RESULTS AND DISCUSSION

4. RESULTS AND DISCUSSION

4.1. GENETIC ASPECTS

4.1.1 Means and variations

Means, phenotypic standard deviations (SD), coefficients of variation (CV%) and determination (R^2) 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 16. 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, 1984; Soliman et al., 1990; Soliman and Khalil, 1993). Results given in Table 16 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 16). Similarly, the Austrian studies (Soliman, 1984; 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. The high CV estimates found in Australian cattle 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 same 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).

4.1.2 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 17). Most of the studies evidenced this trend (e.g. Bttatia, 1980; Berger et al., 1981; El-Kaschab et al., 1981; White et al., 1981; Soliman, 1984; Reis and Silva, 1988; Ponce De Leon and Hernandez, 1988; Soliman and Khalil, 1989; Soliman et al., 1990; Ashmawy and Khalil 1990; Soliman and Khalil, 1993).

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

Table (16). Means, standard deviations (SD), Percentages of variation (CV%) and coefficients of determination (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
<u>First lactation</u>				
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
<u>Second lactation</u>				
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	652.0	15.1	0.527
<u>Third lactation</u>				
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
<u>All lactations</u>				
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	727.3	10.8	0.590

Table (17). 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.

lactations are presented in Table 18. 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 18), 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. **Wilcox et al., 1971; Tong et al., 1979; Karras and Schlote, 1982; Pape et al., 1983; Romberg et al., 1983; Meyer, 1984; Soliman, 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 milk and fat yield traits. 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.

The percentages of variance component attributable to the sire for all milk traits were moderate and ranged from 5.4% to 7.8% (Table 18). 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. On the other side, it was larger than that of 2.6 to 8.0% reported by **Soliman and Khalil (1993)** on Fleckvieh 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., 1987a**).

Moderate sire heritabilities concurring with moderate sire variance component estimates were obtained (Table 18). However, heritability estimates of yield traits agreed with those previously published (**Wilcox et al, 1971; 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, 1984; 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 components (genetic, permanent and remainder) increased with increasing production level. The 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 (**Auran, 1976; Pedersen, 1980; Danell, 1982**).

Table (18). 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 Fleckvieh records.

	Sire		Remainder			
Trait	σ^2_s	V%	σ^2_e	V%	h^2	SE
<u>**First lactation**</u>						
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
<u>**Second lactation**</u>						
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
<u>**Third lactation**</u>						
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

(2) Culling of cows can be expected to influence variation, both between and within progeny. Thus, the heritability estimates may therefore be biased downwards (Ronningen, 1967; 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 18). Most of the previous studies evidenced this trend (Alps, 1971; Tong et al., 1979; Karras and Schlote, 1982; Pape et al., 1983; Romberge et al., 1983; Alps and Averdunk, 1984; Meyer, 1984; Soliman, 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 18) 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 lactation, 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 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.

(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 of second and later lactations (Tong et al., 1979).

(6) In some situations, several sires were used in a single herd and a few in just one year and season. For such a case, the herd and age effects (i.e. some of the genetic contributions from the sire) might have also been removed.

4.1.3 Heritabilities across lactations and repeatability estimates

The cow contributed significantly ($P<0.001$) to the variation of all milk traits (Table 19). This is in full agreement with findings of most available literature (e.g. **Camoens et al., 1976; Soliman, 1984; Soliman and Khalil, 1989; Soliman et al., 1990; Soliman and Khalil, 1993**).

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 20). 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**). Furthermore, estimates from the first lactation are higher than those estimates from all lactations (Table 20). This notation is typically found by **Tong et al., (1979)** and **Berger et al. (1981)**. This trend appears to depend on the sample examined.

Fairly moderate or slightly high repeatability estimates (t) for all milk traits were obtained as showed in **Table 20**. 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.

Estimates of repeatability (t) shown in **Table 20**, indicate that **MY** and **CY** are more repeatable than that of **FY** and **PY**. **Butcher and Freeman (1968)** and **Camoens et al. (1976)** reported that **MY** is slightly more repeatable than **FY**. Also, **Gaunt et al. (1968), Gacula et al. (1968), Wilcox et al. (1971), 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 **Gacula et al. (1968), 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.

Table (19). 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 wintin 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.

Table (20). Estimates (σ^2) and percentages (V%) of variance 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 Fleckvieh records.

	Sire		Cows within sire		Remainder			
Trait	σ^2_s	V%	$\sigma^2_{c:s}$	V%	σ^2_e	V%	t+	h^{2}+
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.

Across all lactations, repeatability estimates are higher than those corresponding estimates of h^2 since the repeatabilities are the upper limit of the heritabilities (Table 20). 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 (Soliman, 1984; 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).

4.1.4 Correlations

(1) Genetic correlation (r_G)

Genetic correlations (r_G) in the first three lactations between milk traits were positive and high (Table 21). Similarly, reviewed estimates of r_G among yield traits of Fleckvieh cattle were, in general, positive and significantly higher and ranged from 0.84 to 0.99 (Foster, 1971; Soliman, 1984; Soliman and Khalil, 1993). These high correlations were evidenced for Braunvieh and Friesian cattle (Gaunt et al., 1968; Bergman, 1969; Wilcox et al., 1971; Peterson et al., 1982; Soliman, 1984; Meyer, 1985; Soliman and Khalil, 1989; Ashmawy 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 21). In the second and third lactations, the same 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 21). 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; Manfredi et al., 1984; Soliman, 1984; Monardes and Hayes, 1985; Meyer, 1985; Wilmink, 1986; 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. Since the

Table (21). 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.

