Models for Estimating Genetic Parameters of Milk Production Dairy Cattle Breeding

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Abstract—**It is well known that the variability of milk yield depends on reproductive factors say: age at calving, calving interval, open interval and number of insemination. Analysis was carried out for a mixed nested model with lactation and sire within lactation and fitting reproductive factors as covariables. Our purposes by using *ANCOVA* were to estimate herit-ability of milk yield and some reproductive traits for each herd and genetic, phenotypic and environm-ental correlations. Again, a number of non-genetic factors have previously been found to be of signifi-cance to milk production. In order to estimate the breeding values for actual milk yield for each herd, the source of variation due to systematic environm-ental effects must be eliminated. The purposes of this investigation were to study the effect of variation between breeding values within herds on actual milk yield using analysis was carried out for a random nested model. The results of the analysis showed that there were highly significance effects of breed-ing values on milk yield within herds.**

Keywords— Mixed Nested Model, ANCOVA, Heritability, Breeding Value.

The study of relationships between animal milk production and other traits is still very current. In this respect, type traits are particularly important. Linear type scoring systems are a part of animal evaluations in most countries with a developed dairy industry [17].

Since the nescience of computerization, together with biostatistics, the opportunity to make substantial genetic progress for milk yield on scientifically sound basis become feasible. There has been an exploration in application of advanced decision making techniques to solving genetic improvement in trait problems.

The traits of greatest importance in dairy cattle breeding are reproductive and phenotypic of dairy cow. Heritability estimates for milk production were evaluated for each herd. Furthermore, to make genetic improve-ment is to identify each animals genetic merit or breeding value for trait to be improved. It will be shown in this paper that phenotypes by themselves may be rather poor estimators of breeding value.

The variability in actual milk production was investigated between and within herds. Preliminary analysis of variance (ANOVA) of the recorded data showed a confounding effect when season crossed herd and age at calving nested within herd. An analytical procedure "the combined analysis" with a heteroscedastic model has been applied. Choosing the most appropriate model depends on decisions concerning the effects that are to be included in the model, especially those accounting for similarities of lactation curves of groups of animals under the influence of a common environmental effect (fixed part) or individual lactation curves of animals (random part) The data were analysed using mixed effect model of weighted least square procedures.

The project of development the cows is considered from projects which was constructed in Libya during interval (1972-1985). It consist of herds distributor in different places in Benghazi area where these herds were designed to contain (4600) cows. The herds under study are AL-Hwari (H), AL-Motkamla (M), and AL-Rahba2 (R2) having average milk yield 6006.7, 3438.5, and 5855.9 respectively.

Estimation of variance components of the genetic and phenotype variances and covariances of the data collected on milk yield were determined for 100-day milk yield as well as for 305-day milk yield. In quantitative genetic work it is possible to partition the phenotypic variance into portions due to inheritance and to environmental effects. This is a powerful analytical device and is the backbone of much of our knowledge of inheritance of quantitative traits in dairy cattle.

Since some of the factors are correlated, analysis of covariance (ANCOVA) would give more appropriate results, two stage nested design with several covariates. ANCOVA is used to improve the precision of an experiment with which comparisons between treatments are made. In fact, this analysis involves adjusting the observed response variable for effect of the concomitant variables on milk yield for the three herds.

Finally, in order to utilize these procedures, one must understand the concept of variance, in this study, the basis for much of this work is the normal distribution.

II. Review in the Literature

Components of variance have been used widely in genetic and animal breeding applications. Some earlier reports of these techniques are by [4], [15], and [26]. Important animal breeding application of variance components estimates are used to predict the breeding values and to indicated sources of variation production records.

Many studies estimated heritability for reproductive traits {age at first calving, number of insemination, days open and calving interval}, and determined its range from (-0.14 – 0.46) by using variance-covariance analysis.

[2] estimated the genetic parameters of milk yield and some reproductive traits of two herds (Al-Jazier and Al-Jalla) were imported as pregnant heifers from west Germany and Denmark respectively. The analysis was done separately for each herd by used [11] half-sib data method to obtain the genetic parameters. He used four statistical models, the general model was included year, sire within year, age at calving, days open, and lactation period as covariate. He indicated that herd differences were observed in milk yield and reproductive traits, heritability estimated for milk yield were 0.33 and 0.13 for Al-Jazier and Al-Jalla herd respectively, this probably is due to the two herds that represent two different sub-population, and heritability estimated for measures of reproductive traits were generally low, its between zero to 0.15, given indication of possible improvement through selection. In fact, measures of fertility were highly correlated both genetically and phenotypically, indicating that the existing of action of genes should be considered in improvement program.

