METHODS AND MATERIALS

Collection of Breeding Data

The data were collected from the performance records of Gir cows maintained at the Kandivili Cattle Breeding Farm of Bombay Gowrakshak Mandali, Bombay. The data comprised of 2,095 lactation records made over a period of 33 years from the year 1936 through 1968, belonging to 502 cows sired by 35 sires and consisted of 348 dam-daughter pairs. Each sire family was represented by at least five daughters for these studies.

History of the Herd

The Gir herd belonged to the Kandivili Cattle Breeding Farm of Bombay Gowrakshak Mandali - a society established in 1887. This herd was established in the year 1924 for the breeding of pure Gir cattle on scientific lines. This institution has been rendering valuable service by supplying purebred Gir cows, heifers and bulls to various government and private breeders. The initial work began with a nucleus herd of 40 cows and one bull. The breeding work was carried out very systematically with the rigid elimination of every possible undesirable variation from genetic improvement point of view and as a consequence the farm-
produced herd strength increased from a nucleus stock of
41 animals in 1924 to 912 animals in 1947. Thereafter, the
strength of animals in the herd has been maintained from year
to year in accordance with the resources available.

Feeding and Management of the Herd

The farm animals have been maintained in good health
and productivity by keeping them under scientific practices of
feeding, housing and management. To ensure the continued
similarity in such practices, best efforts were made by the farm
staff to eliminate all possible variations in the feeding and
management of animals. The feed stuffs available for the farm
animals were jungle grass, hay, para, elephant and guinea grass,
jowar and maize fodder and legumes such as udid, methi, tur,
lucerne, berseem and carrots. Throughout the year each animal
was fed sufficient quantity of dry and green fodder in addition
to a concentrate ration at the rate of 1 kg for 2.5 kg of milk
production. The newly born calves were fed the dam's milk
daily according to specific feeding schedule for the first
6 months period. After one month of age, they were also given
daily some quantity of green feed and concentrate ration. The
animals were given, as far as possible, prompt attention for the
veterinary treatment. The cows were milked twice a day at
12 hours' interval. The milking was done by hand and the milkers
did this job efficiently so as to ensure complete milking of the
animal. The change of milkers from animal to animal was avoided
as far as possible.
Standardization of the Data

The lactation milk yield in the first 300 days or less was considered. Milk production after 300 days was not included in the lactation yield. Animals recording incomplete lactation due to having lactation length of less than 120 days, abortions, premature births, stillbirths, sickness, mastitis, loss of teats, culling or death, etc. were excluded from the data. However, milk yield records of animals which aborted but underwent a normal lactation were included in the data.

The data on the following traits were included:

1. Lactation milk yield records in kg on 300-days' basis for the first five individual lactations.
2. Part lactation milk yield records in kg on ten different periods of monthly consecutive and cumulative milk yield records for the 270 days of first lactation from the date of parturition.
3. Age at first calving in months.
4. Lactation length in days from first to fifth lactation.
5. Dry period in days from first to fifth lactation.
6. Inter-calving period in days from first to fifth lactation.
7. Service period in days from first to fifth lactation.
8. Gestation period in days from first to fifth lactation.
10. Sex ratio at birth.
12. Twinning percentage.

**Statistical Methods**

Since the number of progeny in different sub-classes were unequal and disproportionate and effects were non-orthogonal, it was thought desirable to analyse the data by least squares technique of fitting constants as recommended by Harvey (1966). Least squares constants of each character for various environmental effects were calculated, and then fitted according to the mathematical model of the character concerned. The constants of these variables which had significant effects were used for the adjustment of data of the traits. In the present investigations, it was considered necessary to study the effects of different factors such as period of calving on age at first calving; period of lactation, season of lactation and age at first calving on completed lactation milk yield; period of calving, season of part record and age at first calving on part lactation milk yield records; period of lactation and season of lactation on the traits such as lactation length, dry period, inter-calving period and service period during first lactation; period of lactation, season of lactation and sex of calf on gestation
period during first lactation; period of lactation, season of lactation, sequence of calving and age at first calving on completed lactation milk yield pooled over first to fifth lactation; period of lactation, season of lactation and sequence of calving on the data of traits like lactation length, dry period, inter-calving period and service period pooled over first to fifth lactation; and of factors like period of lactation, season of lactation, sequence of calving and sex of calf on the data of gestation period pooled over first to fifth lactation. Since the data collected were of records performed over a period of 33 years, to eliminate the effect of time the total period of 33 years was divided arbitrarily into seven periods of five years each except the seventh period which was of three years duration for all the traits during different lactations. It was assumed that time-bound changes in the traits within a period of five years or less would be small. The animals were allocated to various periods depending upon the period wherein the maximum part of their lactation of 300 days and partial lactation of different lengths were performed. The data on milk production and other traits of first to fifth lactation were also grouped into various seasons following similar criterion. The data on partial lactation milk yield records were also grouped into various seasons on almost similar criteria. For studies of the effect of sequence of calving, the data on milk production and other economic traits were grouped according to the parity of calving.
Three distinct seasons were used viz; hot season starting from the months of March to May, autumn season beginning from the month of June to September and comfort season extending from October to February. The seasons were formed after taking into consideration the climatological data of Bombay over a period of 30 years as presented in Table 8.