Traits correlated	First lactation $r_G \pm SE$	r_P	r_E	Second lactation $r_G \pm SE$	r_P	r_E	Third lacation $r_G \pm SE$	r_P	r_E	All lactations $r_G \pm SE$	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

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 21), i.e. part-whole relationship was evidenced. An unity estimate of r_G among MY and CY was also reported by **Wilmink (1986) and 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 in the first lactation, from 0.89 to 1.00 in the second lactation and from 0.88 to 1.00 in the third lactation (Table 21). 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 most parities were higher than those of MY and FY (Table 21). These findings are in agreement with other investigations (e.g. **Butcher et al., 1967; Tong et al., 1977; Hargrove et al., 1981; Miller et al., 1981; Peterson et al., 1982; Manfredi et al., 1982; Soliman, 1984; Meyer, 1985; Wilmink, 1986; 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 21), 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 out of ten of r_G 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. **Forster, 1971; Hardie et al., 1978; Hoque and Hodges, 1980; Hargrove et al., 1981; Hudson and Van Vleck, 1982; Wilmink, 1986; 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) <u>Environmental correlation (r_E)</u>

Estimates of environmental correlation are presented in Table 21. 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 (Table 21). Comparable estimates were reported by **Soliman and Khalil (1993)** for milk, fat and protein yield traits on the same breed. It has been shown that (Table 21) the r_E increased from first to second lactation and decreased thereafter. **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 milk, fat and protein yields. Non-genetic effects, such as nutrition, not only increase the 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 is higher than those of milk and fat in the second and third lactations, while the reverse was observed in the first lactation. This may indicate that the 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 and Robertson, 1966**).. Estimates of r_P between FPY with FY are larger than the correlations of FPY with PY (Table 21).

Estimates of correlation 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 21). The same findings were reported by **Soliman and Khalil (1993)**. These results indicate that these relationships are 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 21**). This is 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 part any improvement in environment (management, feeding, housing, ...etc.) may have a reflection on the genetic progress achieved through selection programmes.

4.2 Sire Evaluation Methods

4.2.1 Estimates of sire transmitting ability (STA)

Sire transmitting abilities (STA) were estimated by procedures of contemporary comparison (CC), ordinary least square (OLS), best linear unbiased predictor without A^{-1} (BLUP1) and BLUP considering restricted maximum likelihood (REML) in estimation of variance components (BLUP2). Considering all sires, the minimum and maximum estimates of STA are presented in Table 22. The difference (and the average difference) between minimum and maximum values of STA for different methods of sire evaluation are also illustrated in Table 22. For BLUP2, BLUP1, OLS and CC methods, there was a difference of 1101, 1255, 1289 and 2371 Kg for MY, respectively. The same trend of differences were also observed for CY (1032, 1177, 1210 and 2231 Kg), FY (45, 51, 53 and 104 Kg), PY (30, 34, 36 and 70 Kg) and FPY (74, 85, 87 and 176 Kg). For all traits, the largest differences were obtained by CC method and the lowest differences were observed by BLUP2 method (Table 22).

For all milk traits, the differences in STA for OLS were much lower than these for CC (Table 22). Miller et al. (1967) showed that the largest difference in STA estimated by CC was 1672 Kg for MY and 58.1 Kg for FY, while the lowest differences for OLS were 1519 and 54.9 Kg, respectively. Raheja (1992) found that the lowest difference (548 Kg) in STA was with CC, while the largest difference (1956 Kg) was recorded by OLS, followed by BLUP (1098 Kg).

The differences in estimates of STA for BLUP1 were slightly larger than those for BLUP2 (Table 22). For MY, Keown (1974) found that the difference in STA for BLUP with A^{-1} was smaller than BLUP without A^{-1} (1123 vs 1260 Kg). Everett and Keown (1984) reported that lower difference was obtained by BLUP with A^{-1} than BLUP without A^{-1} (245 vs 443 Kg for MY). A reverse trend for MY was found by Sadek et al. (1993) who reported slightly larger estimates of STA in BLUP with A^{-1} than those of BLUP without A^{-1} (340 vs 325 Kg).

For all milk traits, differences in STA estimated by OLS are nearly similar to estimates of STA obtained by BLUP1 (Table 22). Therefore, both methods have the same trend in the evaluation of sires. Similarly, Keown (1974) found that the difference in STA was slightly greater for OLS than for BLUP without A^{-1} (1280 vs 1260 Kg). Raheja (1992) reported that differences in estimates of STA obtained by OLS were larger than those estimated by BLUP without A^{-1} (1956 vs 1098 Kg for MY).

Differences in STA estimated by OLS for all traits were larger than those estimated by BLUP2 (Table 22). Keown (1974) reported that differences in STA

Table (22). Minimum and maximum values for sire transmitting abilities estimated by best linear unbiased predictor (BLUP) considering REML in estimation of variance component (BLUP2), BLUP without A^{-1} (BLUP1), ordinary least-squares (OLS) and contemporary comparison (CC),

Trait*	All sires				Top 10 sires
	Minimum	Maximum	difference	average**	difference
MY					
BLUP2	-347	754	1101	16.0	515
BLUP1	-427	828	1255	18.1	561
OLS	-446	843	1289	18.6	574
CC	-878	1493	2371	34.3	1050
FY					
BLUP2	-15	30	45	0.7	21
BLUP1	-18	33	51	0.7	23
OLS	-19	34	53	0.8	24
CC	-37	67	104	1.5	48
PY					
BLUP2	-10	20	30	0.4	13
BLUP1	-12	22	34	0.5	14
OLS	-13	23	36	0.5	14
CC	-28	42	70	1.0	32
FPY					
BLUP2	-25	49	74	1.1	35
BLUP1	-31	54	85	1.2	38
OLS	-32	55	87	1.3	38
CC	-66	110	176	2.6	78
CY					
BLUP2	-323	709	1032	15.0	488
BLUP1	-398	779	1177	17.1	535
OLS	-416	794	1210	17.5	545
CC	-823	1408	2231	32.3	1002

* Number of sires used for evaluation was 69 sires; each had at least 100 daughters.

