MATERIALS AND METHODS

3.1. Generation Information about data

a. Source and type of data

The breeding records incorporated in this present investigation comprised of 689 Sahiwal, 639 Brown Swiss x Sahiwal and 3802 Holstein-Friesian x Sahiwal crossbred females, extended over a period of 15 years from 1961-1975. These data were collected from National Dairy Research Institute, Karnal and six Military Dairy Farms of Northern India (Ambala, Bareilly, Birdhantouri, Jullundur, Lucknow and Noerut). The record of Sahiwal and its exotic crossbred females available on the farms were obtained from pedigree book history sheets and the components of first lactation yield were noted from milk record registers.

b. Brief history of the herd

Sahiwal and its Brown Swiss and Holstein-Friesian crossbred cattle included in this study were farm born. Brown Swiss x Sahiwal crossbreeding started at N.D.R.I. farm in 1963. The exotic blood of Ayrshire, Shorthorn, Jersey and Holstein-Friesian was introduced for upgrading the indigenous cattle
(Red Sindhi, Sahiwal, Marana and Tharparker) at Military Dairy Farms round about the beginning of the present century. Friesians were used extensively for crossbreeding at Military Farms due to its superiority in milk production and adaptability (Ferzan, 1927; McGuckin, 1937; Prasad, 1981).

e. Breeding Policy

The breeding policy at NDAI Farm continued to maintain purebred Zebu stock and crossbreeding them with exotic bulls to get 50 and 75 percent exotic blood and further to evolve a breed by inter se matings (well adapted and economic milk producers).

At Military Dairy Farm the attempt was made to maintain exotic gene plasma close to half or 5/8 level, but a range of exotic inheritance (1/64 to 63/64) was produced with forward and backward crossings. The animals recorded at different farms are given in Table 16.

The sirees of females with half or above exotic inheritance were Friesian or Brown Swiss, and with low exotic inheritance were Sahiwal purebreds (Scheme-1).

Scheme-I. Breeding Plan at Military Dairy Farms of North-Western India (Diagramatic)
d. Climatic conditions

All the seven farms considered in this study are situated in North-Western India. The climatic conditions of all the farms are almost similar, therefore, these farms were grouped under one belt of dry Northern region of the country.

e. Managemental Practices

The standard feeding under loose housing system with uniform managerial practices are almost similar at these Military Farms, because they follow common instructions given by Central Directorate of Military Farms, New Delhi. Weaning was practiced at birth and cows were milked by hand. Most of the cows were milked twice a day but animals giving more than 12 kg were milked thrice a day. A few high yielding cows (10 kg) were milked four times a day. Animals that were born at one farm but were shifted to another farm during early growth and completed their production at another farm were considered to be part of such herds.

Milk yield was recorded at each milking for each animal. The animals with breeding troubles, low production or female calves failed to meet the rearing standard (growth rate) were culled from time to time. Birth weight of the calf was recorded within eight hours of birth, weekly weights were recorded for each female calves upto one year and thereafter monthly weights were recorded upto first calving. The Friesian crosses were bred at the age of 21-24 months or at body weight of 340 kg. The corresponding figures for indigenous animals were 24-27 months or 320 kg body weight. Recently it was modified to 15 months age or 260 kg.
<table>
<thead>
<tr>
<th>Exotic inheritance groups</th>
<th>F 1</th>
<th>F 2 &amp; F 3</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1/8</td>
<td>2/8</td>
<td>3/8</td>
</tr>
</tbody>
</table>