The mathematical models used for adjusting the data for various effects were as under:

1. Age at first calving

\[ Y_{jm} = \mu + P_j + e_{jm} \]

Where,
\[ Y_{jm} \] is the observed average age at first calving of the cow and in the \( j \)th period.
\[ \mu \] is the population mean.
\[ P_j \] is a constant for the \( j \)th period of calving of cow.
\( (j = 1, 2, 3, \ldots, 7) \).
\[ e_{jm} \] is the random error.

2. Lactation milk yield of the first and subsequent lactations

\[ Y_{jkm} = \alpha + P_j + m_k + \beta(x_{jkm}) + e_{jkm} \]

Where,
\[ Y_{jkm} \] is the observed average of lactation milk yield of the \( m \)th cow in the \( j \)th period and \( k \)th season.
\[ \alpha \] is \( \mu - \bar{x} \)
\[ P_j \] is a constant for the \( j \)th period of lactation of cow.
\( (j = 1, 2, 3, \ldots, 7) \).
<table>
<thead>
<tr>
<th>S. No.</th>
<th>Month/Season</th>
<th>Atmospheric Temperature</th>
<th>Relative Humidity</th>
<th>Rainfall</th>
<th>Monthly No. of Rainy days</th>
<th>Lat. 18° 46' N, Long. 72° 49' E</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>°C</td>
<td>°C</td>
<td>mm.</td>
<td>mb.</td>
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</tr>
<tr>
<td>1</td>
<td>March</td>
<td>25.5</td>
<td>31.0</td>
<td>22.7</td>
<td>35.0</td>
<td>22.0</td>
</tr>
<tr>
<td>2</td>
<td>April</td>
<td>26.2</td>
<td>31.9</td>
<td>22.2</td>
<td>34.8</td>
<td>22.4</td>
</tr>
<tr>
<td>3</td>
<td>May</td>
<td>27.9</td>
<td>35.1</td>
<td>26.9</td>
<td>34.6</td>
<td>22.8</td>
</tr>
<tr>
<td>4</td>
<td>June</td>
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<td>24.8</td>
</tr>
<tr>
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<td>27.6</td>
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<td>22.5</td>
<td>34.4</td>
<td>23.5</td>
</tr>
<tr>
<td>6</td>
<td>August</td>
<td>27.1</td>
<td>35.0</td>
<td>22.4</td>
<td>31.8</td>
<td>23.1</td>
</tr>
<tr>
<td>7</td>
<td>September</td>
<td>27.0</td>
<td>35.0</td>
<td>22.2</td>
<td>31.7</td>
<td>22.2</td>
</tr>
<tr>
<td>8</td>
<td>October</td>
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<td>22.0</td>
<td>32.2</td>
<td>22.0</td>
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<tr>
<td>9</td>
<td>November</td>
<td>25.6</td>
<td>35.0</td>
<td>22.2</td>
<td>35.1</td>
<td>22.2</td>
</tr>
<tr>
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<td>22.0</td>
<td>34.8</td>
<td>22.0</td>
</tr>
<tr>
<td>11</td>
<td>January</td>
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<td>35.0</td>
<td>22.0</td>
<td>33.7</td>
<td>22.0</td>
</tr>
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<td>12</td>
<td>February</td>
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<td>22.0</td>
<td>33.9</td>
<td>22.0</td>
</tr>
<tr>
<td>13</td>
<td>March</td>
<td>24.2</td>
<td>35.0</td>
<td>22.0</td>
<td>36.1</td>
<td>22.0</td>
</tr>
<tr>
<td>14</td>
<td>April</td>
<td>24.2</td>
<td>35.0</td>
<td>22.0</td>
<td>36.1</td>
<td>22.0</td>
</tr>
<tr>
<td>15</td>
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<td>24.2</td>
<td>35.0</td>
<td>22.0</td>
<td>36.1</td>
<td>22.0</td>
</tr>
<tr>
<td>16</td>
<td>June</td>
<td>24.2</td>
<td>35.0</td>
<td>22.0</td>
<td>36.1</td>
<td>22.0</td>
</tr>
<tr>
<td>17</td>
<td>July</td>
<td>24.2</td>
<td>35.0</td>
<td>22.0</td>
<td>36.1</td>
<td>22.0</td>
</tr>
<tr>
<td>18</td>
<td>August</td>
<td>24.2</td>
<td>35.0</td>
<td>22.0</td>
<td>36.1</td>
<td>22.0</td>
</tr>
<tr>
<td>19</td>
<td>September</td>
<td>24.2</td>
<td>35.0</td>
<td>22.0</td>
<td>36.1</td>
<td>22.0</td>
</tr>
<tr>
<td>20</td>
<td>October</td>
<td>24.2</td>
<td>35.0</td>
<td>22.0</td>
<td>36.1</td>
<td>22.0</td>
</tr>
</tbody>
</table>
3. Average lactation milk yield on pooled data of the first five lactations