A high genetic correlation between part lactation and lactation yield has been found. [27] estimates this correlation (between 150-day milk yield and 305-day milk yield) to 0.96 for first lactation cows. [21] obtained estimated of the genetic correlation between second and third monthly milk yield and lactation yield of size 0.85 and 0.89, respectively about the same estimate was found by [21] between maximum daily milk yield and yearly milk yield. Many studies reported a significant positive correlation between milk yield, and age at first calving see [9], [10], and [16]. A few studies have investigated the genetic relationship between milk yield and age at calving, some reported a positive genetic correlation between two traits. [14] used 1788 first lactation records of Canadian Holstein estimated genetic correlation between milk yield and age at first calving as 0.27.

Many studies investigated the relationship between milk yield and number of insemination, they found a significant and positive correlation between two traits, ranged from 0.14 to 0.70 ([5] and [19]).

Many studies reported a positive significant phenotypic and genetic correlation between milk yield and days open ranged from 0.35 to 0.72 ([1] and [20]) this indicates that, selection for higher producing cows will increase days open. Others reported a positive and significant phenotypic correlation (0.16-0.37) between milk yield and calving interval ([5], [8], [9] and [18]). The figure indicates that high producing cow will have longer calving interval than low producing cow.

[13] reported that high producing herds averaged shorter calving intervals than herds with lower milk yield, however, [25] reported that, there was no correlation between length of calving interval and milk yield.

III. Material, Methods, and Analytical Results

The objective of the present study is to compare some genetic and environmental traits effect on milk yield for above herds. The three herds have practiced milking 2× times per day. The herds are housed in closed stall type buildings. Data for Friesian cattle for three herds from two years (1999-2000) were recorded for each cow. The available data, covering 1365 records of Holstein-Friesian cattle population were imported from Germany as pregnant heifers in 1999, see [7].

Notice that, an incomplete record was deleted due to death or sale.

In order to identify whether the milk yield of three regions or herds H, M, R2 significantly differ with respect to the following variables:

(i) X_1: Age at calving (in months).
(ii) X_2: Calving interval (in days).
(iii) X_3: Open interval (in days).
(iv) X_4: Number of insemination.
(v) X_5: Lactation interval (in days).
(vi) X_6: The production at 100 - days.
(vii) X_7: The production at 305 - days.
(viii) X_8: The total production (in k.g).

The data used in this investigation were included productive and reproductive traits; productive traits were: actual milk yield and corrected milk yield and reproductive traits were: age of calving, insemination number, open days, and calving interval. It consists of 1365 records, 588 cow at AL-Hwari herd, 424 cow at AL-Motkamla herd, and 353 cow at AL-Rahba2 herd. After deletion of those sires with one daughter, the total number was 1261 cow bred by 267 bull, it was analyzed using the following mixed ANCOVA model:

$$Y_{ijk} = \mu + \alpha_i + \beta_{j(i)} + \sum_l \sum_i \sum_j \sum_k \gamma_l (X_{lijk} - \bar{X}_{l\ldots}) + \varepsilon_{ijk} \qquad (1)$$

$$(i = 1,2,\ldots, a;\ j = 1,2,\ldots, b_i;\ k = 1,2,\ldots, n_{ij});$$

$$\sum_i b_i = b,\ \ \sum_j n_{ij} = N_{i.},\ \ \sum_i \sum_j n_{ij} = N.$$

Where Y_{ijk} is the *k*th observation (milk yield), μ is the general mean, α_i the fixed effect due to *i*th level of factor-*A*; lactation, $\beta_{j(i)}$ is the random effect of *j*(*i*)th level of factor-*B*; sire within *i*th level of factor-*A*; lactation. γ_1 is the regression coefficient of milk yield on age at calving (X_1), γ_2 is the regression coefficient of milk yield on interval calving (X_2), γ_3 is the regression coefficient of milk yield open days (X_3), γ_4 is the regression coefficient of milk yield on the number of insemination (X_4), and ε_{ijk} is error term associated with each observation.

This study was made to determine estimates of some genetic parameters. Analysis was carried out for a mixed nested model with lactation as fixed and sire within lactation as random effects and fitting age at calving, calving interval, days open and insemination number as covariables.

Let us consider there will be two factors *A* and *B* having different levels. The level of factor-*B* are nested within the levels of factor-*A*.

The regression coefficients for each treatment are identical. The concomitant variables are not effected by treatments and nonstochastic.