** average= difference value divided by number of sires.

estimated by OLS were larger than those estimated by BLUP with A^{-1} (1280 vs 1123 Kg for MY).

As expected, the differences in STA estimated by CC were much larger than those estimated by BLUP without A^{-1} (Table 22). On the contrary, Raheja (1992) reported that differences in STA estimated by CC were much lower than those estimated by BLUP without A^{-1} (548 vs 1098 Kg for MY).

When considering the first top ten sires (Table 22), we can find that the differences between maximum and minimum values in STA were smaller than that when considering all the sires list. For all milk traits, the lowest differences in STA of the top ten sires were recorded by BLUP2 while the largest estimates were recorded by CC (Table 22). Estimates of BLUP2 vs CC were 515 vs 1050 Kg for MY, 21 vs 48 Kg for FY, 13 vs 32 Kg for PY, 35 vs 78 Kg for FPY and 488 vs 1002 Kg for CY. Raheja (1992) found that estimates of average difference between the top ten sires in STA of MY (31.0, 119.7 and 52.2 Kg in CC, OLS and BLUP, respectively) were larger than those between all sires (14.0, 50.2 and 28.2 Kg, respectively). Sadek et al. (1993) reported that the average difference in STA of MY between top ten sires was larger than that between all sires (10.1 vs 4.11 Kg in BLUP without A^{-1} and 11.0 vs 4.31 Kg in BLUP with A^{-1}).

Figures given in Table 23 show that percent of sires that are common between BLUP2 and BLUP1 or between BLUP2 and OLS ranged from 90 to 100% (i.e. the same top ten sires in BLUP2 are found in BLUP1 and OLS). For CC vs BLUP2, percentages of common sires between these two methods ranged from 70 to 90%. The percentages of sires remaining in the same position (i.e. don't change their rank) ranged from 70 to 80% for MY, PY and CY; from 50 to 60% for FY and FPY when comparing BLUP1 or OLS with BLUP2, while they ranged from 20 to 30% when comparing CC with other methods (Table 23).

Among all sires, percentages of sires who had negative estimates of STA for OLS, BLUP1, BLUP2 and CC are 57, 57, 57 and 55% for MY; 49, 52, 52, and 54% for FY; 51, 52, 49 and 51% for PY; 54, 55, 54 and 54% for FPY and 55, 57, 57 and 55% for CY. Across all methods, the largest average of percentage of negative estimates of STA was recorded by BLUP1 (55%), followed by BLUP2 and CC (54%), while the lowest average was recorded by OLS (53%). Keown (1974) found that the percentages of negative estimates of STA were 46, 46 and 27% for OLS, BLUP1 and BLUP2, respectively. Raheja (1992) found that the percentages of negative estimates of STA were 74, 67 and 62% for OLS, BLUP1 and CC, respectively. The same author added that the overall ranking of sires did not change much between OLS and BLUP1.

Among all traits, the largest percent of negative STA was recorded for MY (57%) followed by CY (56%), FPY (54%), FY (52%), while the lowest percent was

Table (23). Percentages of sires common (CS) and remaining in the same position (RS) in different methods of sire evaluation compared with BLUP2 for different milk traits.

Trait and comparison	BLUP1 vs BLUP2	OLS vs BLUP2	CC vs BLUP2
MY			
% CS	100	100	80
% RS	70	70	20
FY			
% CS	100	100	90
% RS	60	60	30
PY			
% CS	100	100	90
% RS	80	70	20
FPY			
% CS	100	100	90
% RS	50	50	30
CY			
% CS	100	90	70
% RS	70	80	20

recorded for PY (51%). Gacula et al. (1968) found that percentages of negative expected breeding values were 40, 60 and 40% for MY, FY and PY, respectively. Schaeffer et al. (1975) found that the percentages of negative values of sire proofs were 36.7% for MY and 56.7% for FY.

Table 24 shows the distribution of the absolute difference among estimates of STA obtained by different methods of sire evaluation. These results showed that the smallest absolute differences between BLUP2 vs BLUP1 and BLUP2 vs OLS were recorded by the largest number of sires. In this respect and for MY and CY, there were about 83% or 72% of sires (57 sires out of 69) representing an absolute difference of <40 Kg in comparisons of BLUP2 vs BLUP1 and BLUP2 vs OLS, respectively. But there were less than 12% of the sires representing an absolute difference of ≥60 Kg in these two comparisons. The reverse trend was observed in comparison of BLUP2 vs CC (i.e. the largest number of sires was found in the largest absolute difference and the smallest number of sires was found in the smallest absolute difference). Similar trends were observed for other milk traits of FY, PY and FPY (Table 24). For comparison of BLUP with and without A^{-1}, Sadek et al. (1993) found that the largest number of sires (59 out of 79) was presented in the small absolute difference of <10 Kg, while the smallest number of sires (2 out of 79) was presented in the largest absolute difference of 40-49 Kg.