\[ Y_{ijkm} = \mu + F_i + P_j + m_k + \beta(x_{jkm}) + e_{ijkm} \]

Where,

- \( Y_{ijkm} \) was the observed average of lactation milk yield of the \( i^{th} \) cow in \( j^{th} \) period and \( k^{th} \) season,
- \( \mu \) was \( \mu - \bar{X} \)
- \( F_i \) was a constant for the \( i^{th} \) sequence of calving of cow,
- \( P_j \) was a constant for the \( j^{th} \) period of lactation of cow \((j = 1, 2, 3, \ldots, 7)\),
- \( m_k \) was a constant for the \( k^{th} \) season of lactation milk yield in cows \((K = 1, 2, 3)\),
- \( \beta \) was the partial regression of lactation milk yield on age at first calving,
- \( x_{jkm} \) was the age at first calving of the \( i^{th} \) cow in \( j^{th} \) period and \( k^{th} \) season,
- \( e_{ijkm} \) was the random error.
4. Part-lactation milk yield records of first lactation

\[ Y_{jkm} = \alpha + \beta_j + \gamma_k + \delta(X_{jkm}) + e_{jkm} \]

Where,

- \( Y_{jkm} \) was the observed average part-production record of the \( m \)-th cow in \( j \)-th period and \( k \)-th season.
- \( \alpha \) was \( \mu - \bar{X} \).
- \( \beta_j \) was a constant for the \( j \)-th period of part-production record of cow. \( (j = 1, 2, 3, \ldots, 7) \).
- \( \gamma_k \) was a constant for the \( k \)-th season of part-production record in cows. \( (K = 1, 2, 3) \).
- \( \delta \) was the partial regression of part-lactation record on age at first calving.
- \( X_{jkm} \) was the age at first calving of \( m \)-th cow in \( j \)-th period and \( k \)-th season.
- \( e_{jkm} \) was the random error.

5. Other traits such as lactation length, dry period, inter-calving period and service period during first lactation

\[ Y_{jkm} = \mu + \rho_j + \sigma_k + e_{jkm} \]

Where,

- \( Y_{jkm} \) was the observed average record of the trait of \( m \)-th cow in \( j \)-th period and \( k \)-th season.
- \( \mu \) was the population mean.
- \( \rho_j \) was a constant for the \( j \)-th period of the trait of cow \( (j = 1, 2, 3, \ldots, 7) \).
- \( \sigma_k \) was a constant for the \( k \)-th season of the trait in cows \( (K = 1, 2, 3) \).
6. Other traits such as average lactation, dry period inter-calving period and service period pooled over first five lactations

\[ Y_{ijkm} = \mu + F_i + P_j + m_k + \epsilon_{ijkm} \]

Where,

- \( Y_{ijkm} \) was the observed average record of the trait of \( m \)th cow in \( j \)th period and \( k \)th season.
- \( \mu \) was the population mean.
- \( F_i \) was a constant for the \( i \)th sequence of calving of cow.
- \( P_j \) was a constant for the \( j \)th period of the trait of cow (\( j = 1, 2, 3, \ldots, 7 \)).
- \( m_k \) was a constant for the \( k \)th season of the trait in cows (\( k = 1, 2, 3 \)).
- \( \epsilon_{ijkm} \) was the random error.