In matrix notation, the model is

$$Y = \begin{bmatrix} 1 & A & B & C \end{bmatrix} \begin{bmatrix} \mu \\ \alpha \\ \beta \\ \gamma \end{bmatrix} + U$$

$$Y = MP + U \,.$$

Where

$$Y' = \begin{bmatrix} y_{111} & y_{112} & \dots & y_{11n_{11}} \cdots & y_{abn_{ab}} \end{bmatrix}$$

$$U' = \begin{bmatrix} \varepsilon_{111} & \varepsilon_{112} & \dots & \varepsilon_{11n_{11}} \cdots & \varepsilon_{abn_{ab}} \end{bmatrix}$$

$$C' = \begin{bmatrix} (x_{111} - \bar{x}_{\dots}) & (x_{112} - \bar{x}_{\dots}) & \dots & (x_{11n_{11}} - \bar{x}_{\dots}) & \dots (x_{abn_{ab_a}} - \bar{x}_{\dots}) \end{bmatrix}_{1\times N}$$

$$I' = \begin{bmatrix} 1 & 1 & \dots & 1 \end{bmatrix}_{1\times N},$$

$$\alpha' = \begin{bmatrix} \alpha_1 & \alpha_2 & \dots & \alpha_a \end{bmatrix}_{1\times a}$$

$$\beta' = \begin{bmatrix} \beta_{1(1)} \; \beta_{2(1)} & \dots & \beta_{b_1(1)} & \dots \beta_{1(a)} & \beta_{2(a)} & \dots \beta_{b_a(a)} \end{bmatrix}_{1\times b}$$

$$\gamma' = \begin{bmatrix} \gamma_1 & \gamma_2 & \dots & \gamma_k \end{bmatrix}_{1\times k},$$

$$A = Diag\begin{bmatrix} I_{N_{11}} & I_{N_{12}} & \dots & I_{N_{ab}} \end{bmatrix}_{N\times a},$$

$$B = Diag\begin{bmatrix} I_{n_{11}} & I_{n_{12}} & \dots & I_{n_{ab_a}} \end{bmatrix}_{N\times b},$$

and $X = \lfloor x_{rijk} \rfloor_{N\times l}$.

Where $I'_{N_{i.}} = [1 \;\; 1 \;\; \dots \;\; 1]_{N_{i.}\times 1}$, $I'_{n_{ij}} = [1 \;\; 1 \;\; \dots \;\; 1]_{n_{ij}\times 1}$

Thus *M* is an $N \times (a+b+l+1)$ matrix with rank $(b+l)$.

The normal equations to estimate the parameter vector *P* is $M'M\hat{P} = M'Y$.

As rank(*M*) = (*b*+*l*), one need to put (*a*+1) restrictions to solve the normal equations. The restriction are $E'_a\hat{\alpha} = 0$ and $D'\hat{\beta} = 0$, where *E* is column vector of *a*-elements unity, $D = Diag\begin{bmatrix} I_{b_1} \; I_{b_2} & \dots & I_{b_a} \end{bmatrix}_{b\times a}$, where $I'_{b_i} = [1 \;\; 1 \;\; \dots \;\; 1]_{b_i\times 1}$.

Under this restriction, the estimates are:

$$\hat{\alpha} = (A'A)^{-1}(A'Y) - (I'I)^{-1}(E_a I'Y) - (A'A)^{-1}(A'C)\hat{\gamma},$$

$\hat{\gamma} = E_{xx}^{-1}E_{xy}$ and $\hat{\mu} = (I'I)^{-1}(I'Y)$;

Now, sum of squares of estimates is given by :

$SS(estimate) = \hat{P}'M'Y = [\hat{\mu}'I' + \hat{\alpha}'A' + \hat{\beta}'B' + \hat{\gamma}C']Y,$ with (*b*+*l*)*d.f*.

The total sum of squares is given by :

$SS(Total) = Y'Y,$ with *N-d.f* ;

and the sum of squares error is given by:

$SS(error) = E_1 = Y'Y - \hat{P}'M'Y,$ with (*N-b-l*)*d.f.*

The main objectives of the analysis are to test the following hypotheses:

(*i*) $H_0: \alpha_i = 0$ against $H_1: \alpha_i \neq 0$.

(*ii*) $H_0: \delta_\beta^2 = 0$ against $H_1: \delta_\beta^2 > 0$.

Before testing these hypotheses, the interest centers on testing the hypothesis:

$H_o: \gamma = 0$ against $H_1: \gamma \neq 0$.