4.2.2 Criteria for comparison of methods

The criteria for judging the merits of different methods of sire evaluation are the correlations between these methods such as Product-moment correlation, Spearman-rank correlation and Kendall-rank correlation (Hargrove et al., 1975; Kennedy and Moxley, 1977; Danell and Eriksson, 1982; Kemp et al., 1984; Vij and Tiwana, 1988; Raheja, 1992). Another criterion useful and helpful in judging the merits of alternatives of sire evaluation methods is the standard error (SE) of each method (Miller et al., 1967; Henderson, 1974; Ufford et al., 1979; Jensen, 1980; Kumar and Narian, 1980; Erikson and Danell, 1984; Raheja, 1992). Sums of squares of difference (SSD) between estimates of STA obtained from the chosen (thought to be ideal) method and from all other methods were also computed (Kemp et al., 1984). Results of these criteria of evaluation are illustrated below.

4.2.2.1 Product-moment and rank correlations

The product-moment correlations (r_{PM}) between all combinations of two methods of BLUP2, BLUP1 and OLS were greater than 0.992 (Table 25). These figures clearly demonstrate the closeness between both of BLUP2 and each of BLUP1 and OLS methods. Consequently, any computerized method (BLUP or OLS)

Table (24). Distribution of the absolute difference (Kg) among STA estimates calculated by BLUP1, OLS and CC relative to BLUP2 for different milk traits.

Trait	Absolute difference (Kg)	BLUP2 vs BLUP1 No. of sires	%	BLUP2 vs OLS No. of sires	%	BLUP2 vs CC No. of sires	%
<u>MY</u>							
	<20	42	60.9	36	52.2	4	5.8
	20-39	15	21.7	14	20.3	4	5.8
	40-59	4	5.8	9	13.0	5	7.2
	60-79	7	10.1	4	5.8	7	10.2
	80-99	1	1.5	5	7.2	4	5.8
	≥100	0	0.0	1	1.5	45	65.2
<u>FY</u>							
	<1	36	52.2	31	44.9	1	1.5
	1	19	27.5	18	26.1	3	4.3
	2	7	10.1	8	11.6	8	11.6
	3	6	8.7	4	5.8	8	11.6
	4	1	1.5	8	11.6	49	71.0
<u>PY</u>							
	<1	33	47.8	30	43.5	4	5.8
	1	24	34.8	20	29.0	9	13.1
	2	9	13.0	10	14.5	8	11.6
	3	3	4.4	6	8.7	5	7.2
	4	0	0.0	3	4.3	43	62.3
<u>FPY</u>							
	<1	23	33.3	18	26.1	1	1.5
	1-2	32	46.4	29	42.0	6	8.7
	3-4	8	11.6	10	14.5	8	11.6
	5-6	6	8.7	7	10.2	1	1.5
	>6	0	0.0	5	7.2	53	76.7
<u>CY</u>							
	<20	44	63.7	40	58.0	4	5.8
	20-39	14	20.3	14	20.3	4	5.8
	40-59	7	10.2	6	8.7	6	8.7
	60-79	4	5.8	5	7.2	6	8.7
	80-99	0	0.0	4	5.8	5	7.2
	≥100	0	0.0	0	0.0	44	63.8

Table (25). Product-moment correlations (r_{PM}), Spearman rank correlations (r_S) and Kendall's rank correlations (r_K) among methods of sire evaluation for different milk traits.

	Methods correlated*					
Trait	BLUP2&BLUP1	BLUP2&OLS	BLUP2&CC	BLUP1&OLS	BLUP1&CC	OLS&CC
r_{PM}						
MY	0.998	0.993	0.655	0.995	0.649	0.646
FY	0.998	0.995	0.617	0.998	0.610	0.614
PY	0.995	0.992	0.541	0.997	0.523	0.527
FPY	0.998	0.995	0.607	0.998	0.601	0.599
CY	0.998	0.996	0.659	0.998	0.653	0.654
r_S						
MY	0.997	0.982	0.707	0.985	0.701	0.688
FY	0.998	0.993	0.650	0.995	0.641	0.656
PY	0.996	0.992	0.585	0.994	0.562	0.575
FPY	0.999	0.993	0.676	0.995	0.672	0.672
CY	0.998	0.993	0.706	0.996	0.703	0.702
r_K						
MY	0.971	0.936	0.508	0.962	0.507	0.496
FY	0.986	0.968	0.502	0.981	0.495	0.509
PY	0.974	0.963	0.441	0.982	0.418	0.430
FPY	0.985	0.962	0.512	0.979	0.510	0.512
CY	0.976	0.953	0.505	0.977	0.503	0.505

* The standard error of all estimates are less than 0.0001.

may be effective in the evaluation of sires. Estimates of r_{PM} between CC and each of OLS, BLUP1 and BLUP2 were the lowest correlations (Table 25). The estimates ranged from 0.523 to 0.659. This means that there was a large discloseness between all computerized methods (BLUP2, BLUP1 and OLS) and the simple method (CC). The same findings were observed by Kennedy and Moxley (1977) for fat percent. They reported a correlation of 0.85 between CC and BLUP. In practice and for comparison of sire proving schemes, these correlations are not effective.