7. Gestation period during first lactation

\[ Y_{ijkm} = \mu + P_j + m_k + S_i + \epsilon_{ijkm} \]

Where,

- \( Y_{ijkm} \) was the observed average record of the gestation period of \( m \)th cow in \( j \)th period and \( k \)th season.
- \( \mu \) was the population mean.
- \( P_j \) was a constant for the \( j \)th period of gestation length of cow (\( j = 1, 2, 3, \ldots, 7 \)).
- \( m_k \) was a constant for the \( k \)th season of gestation period in cows (\( k = 1, 2, 3 \)).
- \( S_i \) was a constant for the \( i \)th sex of calf of cow (\( S = 1, 2 \)).
- \( \epsilon_{ijkm} \) was the random error.
8. Average gestation period pooled over first five lactations

\[ Y_{ijkm} = \mu + F_i + P_j + m_k + S_i + e_{ijkm} \]

Where,

\( Y_{ijkm} \) was the observed average record of the gestation period of \( m \)th cow in \( j \)th period and \( k \)th season.

\( \mu \) was the population mean.

\( F_i \) was a constant for the \( i \)th sequence of calving of cow.

\( P_j \) was a constant for the \( j \)th period of gestation length of cow (\( j = 1, 2, 3, \ldots , 7 \)).

\( m_k \) was a constant for the \( k \)th season of the gestation period in cows (\( k = 1, 2, 3 \)).

\( S_i \) was a constant for the \( i \)th sex of calf of cow (\( S = 1, 2 \)).

\( e_{ijkm} \) was the random error.

Assumptions in the models used

1. Different effects were independent and fixed.
2. Different effects were additive.
3. The interaction effect among fixed effects were assumed to be zero.
4. The sum of effects of each character added up to zero.
5. The error followed normal distribution with zero mean and population variance \( \sigma^2 \).
Studies on Genetic and Phenotypic Parameters

The data adjusted for various environmental effects were used for the estimation of various phenotypic and genetic parameters under study.

A. Determination of Statistical Measures

The statistical measures such as arithmetic means, standard deviations and coefficient of variability along with standard errors were determined for the various traits (lactation-wise and on all lactations' basis) by using standard techniques as given by Snedecor and Cochran (1968).

B. Estimation of Genetic Parameters

1. Estimation of heritability parameter

Two methods were used to estimate the heritabilities. Method-I Intra-sire regression of offspring on dam

The intra-sire regression of offspring on dam was calculated by pooling the corrected sum of cross-products and corrected sum of squares over all the sires and the heritability estimate was obtained by multiplying by 2 the computed regression as per the formula

\[
b_{yx} = \frac{\sum_{j=1}^{k} \left( \frac{n_j}{n} \sum_{i=1}^{n_j} x_{ij} y_{ij} \right) - \frac{n}{k} \left( \sum_{j=1}^{k} \sum_{i=1}^{n_j} x_{ij} \right)^2}{\sum_{j=1}^{k} \left( \frac{n_j}{n} \sum_{i=1}^{n_j} x_{ij}^2 \right) - \frac{n}{k} \left( \sum_{j=1}^{k} \sum_{i=1}^{n_j} x_{ij} \right)^2}
\]
Where,
\( w_{i} = 1, \ldots, n_{j} \) Number of dam-daughter comparisons for the \( j \)th sire.

\( w_{j} = 1, 2, \ldots, K \).

**Standard error of heritability estimate**

This estimate was calculated by multiplying the standard error of offspring-parent regression by 2. The standard error of regression was calculated by taking the square root of the sampling variance (\( S_{b}^{2} \)). Thus,

\[
S_{b}^{2} = \frac{N - K - 1}{n}
\]

Where,
\( N \) Total number of dam-daughter comparisons for all the sires.

\( K \) No. of sires.

\[
SE(b) = \sqrt{\frac{S_{b}^{2}}{\frac{k}{j=1} \left( \frac{n_{j}}{\sum_{i=1}^{n_{j}} y_{ij} - \frac{1}{n_{j}} \sum_{i=1}^{n_{j}} y_{ij}} \right) - \frac{b^{2}}{\frac{k}{j=1} \left( \frac{n_{j}}{\sum_{i=1}^{n_{j}} x_{ij} - \frac{1}{n_{j}} \sum_{i=1}^{n_{j}} x_{ij}} \right)}}}
\]

\[
SE(h^{2}) = 2 SE(b)
\]
Method II Intraclass paternal half-sib correlation methods

The estimation of heritability value was also done by using paternal half-sib correlation derived from the analysis of variance, according to Winsor and Clarke (1940).