Table 16. Animals recorded at different farms

<table>
<thead>
<tr>
<th>Farms</th>
<th>Zebu</th>
<th>Sahiwal</th>
<th>Brown Swiss x Sahiwal</th>
<th>Friesian x Sahiwal</th>
</tr>
</thead>
<tbody>
<tr>
<td>(A) M.O.R.I., Karnal</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cattle Farm</td>
<td>477</td>
<td>12</td>
<td>16</td>
<td>238</td>
</tr>
<tr>
<td>(B) Military Farms</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(1) Ambala</td>
<td>87</td>
<td>162</td>
<td>15</td>
<td>69</td>
</tr>
<tr>
<td>(2) Bareilly</td>
<td>78</td>
<td>64</td>
<td>56</td>
<td>82</td>
</tr>
<tr>
<td>(3) Birdhanteeri</td>
<td>5</td>
<td>39</td>
<td>39</td>
<td>35</td>
</tr>
<tr>
<td>(4) Jullundur</td>
<td>82</td>
<td>57</td>
<td>92</td>
<td>71</td>
</tr>
<tr>
<td>(5) Lucknow</td>
<td>14</td>
<td>22</td>
<td>30</td>
<td>146</td>
</tr>
<tr>
<td>(6) Meerut</td>
<td>212</td>
<td>45</td>
<td>53</td>
<td>132</td>
</tr>
<tr>
<td>Total</td>
<td>689</td>
<td>308</td>
<td>409</td>
<td>380</td>
</tr>
</tbody>
</table>

Total: 5130
body weight (which over the earlier) for all breeds.

f. Feeding

The standard feeding schedule as prescribed by Directorate of Military Farms is based on body weight, genetic group and considering the maintenance, growth, production, pregnancy and climatic conditions. The young stock is housed and reared separately in following groups:

1. Birth to 6 months
2. Six months to one year
3. One year to two year
4. Two year to mating

9. Recording of observations

The available observations were recorded from history and pedigree sheets and milk record registers of females for the following traits:

A. Body weights at different ages (kg)

1. Weight at birth
2. Weight at two months
3. Weight at four months
4. Weight at six months
5. Weight at nine months
6. Weight at twelve months
7. Weight at fifteen months
8. Weight at eighteen months
9. Weight at fertile service
10. Weight at first calving
The growth rate at different intervals of age were worked out from the above information.

11. Growth rate from birth to 2 months of age
12. Growth rate from 2 to 4 months age
13. Growth rate from 4 to 6 months age
14. Growth rate from 6 to 9 months age
15. Growth rate from 9 to 12 months age
16. Growth rate from 12 to 15 months age
17. Growth rate from 15 to 18 months age

B. Production Traits

18. Age at first calving (months)
19. First lactation length (days)
20. First lactation yield (kg)
21. First, second and third 300 days or less, as standard yield (kg)
22. First dry period (days)
23. The components of first lactation yield are:
   (a) Initial yield (kg): Average daily yield from 2 days production after colostrum period.
   (b) Ascending yield: Average daily yield from 16th and 17th days production after calving.
   (c) Peak Yield: Average one day yield from maximum yield of two consecutive days.
   (d) Descending yield: The average daily yield from 120th and 121st days production after calving.
   (e) Milking daily average yield: Complete lactation production divided by days in milk.
3.2. Classification of Data

The data of Sahiwal, BS x Bu and Friesian x Sahiwal were classified according to the farm, genetic groups, parity, season and periods for all the traits.

a. Farm

Although standard managerial practices were followed at all the farms but variation from farm to farm existed due to availability of green fodder, housing, land, irrigation, climate, genetic composition of the herd and other uncontrolled conditions.

b. Genetic Groups

The Friesian x Sahiwal crosses were grouped in seven classes with an interval of 12.5% level of exotic inheritance (1/6, 2/6, 3/6, 4/6, 5/6, 6/6 and 7/6). Exotic inheritance less than 12.5% fraction was clubbed with nearest level of blood group. Sahiwal animals were considered as one genetic group. Brown Swiss x Sahiwal females were grouped in five classes (6/6, 4/6, 3/6, 2/6 and F4-F3).

c. Parity of Birth

Parity of birth could have significant effect on birth weight and weight at subsequent months. The data classified in four parity groups: (1) First (2) Second (3) Third, and fourth (4) Fifth and above sequence of calving.
d. Season of birth/saving

The year was divided into four seasons based on climate: (i) November - January (Winter) (ii) February - April (Spring) (iii) May - July (Summer) (iv) August - October (Monsoon).

e. Period of birth/saving

The data collected for 15 years in case of Sahiwal and Friesian x Sahiwal crosses and 12 years in case of Brown Swiss x Sahiwal crosses were divided into 5 and 4 periods of 3 years each.