However, If $H_0: \gamma = 0$ is rejected, the analysis involves the test of the hypotheses (*i*),(*ii*). Under null hypothesis $H_o: \delta_\beta^2 = 0$, the model is: $Y = M_1P_1 + U$,

where $M_1 = [1 \;\; A \;\; C]$, $P'_1 = [\mu \;\; \alpha \;\; \gamma]$ and rank(M_1) =(*a*+*l*), since M_1 is not full rank, the estimate of μ and α will be obtained similarly as those are obtained for the model except that the estimate of parameter vector γ is obtained by: $\hat{\hat{\gamma}} = (E_{xx} + B_{xx})^{-1}(E_{xy} + B_{xy})$ and

$SS(estimate) = \hat{P}_1'M_1'Y$ with (*a*+*l*)*d.f* .

$SS(error) = E_2 = Y'Y - \hat{P}_1'M_1'Y$ with (*N-a-l*)*d.f.*

$SS(\beta_{j(i)}) = E_2 - E_1$ with (*b-a*)*d.f.*

Thus for null hypothesis $H_o: \delta_\beta^2 = 0$ the test statistic is: $F = \dfrac{(E_2 - E_1)/(b-a)}{E_1/(N-b-1)}$, this *F-statistics* follows variance ratio distribution with (*b-a*) and (*N-b-*1)*d.f* .

Under null hypothesis $H_o : \alpha_i = 0$ the model becomes: $Y = M_2 P_2 + U$,where $M_2 = [1 \quad B \quad C]$, $P_2' = [\mu \quad \beta \quad \gamma]$, the rank of matrix M_2 is (*b*-*a*+*l*+1).

At this stage the estimate $\hat{\gamma}$ will be replaced by: $\hat{\hat{\hat{\gamma}}} = (E_{xx} + A_{xx})^{-1}(E_{xy} + A_{xy})$

So that,

$SS(estimate) = \hat{P}_2' M_2' Y$ with (*b*-*a*+*l*+1)*d.f*

$SS(error) = E_3 = Y'Y - \hat{P}_2' M_2' Y$ with *N*-(*b*-*a*+*l*+1)*d.f*

$SS(\hat{\alpha}) = E_3 - E_1 = \hat{\alpha}' A' Y$ with (*a*-1)*d.f* under H_o.

Thus, the test statistic for the hypothesis $H_0 : \alpha_i = 0$ is given by:

$F = \dfrac{(E_3 - E_1)/(a-1)}{E_1/(N-b-1)}$, this *F* has the variance ratio distribution with (*a*-1*)* and (*N*-*b*-1*)d.f* .

The variance component of factor *B*(*A*) is computed by the formula:

$\hat{\delta}^2_{\beta(\alpha)} = \dfrac{MSB(A) - MS(C)}{K}$, where

$$K = \frac{N - \sum_i \sum_j \frac{n_{ij}^2}{n_{i.}}}{b-a}.$$

Estimation of the genetic and phenotypic variances and covariances of the data on milk yield were determined using between sires δ_s^2 and the within sire or error component of variance δ_ε^2. For more details, see ([3], [7]).

IV. *Heritability*

The heritability was defined as part of phenotypic variance due to variation of genetic components between sires, and it was estimated by paternal half sib group using the following formula:

$$h^2 = 4t = 4 \times \frac{\delta_s^2}{\delta_s^2 + \delta_\varepsilon^2}, \qquad (2)$$

where h^2 is the heritability estimate of the trait, and t is the intraclass correlation.

The genetic, phenotypic and environmental correlation between traits can be calculated using the following formulas respectively:

$$r_{g_1,g_2} = \frac{\delta_{s_1 s_2}}{\sqrt{\delta_{s1}^2 . \delta_{s2}^2}}, \qquad (3)$$

where r_{g_1,g_2} is the correlation between traits, $\delta_{s_1 s_2}$ is the covariance component of sire, $\delta_{s_1}^2$ is the variance component of sire for one trait, $\delta_{s_2}^2$ is the variance component of sire for the other trait.

The phenotypic correlation is:

$$r_{p_1,p_2} = \frac{\delta_{w_1 w_2} + \delta_{s_1 s_2}}{\sqrt{(\delta_{w_1}^2 + \delta_{s2}^2)(\delta_{w_2}^2 + \delta_{s2}^2)}}, \qquad (4)$$

where r_{p_1,p_2} is the phenotypic correlation between two traits, $\delta_{w_1 w_2}$ is covariance component of error, $\delta_{w_1}^2$ is the variance component of error for one trait, $\delta_{w_2}^2$ is the variance component of error for another trait.