Thus,

\[ h^2 = \frac{4 \cdot \sigma_s^2}{\sigma_s^2 + \sigma_w^2} = 4 \cdot \text{Cov}_{HS}. \]

Except for a small fraction of epistatic variance the sire component consists of additive genetic variance. Mathematical model used was:

\[ Y_{ij} = \mu + S_i + e_{ij} \]

Where,

- \( Y_{ij} \) was the observation under \( j \)th daughter of \( i \)th sire.
- \( \mu \) was the population mean.
- \( S_i \) was the effect of the \( i \)th sire common to all its daughters (\( i = 1, 2, 3, \ldots, s \)).
- \( e_{ij} \) was random error peculiar to \( j \)th individual from \( i \)th sire (\( j = 1, 2, \ldots, n_i \)).

Assumptions

i) \( E(S_i) = E(e_{ij}) = 0 \)
ii) \( E(S_i)^2 = \sigma_s^2 \)
iii) \( E(e_{ij})^2 = \sigma_w^2 \)
### ANALYSIS OF VARIANCE TABLE

(When unequal number of progeny per sire is available)

<table>
<thead>
<tr>
<th>Source</th>
<th>Degrees of freedom</th>
<th>Mean sum of squares</th>
<th>Expectation of mean squares</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total</td>
<td>n - 1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Among sires</td>
<td>S - 1</td>
<td>$SS / S - 1 = MS_s$</td>
<td>$\sigma_w^2 + K\sigma_s^2$</td>
</tr>
<tr>
<td>Progeny within sires</td>
<td>N - S</td>
<td>$SS / N - S = MS_w$</td>
<td>$\sigma_w^2$</td>
</tr>
</tbody>
</table>

Coefficient $K$ was the estimated average number of daughters per sire. This value was obtained by the formula suggested by Snedecor and Cochran (1968).

$$K = \frac{1}{S - 1} \left( N - \frac{\sum n_i^2}{N} \right)$$

Where,
- $K$ was the average estimated number of daughters per sire.
- $S$ was the number of sires.
- $N$ was the total number of the daughters, and
- $\sum n_i^2$ was the sum of squares of actual number of daughters per each sire.

The sire component of variance was obtained as:

$$\sigma_s^2 = \text{Cov}_{HS} = \frac{MS_s - MS_w}{K}$$

$$t = \frac{\sigma_s^2}{\sigma_s^2 + \sigma_w^2}$$
Standard error of heritability estimate

This estimate was computed by the method as suggested by Swiger et al. (1964) assuming normality of the intraclass correlation. Thus,

$$\text{SE}(h^2) = \frac{4 \sqrt{v_t}}{2(n-1)(1-t)\left(1+(k-1)t\right)^2} \frac{1}{k^2(n-5)(S-1)}$$

Where,

$$\sqrt{(v_t)}$$ was the square root of variance of intraclass correlation.

$t$ was intraclass correlation value which is equal to $h^2/4$.

$n$ was total number of observations, and

$S$ was total number of sires.

2. Estimation of Repeatability Parameter

Method of estimation

The repeatability parameter was estimated by the paternal half-sib intraclass correlation method as described by Winsor and Clarke (1940).

$$r = \frac{V_G + V_{EP}}{V_G + V_{EP} + V_{ES}} = \text{Repeatability}$$

The number of measurements per individual were equal.
ANALYSIS OF VARIANCE TABLE

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Degrees of freedom</th>
<th>Mean squares</th>
<th>Expectation of mean squares</th>
</tr>
</thead>
<tbody>
<tr>
<td>Among individuals</td>
<td>N - 1</td>
<td>MS _w</td>
<td>\sigma^2 + K\sigma^2_w</td>
</tr>
<tr>
<td>Within individuals</td>
<td>N(M-1)</td>
<td>MS_e</td>
<td>\sigma^2_e</td>
</tr>
</tbody>
</table>

Where,

- N \_w is the number of individuals.
- M \_w is the number of measurements per individual; equal number for each cow.

The among individual variance component \( \sigma^2_w \) had a value because of differences among individuals while \( \sigma^2_e \) was a value representing the differences among measurements within the individuals. The component \( \sigma^2_w \) estimated all the genetic variance and the portion of the permanent environmental effects.

\[
\sigma^2_w = \frac{MS_w - MS_e}{K}
\]

\[
 repeatability = \frac{\sigma^2_w}{\sigma^2_w + \sigma^2_e}
\]

With equal numbers per group, the formula as given by Swiger et al. (1964) was used for the estimation of standard error. Thus,
Where,
\( M \) was the number of records per cow.
\( m \) was the total number of records = \( KM \), and
\( N \) was the total number of cows.

**Estimation of Correlations**

The phenotypic, genetic and environmental correlations were estimated by using the estimated components of variance and covariance among various traits. The components of variance and covariance among traits were computed by using Henderson's Method I (Henderson, 1953).

