Analysis of variance from mixed models in (1) and (2).

Source of Variation	df	Sum Squares	EMS
Sire	S-1	R(μ,F,S,B) -R(μ,F,B)	$\sigma^2_e + K1\sigma^2_s$
Fixed	F-1	$F'Z^{-1}$ F(adjusted for sires)	$\sigma^2_e + KK^2_f$
Covariate	1	$B'Z^{-1}B$	$\sigma^2_e + KK^2_b$
Remainder	n-(S+F-1)	Y'Y - R(μ,F,S,B)	σ^2_e

Where:

R = The reduction in sum of squares;

S = The number of sires;

n = The total number of observations;

F = The number of each other fixed effects;

σ^2_s = Variance component of between sire groups, estimated from indirect analysis of Henderson (1953) as:

$\sigma^2_s = (MS_s - MS_e)/K1$

and it is equivalent to covariance of paternal half-sisters;

σ^2_e = Variance component of between cows within sire.

Accordingly, estimates of sire (σ^2_s) and remainder (σ^2_e) components of variances and covariances were obtained. Genetic variance for each trait was estimated as four times the estimated variances of sire component. Genetic covariance between traits i and j was estimated as four times the estimated sire covariance between the two traits, $4\hat{\sigma}_{si,sj}$. Phenotypic covariance was $\hat{\sigma}_{si,sj}$ + $\hat{\sigma}_{ei,ej}$ where $\hat{\sigma}_{eiej}$ is an environmental covariance.

3.5.3 Estimation of genetic parameters:

Models (1) and (2) utilized to obtain estimates of variance components for sire (σ^2_s) and remainder (σ^2_e).

The heritability (h^2_s) for each trait was estimated as four times the intraclass correlation coefficient between sire groups, i.e.

$h^2_s = 4\sigma^2_s / (\sigma^2_s + \sigma^2_e)$ ...... (14)

The standard error for heritability was calculated using formula of Becker (1984) as:

$SE(h^2) = 4\ Var\ (\sigma^2_s) / \sigma^2_s + \sigma^2_e$ .... (15)

The phenotypic correlation coefficients (r_p) were estimated according to the formula given by Falconer (1981)

$r_p = Cov_s + Cov_e / \sqrt{(\sigma^2_{s1} + \sigma^2_{e1})(\sigma^2_{s2} + \sigma^2_{e2})}$ ..... (16)

where

σ^2_{e1} = The remainder component of variance of the 1st trait;

σ^2_{e2} = The remainder component of variance of the 2nd trait;

σ^2_{s1} = The sire component of variance of the 1st trait;

σ^2_{s2} = The sire component of variance of the 2nd trait;

Cov_e = The remainder component of covariance of the two traits;

Cov_s = The sire component of covariance of the two traits estimated as $(MCP_s - MCP_e)/K$

MCP_s = The mean cross product of sire of the two traits;

MCP_e = The remainder mean cross product of the two traits;

K = The coefficient of the mean number of cows (daughters) per sire group;

The genetic correlation coefficient (r_G) between any two different traits studied was estimated using the following formula:

$$r_G = Cov_s / \sqrt{\sigma^2_{s1} \cdot \sigma^2_{s2}} \quad \ldots\ldots. \quad (17)$$

The symbols were as defined before.

The standard errors of the genetic correlation $SE(r_G)$ was approximately estimated using the formula of Turner and Young (1969) as :

$$SE(r_G) = \frac{1 - r^2_G}{\sqrt{2}} \sqrt{\frac{SE(h^2_1) \cdot SE(h^2_2)}{h^2_1 \cdot h^2_2}} \quad \ldots.. \quad (18)$$

3.5.4 <u>Best Linear Unbiased Prediction (BLUP):</u>

Rewriting the mixed linear model in matrix notation or the linear equation describing the previous mixed models is:

$$Y = Xf + Zs + Wb + e \quad \ldots\ldots.. \quad (19)$$

Where:

Y = The n x 1 observation vector (the records);

n = The total number of observations on each trait analysed separately;

X = A fixed and known n x p matrix;

f = An unknown p x 1 fixed vector of fixed effects;

p = Number of levels of f;

Z = A fixed and known n x q matrix whose elements are equal to zero or one;

s = A q x 1 nonobservable random vector (some or all of its elements represent breeding values of sires);

q = The number of levels of s;

W = n x 1 covariate vector (independent variables);

b = Vecotr of partial regression of Y on W;

e = Is an nx1 nonobservable random vector (the error vector).

$$E\begin{bmatrix} s \\ \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ \\ 0 \end{bmatrix} \qquad Var\begin{bmatrix} s \\ \\ e \end{bmatrix} = \begin{bmatrix} G & 0 \\ \\ 0 & I \end{bmatrix}\sigma^2_e \qquad \ldots\ldots \quad (20)$$

Thus, every elements of s and e has mean zero. The variance-covariance matrix of the elements of s is $G\sigma^2_e$, where G is a nonsingular, symmetric matrix. In the present study, the elements of s cannot be correlated, in which case off-diagonal elements of G are zero. The elements of e are uncorrelated and have common variance, σ^2_e. It was proved by Henderson (1977 and 1978) that BLUP of all elements of $\hat{S}$ of equation (19).

It was also proved by Henderson (1975) that $\hat{f}$ of (19) is a generalized least-sqares solution. These solutions are called mixed model solution which give a BLUP estimate for each sire. The mixed model equations (Henderson, 1984) are:

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z+G & Z'W \\ W'X & W'Z & W'W \end{bmatrix} \begin{bmatrix} \hat{f} \\ \hat{s} \\ \hat{b} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'Y \\ W'Y \end{bmatrix} \qquad \ldots\ldots\ldots \quad (21)$$

Where $G = \sigma^2_e/\sigma^2_s$ or $(4 - h^2)/h^2$ for each trait which was added to the diagonals of sire effect in the matrix. The above matrix model equations are given by:

$$\begin{bmatrix} \hat{f} \\ \hat{s} \\ \hat{b} \end{bmatrix} = \begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z+G & Z'W \\ W'X & W'Z & W'W \end{bmatrix}^{-1} \begin{bmatrix} X'Y \\ Z'Y \\ W'Y \end{bmatrix} \quad \ldots\ldots \quad (22)$$

The above analysis was carried out to estimate sire and remainder components of variance and to predict sire transmitting abilities for each trait, i.e. Best Linear Unbiased Predication (BLUP) values for sire effects absorbed by Maximum Likelihood were obtained. BLUP estimates for each of the first three lactations were obtained by using at least five daughters per sire.