In addition, the environmental correlation is:

$$r_{e_1,e_2} = \frac{\delta_{w_1 w_2} - 3\delta_{s_1}\delta_{s_2}}{\sqrt{(\delta_{w1}^2 - 3\delta_{s1}^2)(\delta_{w2}^2 - 3\delta_{s2}^2)}}. \qquad (5)$$

The breeding value can be estimated by using the data of sibs records by the following formula:

$$BV = b_1(x_i - \bar{x}_p) + b_2(\bar{x}_{hs} - \bar{x}_p) + b_3(\bar{x}_{fs} - \bar{x}_p)$$

Where *BV* is breeding value of individual, x_i is the individual trait, $\bar{x}_{hs}$ is the mean of half sibs, $\bar{x}_{fs}$ is the mean of full sibs, $\bar{x}_p$ is the population mean and b_i's are the regression coefficient and computing by:

$$b_1 = \frac{h^2}{(2-h^2)},$$

$$b_2 = \frac{4nd(1-h^2)h^2}{[4+(n-2)h^2][4+(n(d+1)-2)h^2]},$$

and

$$b_3 = \frac{2nh^2(1-h^2)}{(2-h^2)[4+(n-2)h^2]}.$$

Where *n* is the number of full sibs per family, h^2 is the heritability estimated of the trait and *d* is the number of dams mated to a sire, see [12].

Also, the estimator of variance components are given by:

$$\hat{\delta}_\alpha^2 = \frac{(a-1)\lambda_0}{b(\lambda_0^2 - \sum_i \lambda_i)}[MS(A) - MS(E)] - \frac{a({\lambda_0}^2 - \sum_i \lambda_i^2)}{(a-1)\lambda_0^2}[MSB(A) - 1]$$

and

$$\hat{\delta}^2_{\beta(\alpha)} = \frac{(MSB(A) - MS(error))}{\lambda_0 / a}$$

For more details, see ([6] and [24]).

The analytical results show that all the concomitant variables are do not have a significant impact on milk yield for all herds, and the lactation showed no significant difference upon 305-days milk yield and total milk yield. Also it can be seen from the analytical results that the effect of sire within lactation is highly significant on milk yield for only two herds AL-Hwari and AL-Rahba2 herds, and not significance on milk yield for AL-Motkamla herd.

Too many studies have reported different estimates of heritability for milk yield in dairy cattle. The estimates ranged from 0.06 to 0.65, also heritability estimates for reproductive traits ranged from –0.13 to 0.77. The heritability estimates for this study of milk yield and reproductive traits for the three herds studied are presented in the following table.

Table 1. Heritability estimated for milk yield and reproductive traits for the three herds.

Traits	AL-Hwari	AL-Motkamla	AL-Rahba2
Actual milk yield	0.52	0.43	0.32
The 305-d milk yield	0.57	0.30	0.25
Age at calving	0.55	0.69	0.45
Calving interval	0.61	0.40	0.51
Open days	0.64	0.40	0.93
Insemination number	0.66	0.27	0.24

Generally, the effect of heritability seems to be higher for AL-Hwari herd except for two traits age at calving and open interval that than for AL-Motkamla and AL-Rahba2 herds for most traits respectively. The different estimate of heritability of milk yield for the three herds may be due to that the effect of herd was important for the trait studied.

Low heritability estimates was obtained (0.24) for the insemination number trait in AL-Rahba2 herd. However, a high heritability for the same herd (0.93) was obtained for open days traits, given indication of possible improve-ment through selection from this herd. Heritability estimated of age at calving was high in AL-Motkamla herd (0.69) and then for the same trait (0.55 and 0.45) for AL-Hwari herd and AL-Rahba2 herd respectively. Again this herd accounted low heritability value for the insemination number traits, insemination number for AL-Hwari herd showed higher estimates (0.66) than those for other herds.

The reason behind that dairy cattle in herds centering of the interest by the age at calving in AL-Motkamla, open interval in AL-Rahba2 herd and with the clearness of the perfect interest in AL-Hwari on all traits.

Genetic, phenotypic and environmental correlations

The phenotypic variance is made of the genetic variance plus environmental variance and interaction between them. It can be seen and measured, but we wish to estimate the genetic variance by more accuracy. Estimation of genetic, phenotypic and environmental correlations are presented in Tables (2), (3) and (4) for AL-Hwari, AL-Motkamla and AL-Rahba2 herds respectively.

Table 2. Correlations among milk yield and reprod- uctive traits for AL-Hwari herd.