1. **Estimation of Phenotypic Correlations**

   Equation used to estimate phenotypic correlation was:

   \[
   r_p = \frac{k \left( \sum_{j=1}^{k} n_j \sum_{i=1}^{n_j} x_{ij} y_{ij} - \left( \sum_{i=1}^{n} x_{ij} \right)^2 \right)}{\sqrt{\sum_{j=1}^{k} \left( \sum_{i=1}^{n_j} x_{ij}^2 \right) \left( \sum_{i=1}^{n_j} y_{ij}^2 \right) - \left( \sum_{i=1}^{n_j} x_{ij} y_{ij} \right)^2}}
   \]

   Where,
   \( r_p = \tau_{x_i y_i} \) was the phenotypic correlation between \( X_i \) and \( Y_i \) traits,
   \( i = 1, \ldots, n \), Number of pairs of observations on \( X_i \) and \( Y_i \) for the \( j^{th} \) sire, and
   \( j = 1, 2, \ldots, K \).
Standard Error of Phenotypic Correlation

This was computed as

\[ SE(r_p) = \sqrt{\frac{1 - r_p^2}{n - 2}} \]

2. Estimation of Genetic Correlations

Hazel et al. (1943) was the pioneer to demonstrate the method of computing genetic correlation from the variance and covariance components obtained by extending the technique of variance component analysis to estimation of covariance components.

ANALYSIS OF VARIANCE TABLE

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Degrees of freedom</th>
<th>Mean Squares</th>
<th>Expectation of mean squares</th>
<th>Estimated value of variance components</th>
</tr>
</thead>
<tbody>
<tr>
<td>Among sires</td>
<td>S-1</td>
<td>MS_s</td>
<td>( \sigma_s^2 + k \sigma_w^2 )</td>
<td>( \sigma_p^2 = \frac{MS_s - MS_w}{K} )</td>
</tr>
<tr>
<td>Within sires</td>
<td>N-S</td>
<td>MS_w</td>
<td>( \sigma_w^2 )</td>
<td>( \sigma_p^2 = \sigma_s^2 + \sigma_w^2 )</td>
</tr>
</tbody>
</table>

Where,

- \( K \) was the average estimated number of daughters per sire.
- \( S \) was the number of sires.
- \( N \) was the total number of daughters.
ANALYSIS OF COVARIANCE TABLE

<table>
<thead>
<tr>
<th>Source of Variation</th>
<th>Degrees of Freedom</th>
<th>Mean Sum of Squares</th>
<th>Expectation of Estimated Covariance of Products of Components of Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Among Sires -1</td>
<td>$MP_s$</td>
<td>$\text{Cov}_w$ + $K\text{Cov}_S$</td>
<td>$\text{Cov}_S = \frac{MP - MP_w}{K}$</td>
</tr>
<tr>
<td>Within Sires</td>
<td>$MP_w$</td>
<td>$\text{Cov}_w$</td>
<td>$\text{Cov}_p = \text{Cov}_S + \text{Cov}_w$</td>
</tr>
</tbody>
</table>

The genetic correlations were computed by the formula as suggested by Hazel et al. (1943).

$$r_{gxgy} = \frac{\sigma_{SXY}^2}{\sqrt{\sigma_{S(x)}^2} \cdot \sqrt{\sigma_{S(y)}^2}}$$

Where,
- $\sigma_{SXY}$ refers to observed genetic covariance between the two traits.
- $\sigma_{S(x)}^2$ and $\sigma_{S(y)}^2$ refer to observed sire component of variance of the two traits.

**Estimation of Standard Error of Genetic Correlation**

This estimate was obtained by the formula as recommended by Robertson (1959b). Thus,

$$SE(r_g) = (1-r_g^2) \cdot \frac{(SE(h_x^2) \cdot SE(h_y^2)}){(2h_x^2 \cdot h_y^2)^{1/2}}$$

Where,
- $h_x^2$ and $h_y^2$ refer to heritabilities of the two characters.
- $SE(h_x^2)$ and $SE(h_y^2)$ refer to their respective standard errors.
Estimation of Relative Efficiency of Selection

Relative selection efficiency on part-lactation milk production records relative to complete lactation milk production records in improving the annual milk production can be determined by using the method as suggested by Lerner and Cruden (1948).

\[ R.E. = \frac{G_x G_y}{h_p} \cdot \frac{\sqrt{h_c^2}}{h_c^2} \]

OR

\[ R.E. = \frac{G_x G_y}{h_p} \cdot \frac{h^2}{h_c^2} \text{ for partial lactation milk production} \]
\[ \text{for complete lactation milk production} \]

Sire Proving with Variable Number of Daughters on Various Part-Milk Yield Records

The object was to know minimum number of daughters required to prove a sire on part-record milk yield.