<table>
<thead>
<tr>
<th>Years</th>
<th>Period I</th>
<th>Period II</th>
<th>Period III</th>
<th>Period IV</th>
<th>Period V</th>
</tr>
</thead>
<tbody>
<tr>
<td>1961-1963</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1964-1966</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1967-1969</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1970-1972</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1973-1975</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

3.3. Statistical Methods

The analysis was done on IBM 1620 (Institute of Agricultural Research Statistics, New Delhi) and 360 (Delhi University Computer Centre), Electronic Computers. In order to study the genetic architecture of growth and production traits, the non-genetic factors affecting the traits were neutralized. As the breeding data was non-orthogonal with disproportionate
sub-class numbers the least square technique was used to overcome these difficulties (Harvey, 1966). Statistical methods were employed according to the type of data for calculating required estimates. The processing of the data was done accordingly.

1. Purebred Sahiwal
2. Brown Swiss x Sahiwal crosses
3. Holstein-Friesian x Sahiwal crosses
   (a) Friesian x Sahiwal crosses (4/8 to 7/8) sired by Friesian bulls.
   (b) Sahiwal x Friesian crosses (1/8 to 3/8) sired by Sahiwal bulls.

3.3.1. Mathematical Estimates

a. The average daily gain (g/day)

The absolute gain in weight per unit time was worked out from different intervals of time as:

\[ \text{Average daily gain} = \frac{W_2 - W_1}{T_2 - T_1} \]

Where, \( W_1 \) and \( W_2 \) are initial and final weights at \( T_1 \) and \( T_2 \) initial and final age of animals.

b. Least square mean

The Model-I of Eisenhart was used for least square analysis (Harvey, 1966). Five way and four way classification with fixed effect without interaction was used for body weights,
growth rate, milk components of first lactation yield and first, second and third lactation yields.

\[ Y_{ijklmn} = u + a_i + b_j + c_k + d_l + f_m + e_{ijklmn} \]

Where,

- \( Y_{ijklmn} \): The observations on \( n \)th animal of \( n \) season,
- \( i \): period,
- \( k \): parity,
- \( j \): genetic group
- \( l \): farm
- \( u \): overall mean when equal sub-class number exist
- \( a_i \): effect of the \( i \)th farm (1-6)
- \( b_j \): effect of the \( j \)th genetic group (1-7)
- \( c_k \): effect of the \( k \)th parity of birth (1-4)
- \( d_l \): effect of the \( l \)th period of birth (1-5)
- \( f_m \): effect of the \( m \)th season (1-4)
- \( e_{ijklmn} \): random error

To study the least square means of first lactation components, first lactation yield and first, second and third lactation yield the parity of birth was eliminated. The restriction was imposed that \( \sum a_i = \sum b_j = 0 \). The coefficients of one effect were subtracted from other coefficients of within the effect by columns and rows. Thus reduced least square equations were produced. Then from the inverse matrix of the reduced equation, the constant estimates were obtained. In the Model the \( a_i \) are expressed as deviations from \( u \). Therefore, it is logical to assume that \( \sum a_i = 0 \) and obtained the constant estimates as deviations from \( u \). Reduced least square equation was obtained after subtracting one coefficient of the effect from
column and rows within the effect and symmetrical set of equations were solved for the inversion of the variance - covariance matrix and constants were worked out from the inverse elements and RMA's of the equations.