Correlations obtained here (Table 25) indicate that the sires were reranked when using the computerized methods (BLUP2, BLUP1, OLS) which are different from those ranks obtained by CC. Theoretically, the CC is biased due to the presence of genetic trend and non-random distribution of herdmates' sires (Kennedy and Moxely, 1977; Freeman, 1988). The closer correspondence between BLUP2 and BLUP1 may be due to their computational similarities which indicate that there is no significant inbreeding in the population considered. The accuracy in estimating variance components by REML procedure and consequently the more precise ratio of variances (σ^2_e/σ^2_s) and also adding the identity relationship coefficient matrix (A^{-1}) did not create great differences between estimates of STA for the two methods. The REML estimation of variance component in a sire model has been shown to lead to substantial reduction in biases due to cow culling (Ouweltjes et al., 1988).

The slight decrease in estimates of Spearman (r_s) and Kendall (r_K) rank correlations among computerized methods (OLS, BLUP1 and BLUP2) may be due to that certain kind of selection may lead to a bias in least-squares estimates (Henderson, 1984). Keown (1974) reported that evaluations of sires by OLS and BLUP1 were similar which indicate that with large numbers of daughters and addition of variance ratio (σ^2_e/σ^2_s) to the diagonals, both items have little effect on the evaluation of sires. This also may be due to that OLS may be affected more by the interaction between sires and herd than BLUP. In comparison including CC and each of OLS, BLUP1 and BLUP2 for all milk traits, estimates of rank correlation (r_s) had the same trend where estimates ranged from 0.562 to 0.707 (Table 25). The estimates ranged from 0.982 to 0.999 between any combination of two methods of BLUP2, BLUP1 and OLS. The same trend was also observed when considering the Kendall rank correlation (r_K). Miller et al. (1967) reported that r_s between CC and each method of OLS and maximum likelihood (ML) was found to be less than that of OLS with ML (0.95 vs 0.99 for MY). Kennedy and Moxley (1977) found a close correlation between CC and BLUP for FY. They concluded that there is no genetic trend and also no large differences in levels of herdmate sires.

With respect to bias, computerized methods (BLUP2, BLUP1 and OLS) appear to be valid theoretically and they could be preferred over the simple method (CC). This trend was evidenced by Kennedy and Moxley (1977).

4.2.2.2 Standard error (SE)

With a slight tendency for closer agreement between computerized methods (BLUP2, BLUP1 and OLS) as compared by the three types of correlations (r_{PM}, r_S and r_K), there would be other bases for detecting which method is more accurate and which method is more preferable over others. The second criterion to assess the accuracy of different methods of sire evaluation is the standard error (SE) of each method and the percentage of reduction in standard error (RSE) due to using one method instead of another. These estimates are represented in Table 26. For all traits, BLUP2 has the lowest estimates of SE, while CC had the largest estimates. For 305-day milk yield, Raheja (1992) found that SE for STA estimated by BLUP was smaller (28.43) than estimates calculated by CC and OLS (30.2 and 63.02). Including REML in calculation of BLUP will increase the accuracy of STA estimates (through reduction of PEV) than BLUP without A^{-1} (Henderson, 1975; Kennedy and Moxley, 1977; Jensen, 1980; Carlson et al., 1984; Everett and Keown, 1984; Mabry et al., 1987). Sadek et al. (1993) found that inclusion of REML in calculations of BLUP caused little increase in sire variance (σ^2_s) and little decrease in error variance (σ^2_e).

Estimates of percentages of reduction in SE (RSE) that gained from using the ideal method instead of other alternative ones illustrate their desirability (Table 27). For all traits, estimates of RSE from using BLUP2, BLUP1 and OLS instead of CC were large and ranged from 45.5 to 56.3% (Table 27). On the other hand, RSE estimates ranged from 11.8 to 17.1% from using BLUP2 instead of BLUP1 or OLS, while they ranged from 2.0 to 4.4% from using BLUP1 instead of OLS. These figures showed that the lowest RSE was between BLUP1 and OLS, which means that both methods are similar and there were no differences between them in ranking of sires. This agrees well with Keown (1974) who come to the conclusion that evaluations of sires by OLS and BLUP1 are similar.

The BLUP2 was the nearer to BLUP1 than OLS since the differences between BLUP2 and OLS were larger than those between BLUP2 and BLUP1 (Table 27). Including REML in calculation of BLUP will lead to a great difference in sire evaluation when compared with both methods of OLS and BLUP without A^{-1} (Keown, 1974; Henderson, 1975; Carlson et al., 1984). Carlson et al. (1984) reported that BLUP without A^{-1} drastically reduced PEV by about 59.3% from CC, while BLUP with A^{-1} reduced PEV by about 17.0% more than BLUP without A^{-1}.

Table (26). The standard error (SE) of each method of sire evaluation for different milk traits.

Method	MY	FY	PY	FPY	CY
BLUP2	24	1.05	0.75	1.80	22.61
BLUP1	27	1.19	0.86	2.05	25.64
OLS	28	1.23	0.90	2.11	26.30
CC	55	2.34	1.65	3.99	52.00

Table (27). Reduction percent in standard error (RSE) gained from using BLUP2 instead of other alternative methods and sums of squares of difference (SSD) between different methods of sire evaluation.