The degree of genetic resemblance between relatives was the basis of estimating the component of additive variance of a trait in the population and that this component \( h^2 \) of a trait calculated on the basis of part-records of variable number of daughters established the correlation between sire's estimated additive genetic merit \( \hat{g} \) and his true additive genetic merit \( g \).

This correlation between \( g \) and \( \hat{g} \) may be expressed in the form of an equation (Searle, 1964) as
Where,

\( n \) was the number of daughters.

\( h^2 \) was the heritability of the part record.

Thus, the correlations calculated on various combinations of part-records of variable number of daughters, was be compared in all possible ways to determine minimum number of daughters required to estimate the true genetic merit of the sire at an early date.

**Construction of Selection Indexes**

The techniques of path coefficients, analysis of covariance and multiple regression as recommended by Hazel (1943) were used for the construction of various selection indexes.

The selection index, \( I \) was of the form:

\[
I = b_1 X_1 + b_2 X_2 + \ldots + b_n X_n = \sum_{i=1}^{n} b_i X_i
\]

Where,

\( X_i \)'s represent the phenotypic values of the different traits, and \( b_i \)'s represent the relative weights given to each of the traits.

In the present study, twenty-four traits of first lactation were used for developing twenty-nine selection indexes. The various traits used in different combinations for constructing selection indexes were age at first calving in months (\( X_1 \));
first lactation milk yield in kg \( (X_2) \); first service period in days \( (X_3) \); first lactation length in days \( (X_4) \); first calving interval in days \( (X_5) \); first dry period in days \( (X_6) \); ten monthly part lactation milk yield records in kg \( (X_7 \text{ to } X_{16}) \); and nine cumulative part lactation records of milk production from first 60-days to first 270-days of lactation in kg \( (X_{17} \text{ to } X_{24}) \). The minimum number of traits combined in a selection index was two.

The major steps followed in constructing a selection index were as under:

The different quantities such as components of phenotypic and genetic variances and covariances, heritabilities and relative economic values were computed for the individual traits selected for developing the indexes. The variance and covariance components among the traits were computed by using Henderson's Method I (Henderson, 1953). Taking into careful consideration the total expenses of various items involved in maintaining an animal as well as the income received on account of sale of total milk produced over a period of time, the net economic value for each of the traits were calculated on an unit basis and expressed in standard units.

Using all the quantities needed, the normal simultaneous equations were set up for each trait to compute the \( b_i \) values. The \( b_i \)'s were partial regression coefficients required to minimise the sum of squares resulting from non-additive genetic effect plus the environmental contribution \( (E_i) \) in the phenotypic value of \( X_i \)'s i.e. \( \sum_{i=1}^{n} \{ (b_i X_i + E_i - (b_i X_i))^2 \} \) or \( \sum_{i=1}^{n} ( H_i - I_i )^2 \), so that the correlation between the true breeding
value of the individual and the selection index value i.e. $r_{IH}$ was maximised and also the dependent variate, $H$ was predicted from the $X_i$'s in the best possible manner.

The values of $b_1$, $b_2$, .... $b_n$ for the traits combined in a selection index were computed by solving the equations as given below:

$$b_1 \sigma^2 x_1 + b_2 \text{COV} x_1 x_2 + \cdots + b_n \text{COV} x_1 x_n = \text{COV} x_1 H.$$  \hspace{1cm} (1)

$$b_1 \text{COV} x_1 x_2 + b_2 \sigma^2 x_2 + \cdots + b_n \text{COV} x_2 x_n = \text{COV} x_2 H.$$  \hspace{1cm} (2)

$$b_1 \text{COV} x_1 x_1 + b_2 \text{COV} x_2 x_2 + \cdots + b_n \sigma^2 x_n = \text{COV} x_n H.$$  \hspace{1cm} (n)

Where,

$\sigma^2 x_1, \sigma^2 x_2, \ldots, \sigma^2 x_n$ are the phenotypic variances of the individual traits associated with $b_i$'s as diagonal members.

$\text{COV} x_1 x_2, \ldots, \text{COV} x_1 x_n$ and $\text{COV} x_2 x_2, \ldots, \text{COV} x_n x_n$ are the phenotypic covariances among the individual traits as off-diagonal members, and

$\text{COV} x_1 H, \text{COV} x_2 H, \ldots, \text{COV} x_n H$ are the covariances of the individual traits with the composite breeding value.