Traits		Age at calving	Calving interval	Open interval	Insem. number
Actual milk yield	**G**	-0.02	-0.18	0.02	0.04
	P	0.01	-0.17	-0.05	0.00
	E	0.05	0.19	-0.07	-0.21
305-day milk yield	**G**	0.01	0.03	0.02	0.01
	P	0.04	0.07	0.07	-0.03
	E	0.03	-0.01	0.01	-0.03
Age at calving	**G**		0.16	0.17	-0.09
	P		0.21	0.21	-0.01
	E		-0.13	-0.14	0.14
Calving interval	**G**			0.99	0.00
	P			0.99	0.00
	E			-0.99	0.00
Open interval	**G**				0.01
	P				0.01
	E				-0.01

G= Genetic correlation, P= phenotypic correlation, E= Environmental correlation.

Table 3. Correlations among milk yield and reprod-uctive traits for AL-Motkamla herd.

Traits		Age at calving	Calving interval	Open interval	Insem. number
Actual milk yield	**G**	0.39	0.01	-0.01	-0.32
	P	0.33	-0.01	-0.01	-0.16
	E	-0.42	0.01	0.01	0.94
305-day milk yield	**G**	0.32	-0.01	0.01	0.01
	P	0.14	0.01	0.01	-0.01
	E	0.74	0.06	0.01	-0.81
Age at calving	**G**		0.22	0.23	-0.31
	P		0.13	0.13	-0.02
	E		-0.32	0.13	0.94
Calving interval	**G**			0.99	0.17
	P			0.99	-0.05
	E			-0.99	0.73
Open interval	**G**				-0.17
	P				-0.06
	E				0.72

G= Genetic correlation, P= phenotypic correlation, E= Environmental correlation.

Table 4. Correlations among milk yield and reprod-uctive traits for AL-Rhba2 herd.

Traits		Age at calving	Calving interval	Open interval	Insem. number
Actual milk yield	G	-0.13	-0.11	-0.03	0.00
	P	-0.03	-0.10	-0.04	0.04
	E	0.35	0.15	0.04	0.00
305-day milk yield	G	-0.02	0.12	0.04	-0.17
	P	-0.04	0.08	0.03	0.01
	E	-0.15	-0.64	-0.20	0.00
Age at calving	G		0.06	0.02	-0.21
	P		0.13	0.05	-0.09
	E		0.02	0.00	0.00
Calving interval	G			0.32	0.06
	P			0.10	0.05
	E			-0.27	0.00
Open interval	G				0.02
	P				0.02
	E				0.00

G= Genetic correlation, P= phenotypic correlation, E= Environmental correlation.

Generally, the genetic and phenotypic correlations between milk yield and reproductive traits seem to be very low for the three herds. Also environmental correlation between milk yield and reproductive traits were low except in AL-Motkamla herd, which have highly environmental correlation between actual milk yield and insemination number, and between 305-day milk yield and age at calving, this means the management of this herd focuses their attention with two traits insemination number and age at calving.

Again, it appears from the above tables that the genetic, phenotypic and environmental correlations between open interval and calving interval for AL-Hwari and AL-Motkamla herds were high and have the same correlations value, this indicating for longer calving interval implies to longer open interval, these correlations are coincide to correlations reported by [2], but these correlations are low and different in AL-Rahba2 herd. The environmental correlation between two traits tells us that the environment has negative effect in the two traits for all herds.

High environmental correlation was found between age at calving, calving interval and open interval with insemination number for AL-Motkamla herd, that is indicating to in AL-Motkamala herd the environment has a big effect suffer on measure the reproductive traits by the reversal of the other herds.

Breeding Value

The data used in this part of study were a division breeding values of actual milk yield by herds into five dissimilar intervals, where the effect of breeding values considered random. Also as before the effect of herds was random. The mathematical model is given by:

$$Y_{ijk} = \mu + \alpha_i + \beta_{j(i)} + \varepsilon_{ijk} \qquad (6)$$

(i=1,2,.,a , j=1,2,.,b , k=1,2,.n_{ij})

Where Y_{ijk} is the actual milk yield, μ is the general mean, α_i is the random effect of the i-th level of herds, $\beta_{j(i)}$ is the random effect of jth level of breeding values within ith level of herds and ε_{ijk} is the error term with mean zero and variance δ_i^2.

With assumption:

$\alpha_i \sim NID(0,\delta_\alpha^2)$, $\beta_{j(i)} \sim NID(0,\delta_{\beta(\alpha)}^2)$, and $\varepsilon_{ijk} \sim NID(0,\delta_i^2)$.

