىء الوراثى لمحصول اللبن الخالى مـن اللدهن والبروتين متقاربة من بعضهما.

٤ – كان لتأثير البقـرة داخل الأب تـأثيرا معنويا عاليا على جميـع الصفـات المدروسة حيث تراوحت نسبة التباين الراجعة للبقرة من ٢٧٫٤ إلى ٤٣٫٤٪. وكانت قيم المعامل التكرارى لصفات اللبن المدروسة متوسطة أو عالية قليـلا حيث تراوحت القيم بين ٠٫٣٣ إلى ٠٫٠٤٩.

٥ – كانت معاملات الإرتباط الوراثى فى الثـلاث مواسم إدرار الأولى بين صفات المحصول عالية وموجبة حيث تراوحت القيم بين ٠٫٨٧ إلى ١٫٠. كذلك كانت معاملات الإرتباط المظهرى لصفات اللبن موجبة وعالية حيث تراوحت القيم بين ٠٫٨٣ إلـى ١٫٠. ولقد لوحـظ نفس الإتجـاه بالنسبة لمعاملات الإرتباط البينى. كانت قيم معـاملات الإرتباط المظهرى والبينى أعلى من مثيلاتها لمعاملات الإرتبـاط الوراثى فى موسمى الإدرار الثانى والثالث.

لذلك ومن الناحية العلمية وتبعا لنظام التسعير الحالى لمحصول اللبن فى الولايات المتحدة وأوروبا فإن النتائج المتحصل عليهـا توضح بأن الإنتخاب لزيادة محصول البروتين سوف تؤدى أيضا إلى زيادة محصول اللبن بمعدل أفضل من الإنتخاب لمحصول الدهن والذى يعد من الناحية الإقتصاديـة أكثر فائدة لمنتجى الألبان. ومن الناحية الإقتصادية أيضا فإنه يبدو أفضلية تحويل إتجاه الإنتخاب لزيادة محصول البروتين بدلا من الإنتخاب لزيادة محصول الدهن.