Comparison	MY	FY	PY	FPY	CY
(i) RSE+					
BLUP2 vs BLUP1	11.8	11.8	12.8	12.2	11.8
vs OLS	13.6	17.1	16.7	14.7	14.0
vs CC	56.3	55.1	54.5	54.9	56.5
BLUP1 vs OLS	2.0	3.3	4.4	2.8	2.5
vs CC	50.5	49.1	47.9	48.6	50.7
OLS vs CC	49.1	47.4	45.5	47.1	49.4
(ii) SSD					
BLUP2 vs BLUP1	59960	117	87	343	51590
vs OLS	117395	214	162	631	85111
vs CC	5098988	8605	4333	25240	4460972
BLUP1 vs OLS	36595	35	33	110	12205
vs CC	4269670	7246	3572	21027	3740560
OLS vs CC	4242559	6869	3319	20001	3611539

+ Percent of reduction in SE due to using BLUP2 instead of BLUP1, using BLUP2 instead of OLS, ... etc.

The largest differences in ranking of sires reached with CC since the largest RSE were found between CC and other computerized methods (BLUP2, BLUP1 and OLS). This means that CC method widely differed from other computerized methods in ranking of sires.

4.2.2.3 Sums of squares of difference (SSD) between methods

Comparisons were made firstly between each method of CC or OLS or BLUP1 and the ideal method (BLUP2), secondly between each of OLS or CC and BLUP1 and finally between CC and OLS. Estimates of SSD are given in Table 27. For all traits, a great closeness between BLUP1 and OLS was evidenced since their estimates of SSD were the lowest (Table 27). Thus, BLUP1 and OLS recorded STA whose estimates were less different from other methods. In contrast, BLUP2 and CC have the largest estimates of SSD. Also, SSD estimates between CC and the remaining other methods (BLUP1 and OLS) were found to be greater than those estimates of SSD between BLUP1 and OLS (Table 27). Over all six combinations of any two methods, the CC method recorded STA whose estimates were more different from other methods, while the BLUP1 and OLS yielded STA whose estimates were more similar.

4.3 Cow Evaluation Methods

4.3.1 Estimates of cow transmitting ability (CTA)

The minimum and maximum estimates of cow transmitting abilities (CTA) estimated by the three methods BLUP, SI and MPPA are presented in Table 28. Szkotnicki et al (1978) found that differences in estimates of CTA for MY were 116 and 173 Kg for Brown Swiss and Canadian cattle, respectively. The differences for FY were 5.0 and 8.6 Kg for the same two breeds. Hintz et al (1978) reported higher differences in CTA for MY where they were 757, 520, 580, 487 and 907 Kg for Ayrshire, Guersey, Holstein, Jersey and Brown Swiss, respectively. The differences between minimum and maximum values of CTA for different methods are illustrated in Table 28. For all milk traits, the largest differences in CTA estimates were recorded by MPPA and the lowest differences were presented by SI (Table 28). The differences in CTA using SI1 (for milk) and SI2 (for carrier) were nearly the same (Table 28). Therefore, both indices have the same trend in the evaluation of cows.

The differences in CTA for BLUP were often larger than those for SI (Table 28). This may be due to that all available records of the cow were used in BLUP , while SI used only the first record of the cow. Van Der Werf et al (1989) reported that SI values are underestimated since young cows are compared with selected older cows.

As expected, the differences between CTA estimated by MPPA were much larger than those estimated by SI (Table 28). These large differences do not introduce a good tool for having the correct culling decision since these large differences may be due to disadvantages in this method; assuming that the genetic correlation among lactations equal unity (Maijala and Hanna, 1974 and Strandberg, 1985).

Among all cows, BLUP recorded the lowest percentages of cows having negative estimates of CTA followed by SI and MPPA for all milk traits (Table 29).

4.3.2 Distribution of absolute differences of CTA

Absolute differences (in Kg) distributed as percentages in different methods of cow evaluation are presented in Table 30. One method of improving the production of a dairy herd is to cull the low producers of 25-30% of the cows (O'Bleness and Van Vleck, 1962; Carter et al., 1963). Accordingly, the percentage of culling of cows depending on their CTA mainly include the inferior 25-30% of cows. Comparing SI relative to BLUP, we found that this percent will cull those cows having CTA $\leq$ 100 Kg for MY or CY (Table 30). When using MPPA as a method for estimating CTA and comparing their estimates

Table (28). Minimum and maximum values for cow transmitting abilities (CTA) estimated by Best Linear Unbiased Predictor (BLUP), Selection Index for milk (SI1), Selection Index for carrier (SI2), and Most Probable Producing Ability (MPPA).

Trait+	Minimum	Maximum	Difference
MY			
BLUP	-992	1561	2553
SI1	-793	867	1660
MPPA	-1584	2121	3705
FY			
BLUP	-52	65	117
SI1	-38	45	83
SI2	-33	40	73
MPPA	-63	82	145
PY			
BLUP	-42	49	91
SI1	-24	31	55
SI2	-24	31	55
MPPA	-48	53	101
FPY			
BLUP	-99	118	217
SI1	-58	80	138
SI2	-58	80	138
MPPA	-116	136	252
CY			
BLUP	-994	1490	2484
SI2	-733	797	1530
MPPA	-1665	2037	3702

+ Number of cows evaluated were 6018.

Table (29). Percentages of negative estimates of cow transmitting ability (CTA) in different methods of cow evaluation.

Trait	BLUP	SI1	SI2	MPPA
MY	52.0	52.7	a	53.5
FY	50.9	52.0	50.3	52.0
PY	47.8	48.8	48.6	49.4
FPY	51.5	51.7	51.7	52.2
CY	51.1	a	52.5	53.3

a SI1 is the index to select for MY, while SI2 to select for CY.