Here $\delta_\alpha^2, \delta_\beta^2,$ and δ_i^2 are the variance components, the weighted least squares (WLS) method gives estimators of the parameters as:

$$\hat{\mu} = \frac{\sum_i (\lambda_i / n_{i.}) Y_{i..}}{\lambda_0 N} = \bar{Y}_{...}$$

, where $\lambda_i = w_i n_{i..}$ and $\lambda_0 = \sum_i \lambda_i$.

The sum of squares are given by :

$$SS(A) = b\sum_i \lambda_i (\bar{Y}_{i..} - \bar{Y}_{...})^2 \quad \text{with } (a-1) d.f,$$

$$SS(B(A)) = \sum_i \sum_j \lambda_i (\bar{Y}_{ij.} - \bar{Y}_{i..})^2 \quad \text{with } a(b-1) d.f,$$

$$SS(error) = \sum_i \sum_j \sum_k \lambda_i (Y_{ijk} - \bar{Y}_{ij.})^2 \quad \text{with } (N-ab) d.f.$$

Under the assumptions the result of analytical is summarized in the following *ANOVA* table. See ([6] and [24]).

Table 5. ANOVA table for Random Nested Model.

S.V.	Sum of Square	d.f	Mean Square	F	P-value
Herd	44423.842	2	22211.92	0.450546	0.648
Breeding value(Herd)	591600.134	12	49300.01	772.1828	0.000
Error	81594.508	1278	63.845		

As can be seen from the analytical results, the effect of herd is not significant on actual milk production; however, there are highly significance effects of breeding values on milk yield within herd. In fact, the component of variance due to breeding value within herd could be estimated by computational technique as follows:

$$\hat{\delta}_{\beta(\alpha)}^2 = \frac{MSB(A) - MS(error))}{\lambda_0 / a} = 5.79 \times 10^{-2}$$

The main factors affecting milk yield are species, sires of bulls, dams of bulls, sires of cows, and dams of cows. The trait of milk yield is also affected by environmental factors such as season of calving, lactation interval, days dry, and age of cow at freshening. It would appear that the variability of milk yield also depends on the non-genetic factors or reproductive factors say; age at calving, calving interval, open period, number of insemination, and kind of insemination.

V. Summary Results and Discussion

The results showed that lactations have no effect on milk yield, but sire within lactation resulted in a highly significant component of variance. Again the above concomitant variables have no significant impact on milk yield.

Components of variance have been evaluated in genetic application such as: heritability and breeding values. The heritability estimates of actual milk yield obtained in this study were higher for AL-Hwari herd (0.52) than AL-Motkamla herd (0.43) and AL-Rahaba2 herd (0.32). Heritability estimates of age at first calving were high in AL-Motkamla herd and gave an indication of possible improvement through selection from this herd, but at the expense of yield at first lactation if the selection criterion will be early age at first calving. Heritability estimates of calving interval and insemination number were high in AL-Hwari herd and gave an indication of possible improvement through selection of two traits from this herd. Heritability estimates of days open were high in AL-Rahba2 herd, given an indication of possible improvement through selection from this herd.

The estimation of genetic correlation between actual milk yield and age at calving were negative (-0.02) and (-0.13) for AL-Hwari and AL-Rahba2 respectively, and (0.39) for AL-Motkamla herd, indicating that higher actual milk yield implies to lower age at calving in AL-Hwari and AL-Rahba2 herds. These genetic correlations between actual milk yield and age at calving were generally lower than the phenotypic correlations for herds AL-Hwari and AL-Rahba2, indicating that the relationship between the traits were more due to non-genetic causes, but in AL-Motkamla the phenotypic correlation is less than genetic correlation. Also environmental correlation between actual milk yield and age at calving were very low (0.05) in AL-Hwari herd, negative correlation (-0.42) in AL-Motkamla herd, and positive correlation (0.35) in AL-Rahba2 herd.

The estimation of genetic correlation between 305-day milk yield and age at calving were very low (0.01) in AL-Hwari herd, positive correlation (0.32) in AL-Motkamla herd and negative (-0.02) in AL-Rahba2 respectively. The phenotypic correlation between 305-day milk yield and age at calving were generally lower than the genetic correlation for all herds unless in AL-Hwari herd. A high environmental correlation between 305-day milk yield and age at calving was (0.75) in AL-Motkamla herd, low correlation (0.03) in AL-Hwari herd and negative correlation (-0.15) in AL-Rahba2 herd. Estimation of the genetic correlation between yield traits and calving interval were negative for actual milk yield (-0.18,-0.11) for AL-Hwari and AL-Rahba2 herds, this indicates to increase of actual milk yield that leads to decrease to calving interval and very low for 305-day milk yield (0.03, 0.12) for AL-Hwari and AL-Rahba2 herds respectively. For AL-Motkamla herd the genetic correlation between traits were very low (0.01) for actual milk yield and negative correlation (-0.01) for 305-day milk yield. Similarly, phenotypic correlation between milk yield traits and calving interval were very small with negative sign for actual milk yield for all herds, and very low for 305-day milk yield with positive sign for all herds. This result is close to result of [25].