Now, the left hand side members of $n$ equations given above were further subjected to reduction process to obtain the final form of their matrix.

The right hand side members of $n$ equations were the covariances of $H$ with $X_i$'s values. Since a trait $X_i = G_i + E_i$ and the $G_i$ was assumed to be independent of $E_i$, $\sigma^2 HX_i = \sigma^2 HG_i = a_1 \sigma^2 G_{i1} + a_2 \sigma^2 G_{i2} + \cdots + a_n \sigma^2 G_{in}$. Therefore, the right hand members of the above $n$ equations can also be expressed in the form of equations as under:
COVX_H = \( \sigma^2 G_1 + a \text{COVG}_G + \ldots + a \text{COVG}_{G(n+1)} \)  
\( \text{(n+1)} \)

COVX_H = \( a \text{COVG}_G + \sigma^2 G_2 + \ldots + a \text{COVG}_{G(n+2)} \)  
\( \text{(n+2)} \)

COVX_H = \( a \text{COVG}_G + \sigma^2 G_2 + \ldots + a \text{COVG}_{G(2n)} \)  
\( \text{(2n)} \)

Where,

\( \sigma^2 G_1, \sigma^2 G_2, \ldots, \sigma^2 G_n \) were the additive genetic variances of the individual traits associated with \( a_1 \)'s as diagonal members.

\( \text{COVG}_G, \text{COVG}_G, \ldots, \text{COVG}_G \) were the genetic covariances among the individual traits as off-diagonal members, and

\( a_1, a_2, \ldots, a_n \) were the relative economic values assigned to the individual traits.

Now, the right hand side equations given above were further solved to obtain the values of COVX_H, COVX_H, \ldots, COVX_H in the final form of matrix. Subsequently, both the final matrixes obtained from the two sets of simultaneous equations i.e. 1 to n and (n+1) to (2n) given above were subjected to inversion process to compute \( b \) values for the different traits. By assuming that \( G_1 \) (additive genetic effect) and \( E_1 \) (combined effects of non-additive genetic effect and environment effects) were independent, vector of \( b \)'s were calculated as

\[ b = P^{-1}Ga \]

Where,

\( P \) and \( G \) were the matrices of phenotypic and genetic variances and covariances respectively, and

\( a \) was the vector of economic weights.
Assumptions used in the construction of selection indexes

i) The relative economic values (a_i's) were linear with G_i's.

ii) The phenotypic and genotypic variances and covariances were estimated without error.

iii) The traits were determined in an additive manner i.e. X_i = G_i + E_i.

iv) The G_i and E_i were mutually independent i.e. \sigma^2 G_i E_i was zero.

v) The regression of H on X_i's in a selection index was linear.

vi) The selection index (I) and aggregate breeding worth (H) were normally distributed with \sigma^2 I and \sigma^2 H.

In order to know which selection index was the most suitable for use as a basis of effective selection among Gir cows, the r_{IH} values were computed for each of the selection indexes constructed. The r_{IH} values were obtained by using the following formula as described by Bogart (1959).

\[ r_{IH} = \frac{\sigma_{IH}}{\sqrt{\sigma^2 I \cdot \sigma^2 H}} \]

Where,

r_{IH} was the correlation between aggregate breeding worth (H) of the individual and selection index (I).

\sigma^2 I was the variance of selection index (I).

\sigma^2 H was the variance of aggregate breeding worth (H), and

\sigma_{IH} was the covariance between selection index and aggregate breeding worth.
Subsequent calculations of \( \sigma^2 I \) and \( \sigma^2 H \) and 
\[ \sigma^2 H = \sum_{i=1}^{n} b_i \sigma^2 G_i \] 
\[ \sigma^2 I = \sum_{i=1}^{n} b_i \sigma^2 X_i \]

Therefore,
\[ \sigma^2 I = b_1 \sigma^2 X_1 + b_2 \sigma^2 X_2 + \ldots + b_n \sigma^2 X_n \] 
\[ \sigma^2 H = \sum_{i=1}^{n} b_i \sigma^2 G_i \] 

Where,
\( X_i \)'s represented the phenotypic values of the different traits, and
\( b_i \)'s represented the relative weights given to each of the traits.

The aggregate breeding value of an animal or a group of animals was defined as the sum of the genetic gains made in the several traits, the gain for each trait being weighted by its relative economic value. Thus, the aggregate breeding value of an animal was:
\[ H = \sum_{i=1}^{n} a_i G_i \]

Where,
\( G_i \)'s represented the breeding values or additive genetic values of the individual traits, and
\( a_i \)'s represented the relative economic values of the individual traits.