Table (30). Distribution of absolute difference (%) among estimates of CTA calculated by SI1, SI2 and MPPA relative to BLUP.

Trait	Absolute difference (Kg)	BLUP vs SI1	BLUP vs SI2	BLUP vs MPPA
MY				
	>300	24.6	a	33.6
	>200-300	17.2	a	24.2
	>100-200	25.9	a	28.3
	>0-100	32.0	a	13.9
	=0	0.3	a	0.0
FY				
	>20	5.8	6.1	6.7
	>10-20	23.4	24.4	44.3
	>0-10	66.8	65.8	48.1
	=0	4.0	3.7	0.9
PY				
	>20	1.1	1.1	4.3
	>10-20	12.6	12.5	36.28
	>0-10	80.2	80.6	59.4
	=0	6.2	5.8	0.02
FPY				
	>30	9.1	8.8	9.8
	>20-30	15.3	16.3	30.3
	>10-20	29.1	32.3	36.3
	>0-10	44.3	40.8	23.3
	=0	2.2	1.8	0.3
CY				
	>300	a	26.5	31.0
	>200-300	a	18.3	30.7
	>100-200	a	24.7	27.7
	>0-100	a	30.4	10.5
	=0	a	0.1	0.1

[a] SI1 is the index to select for MY, while SI2 to select for CY.

with those estimates of BLUP, we found that percent of culling (25-30%) will include those cows having CTA greater than 100 Kg till 200 Kg for MY or CY. Using CTA estimates of FY, PY and FPY as a criteria for culling decision, the appropriate culling percent (25-30%) will include those cows having CTA equal to zero and those having 10 Kg or less in comparison of SI1 vs BLUP or SI2 vs BLUP or MPPA vs BLUP (Table 30). For FPY trait, the appropriate culling percent will include those cows having 10 Kg or less in comparison of SI1 vs BLUP and SI2 vs BLUP but it will include those cows having 20 Kg or less in comparison of MPPA vs BLUP.

Using estimates of CTA to decide the culling percentage of cows, both BLUP and SI are coupled in deciding the inferior cows, while MPPA will include some cows whose having large CTA in the culling percent.

4.3.3 Criteria for judging merits of methods

The criteria for judging the merits of different methods of cow evaluation are the correlations between these methods such as Product-moment correlation, Spearman-rank correlation and Kendall-rank correlation (Hargrove et al. 1974; Kress et al., 1977; Kennedy and Moxley, 1977; Dempfle and Hagger, 1979; Danell and Eriksson, 1982; Kemp et al., 1984; Mabry et al., 1987; Vig and Tiwana, 1988; Tajani and Rai, 1990). Another criterion useful and helpful in judging the merits of alternatives of cow evaluation methods is the standard error (SE) of each method (Miller et al., 1967; Henderson, 1974; Ufford et al., 1979; Jensen, 1980; Kumar and Narian, 1980; Eriksson and Danell, 1984; Raheja, 1992). Sums of squares of difference (SSD) between the chosen (ideal) and the other methods were also calculated (Kemp et al., 1984). Results of these criteria of evaluation are presented below.

4.3.3.1 Product-moment and rank correlations

For all milk traits, the product-moment correlations (r_{PM}) between all combinations of two methods of BLUP, SI and MPPA were greater than 0.50 (Table 31). Estimates of r_{PM} between two types of SI were near to unity. These figures fairly demonstrate the closeness between both two types of SI. Consequently, any type of SI may be effective in the evaluation of cows using only the first cow record. The product-moment correlations between SI and MPPA were considerable lower than those estimates between any two types of combination (Table 31). The estimates ranged from 0.50 to 0.627. This means lack of agreement between SI and MPPA. It may also indicate that the largest differences in reranks of cows were between these two methods of evaluation. Schaeffer et al. (1982) reported that r_{PM} between BLUP and CC for CTA of MY

Table (31). Product-moment correlations (r_{PM}), Spearman's rank correlations (r_S) and Kendall's correlations (r_K) among methods of cow evaluation for different milk traits.

Trait	BLUP&SI1	BLUP&SI2	BLUP&MPPA	SI1&SI2	SI1&MPPA	SI2&MPPA
	Methods correlated+					
r_{PM}						
MY	0.709	a	0.813	a	0.611	a
FY	0.706	0.705	0.804	0.997	0.593	0.593
PY	0.664	0.664	0.588	0.997	0.502	0.500
FPY	0.701	0.701	0.779	1.000	0.574	0.574
CY	a	0.720	0.786	a	a	0.627
r_S						
MY	0.700	a	0.791	a	0.588	a
FY	0.684	0.684	0.771	0.997	0.566	0.566
PY	0.637	0.637	0.538	0.996	0.478	0.475
FPY	0.683	0.683	0.743	1.000	0.554	0.554
CY	a	0.709	0.762	a	a	0.600
r_K						
MY	0.514	a	0.604	a	0.415	a
FY	0.514	0.514	0.594	0.974	0.410	0.410
PY	0.480	0.480	0.403	0.979	0.346	0.345
FPY	0.508	0.508	0.563	1.000	0.398	0.398
CY	a	0.522	0.575	a	a	0.428

+ Standerd errors for all estimates were less than of 0.0001.
a SI1 is the index to select for MY, while SI2 to select for CY.

and FY were 0.88 and 0.65, respectively. Van Der Werf et al. (1989) reported that r_{PM} between animal model (AM) and SI were very high (0.98).