Environmental correlation between the yield traits and calving interval were found negative for 305-day milk yield for AL-Hwari and AL-Rahba2 and for low positive sign in actual milk yield for the same herds. Again, estimated genetic correlation between milk yield and open interval were negative for actual milk yield (-0.01,-0.03) for AL-Motkamla and Rahba2 herds from the tables, this indicating to increase of actual milk yield leads to decrease to open interval, and the genetic correlation between 305-day milk yield and open interval was very low for these two herds. For AL-Hwari herd the genetic correlation between milk yield traits and open interval have very low correlation. Phenotypic correlation between milk yield and open interval accounted same behavoiur as with milk yield traits and calving interval for all herds. Environmental correlation between the yield traits and open interval were found very low for actual milk yield (0.01,0.04) for AL-Motkamla and AL-Rahba2, and negative correlation (-0.07) for AL-Hwari herd, and for 305-day milk yield were very low the same correlation between traits (0.01) for AL-Hwari and AL-Motkamla herds, negative environmental correlation (-0.20) for AL-Rahba2 herd. (0.19, 0.15) for the same herds. In AL-Motkamla herd this correlation was very low (0.01) for actual milk yield and (0.06) for 305-day milk yield.

Estimated genetic correlation between milk yield trait and insemination number were for actual milk yield very low for AL-Hwari herd, negative for AL-Motkamla herd and no correlation for AL-Rahba2 herd, and for 305-day milk yield were very low the same correlation value (0.01) for AL-Hwari and AL-Motkamla, and negative correlation for AL-Rahba2 herd. Phenotypic correlation between milk traits and insemination number were found very low for AL-Rahba2, negative for AL-Motkamla herd and no correlation between actual milk yield and insemination number and negative correlation between 305-day milk yield and insemination number for AL-Hwari herd. Environmental correlation between milk traits were found negative for AL-Hwari herd. A high environmental correlation between actual milk yield and insemination number (0.94) and negative correlation between 305-day milk yield and insemination number for AL-Motkamla herd and no environmental correlation between milk traits and insemination number for AL-Rahba2 herd.

The genetic, phenotypic, and environmental correl-ations between age at calving and reproductive traits (calving interval, open interval and insemination number) were low for traits calving interval and open interval and negative for insemination number for all herds, indicating that the age at calving increases the calving interval and open interval increases too and number of insemination decrease. The estimates of genetic correlation among the measure of reproductive traits were high between calving interval and open interval and for AL-Hwari and AL-Motkamla herds and no environmental correlation between calving interval and insemination number for AL-Hwari herd, negative correlation (-0.17) in AL-Motkamla herd and very low correlation (0.06) in AL-Rahba2 herd. A high phenotypic and negative environmental correlation between calving interval and open interval were also found for AL-Hwari and AL-Motkamla herd, and low phenotypic and negative environmental correlations for AL-Rahba2 herd.

No genetic, phenotypic and environmental correlation between calving interval and insemination number for AL-Hwari herd, negative genetic and phenotypic correlation between calving interval and insemination number for AL-Motkamla herd and high environmental correlation between traits. And very low genetic and phenotypic correlation between calving interval and insemination number for AL-Motkamla herd and no environmental correlation between traits.

The study also discussed the effect of variation between breeding values within herds on actual milk yield, the analysis was carried out for a random nested model and resulted in highly significant effects of the breeding values.

The heritability estimates of actual milk yield obtained in this study were higher, indicating that, genetic progress is expected from selection. The difference in heritability estimates of milk yield could be attributed to the fact that the three herds represent three different sub-population which probably vary in their genetic variance. This result is degree with the results of [2]. Heritability estimates for measures of reproductive traits were generally high compared to the results which were obtained by [2], indicating that genetic progress through selection will have more effect.

The genetic correlation between milk yield and reproductive traits were generally very low, this means the relationship between traits were more due to non-genetic causes. The effect of herd is not significant on actual milk production, and there were highly significance effects of breeding values within herd on actual milk yield.

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