Estimates of r_{PM} between BLUP and SI were less than those between BLUP and MPPA (Table 31). The estimates ranged from 0.664 to 0.720 for BLUP vs SI1 or SI2, while they ranged from 0.588 to 0.813 for BLUP vs MPPA. The lower correlation between BLUP and SI may be due to the fact that SI constructed here included less information than BLUP (first lactation only for the former method vs all lactations for the later method). Consequently young cows could be compared with those selected older cows (Van Der Werf et al., 1989). The latter authors added that BLUP showed an advantage over SI accounting for bias from selection on sequential records of the cows. Considering the other two types of correlation (r_S and r_K), the same trend was observed with the decrease of their estimates (Table 31).

4.3.3.2 Standard error (SE) and sums of squares of difference (SSD) between methods

With the clear disagreement among the three methods (BLUP, SI and MPPA) as compared by the three types of correlations of r_{PM}, r_S and r_K (Table 31), there would be other bases for detecting which method is more accurate and which is more preferable over others. The other criteria to assess the accuracy of different methods of cow evaluation are the standard error (SE) of each method and the percentage of reduction in standard error (RSE) due to using one method instead of another. Estimates of these criteria of cow evaluation are described below (Tables 32 & 33).

Across all milk traits, BLUP has the lowest SE estimates, while MPPA had the largest estimates and SI was in between (Table 32). Bias owing to the genetic trend and the limited amount of information used in construction of SI may be the main causes for increasing SE of SI when compared with BLUP (Sorensen et al., 1988). When using BLUP, Ufford et al. (1979) reported that records additional to the first lactation would be expected to contribute more accuracy. Within-herd evaluation of cows, Schaeffer et al. (1982) reported that using BLUP is more accurate than traditional CC. Chyr et al. (1979) reported that BLUP procedure (with or without A^{-1}) were more effective in eliminating temporary environmental effects relative to herdmate comparison in cow evaluation. They added that standard deviation (SD) of herdmate comparison was larger than that of BLUP without A^{-1} (1174 vs 1145). Estany et al. (1988) found that there was about 6% loss in efficiency due to use of SI instead of BLUP. However, using REML in estimation of variance components for BLUP will also increase the accuracy of estimates of CTA through the reduction of PEV (Henderson, 1975; Kennedy and Moxley, 1977; Jensen, 1980;

Table (32). The standard error (SE) of each method of cow evaluation for different milk traits.

Method	MY	FY	PY	FPY	CY
BLUP	2.26	0.11	0.07	0.17	2.10
SI1	4.60	0.19	0.12	0.32	a
SI2	a	0.18	0.12	0.32	4.75
MPPA	6.08	0.26	0.18	0.43	6.01

[a] SI1 is the index to select for MY, while SI2 to select for CY.

Table (33). Reduction of percent in standard error (RSE) gained from using BLUP instead of other methods and sums of squares of difference (SSD) between different methods of cow evaluation.

Comparison		MY	FY	PY	FPY	CY
(i) <u>RSE</u>[+]						
BLUP	vs SI1	50.9	42.1	41.7	46.9	a
	vs SI2	a	38.9	41.7	46.9	55.8
	vs MPPA	62.8	57.7	61.1	60.5	65.1
SI1	vs SI2	a	-5.6	0.0	0.0	a
	vs MPPA	24.3	26.9	33.3	25.6	a
SI2	vs MPPA	a	30.8	33.3	25.6	21.0
(ii) <u>SSD</u>						
BLUP	vs SI1	277498979	453949	206467	1327500	a
	vs SI2	a	472610	206537	1329120	303874108
	vs MPPA	303947115	561763	542120	1784282	332916884
SI1	vs SI2	a	6201	954	26210	a
	vs MPPA	607760656	1055520	628005	3187028	a
SI2	vs MPPA	a	1082979	627085	3196110	595819348

[+] Percent of reduction in SE due to using BLUP instead of SI1; using BLUP instead of SI2; ... etc.

[a] SI1 constructed to select for MY, while SI2 constructed to select for CY.

Carlson et al., 1984; Everett and Keown, 1984; Mabry et al., 1987). The only advantage of SI over the BLUP procedure in cow evaluation is that, it can be used when the cost of computation effectively rules out the more sophisticated BLUP approach of simultaneously estimating the breeding values of all bulls and cows in the national herd (Henderson, 1975; Dempfle, 1982; Hill and Swanson, 1983).

Percentages of reduction in estimates of SE (RSE) from using the ideal method instead of alternative ones are given in Table 33. Across all traits, RSE from using BLUP instead of MPPA were large and ranged from 57.7 to 65.1% (Table 33). On the other hand, estimates of RSE ranged from 38.9 to 55.8% from using BLUP instead of any one of the two types of SI, while they ranged from 21.0 to 33.3% from using any type of SI instead of MPPA. The lowest estimates of RSE was between SI1 and SI2 (Table 33). In this respect, using SI1 instead of SI2 will lead to a reduction in estimates of RSE of 0.0 to 5.6%. This means that both indices are similar and there were no differences between them in ranking of cows. Schaeffer et al. (1982) concluded that evaluations of cows by BLUP are more accurate than traditional contemporary comparisons.

In general, accuracy of SI was the nearer to BLUP than MPPA. This trend is clear since the sums of squares of differences (SSD) between BLUP and both types of SI were smaller than those between BLUP and MPPA (Table 32). This trend is more evidenced since SSD between MPPA and both types of SI were greater than estimates of SSD between MPPA and BLUP.