**Standard error**

The standard error of u was worked out from the inverse matrix

\[ \text{SE} u = \sqrt{(C_{ii}) s^2} \]

Where,

- \( u \) = population mean when equal frequencies exist among the classes.
- \( C_{ii} \) = corresponding diagonal inverse element for that constant
- \( s^2 \) = error mean square

**Estimation of variance components**

The sum of squares for each effect was obtained in the general way as shown below:

\[ S_i, S_q, = \hat{B}' Z^{-1} B \]

Where \( \hat{B} \) is a row vector of constant estimates for a given set (such as \( a_k \)); \( Z^{-1} \) is the inverse of the segment of the inverse of the variance - covariance matrix, corresponding, by row and column, to this set of constants; and \( B \) is a column vector of the set of constants.

The analysis of variance model in general was followed for various traits under study (Harvey, 1966).
d. Test of all comparisons among means

In a group of more than two means, $F$ test will not give any clue as to how many differences were significant at known probability, therefore to overcome this difficulty, Tukey's test (1953) was applied to test the differences among all means.

$$D = q \sqrt{\frac{\text{Error mean square}}{n_2}}$$

$D =$ differences between two means.

$q =$ Table value at $n_1$ and $n_2$ degrees of freedom,

$n_1 =$ number of subclass means used.

$n_2 =$ error degree of freedom.

The differences between two means are greater or equal to $D$ value, indicate the significance at 5% or 1% level of probability.

e. Correction of the data for genetic study

Various non-genetic factors (farms, parity, season and period) and genetic groups affecting the traits were worked out by analysis of variance. The constants of all levels of all the factors affecting the traits were obtained and individual observations were corrected for the significant effect of non-genetic factors. The adjusted body weight, growth rate and production traits were obtained as given below:

$$y_{ijklmn} = y_{ijklmn} - (a_i + b_j + c_k + d_l + f_m)$$
Where,

\[ Y_{ijklmn} = \text{The actual body weight record of the animal at given age.} \]

\[ a_1 = \text{fear constant} \]

\[ b_j = \text{genetic group constant} \]

\[ c_k = \text{parity of birth constant} \]

\[ d_i = \text{period of birth constant} \]

\[ e = \text{constant for season of birth} \]

f. Regression Analysis

The adjusted data was used for the regression analysis. Various regression models were used to estimate the first total lactation production from growth rate and body weights (premanifested traits), lactation length and first lactation components.

(a) Linear regression model with one trait

\[ Y = a + bx + e \]

(b) Multiple linear regression model, taking two or more than two traits:

\[ Y = a + b_1x_1 + b_2x_2 + \ldots + b_nx_n + e \]

(c) Quadratic or curvilinear regression model with one, two or more than two traits:

\[ Y = a + b_1x_1 + b_1^2x_1^2 + b_2x_2 + b_2^2x_2^2 + \ldots + b_nx_n + b_n^2x_n^2 \]

Where,

\[ a = \text{intercept value} \]

\[ y = \text{dependent traits} \]
\[ b_1 - b_n = \text{coefficient of linear regression} \]

\[ x_1 \text{ to } x_n = \text{independent traits} \]

\[ e = \text{residual error} \]

\[ (d) \text{ F test} \]

The significant test for the regression was estimated as:

\[ F = \frac{\text{Regression mean square}}{\text{Residual mean square}} \]

at \( n_1 \) (degree of freedom of regression) and \( n_2 \) (degree of freedom of error) degrees of freedom.

\[ (e) \text{ The coefficient of determination (R}^2) \text{ value was calculated:} \]

\[ R^2 = \frac{\text{Sum of square due to regression}}{\text{Total sum of square}} \]

9. Age (months) and first lactation production (kg) relationship

To study the effect of age at first calving, on first lactation yield and first lactation length, the 4 sets (1. Sahiwal, 2. B.S \( \times \) Sb, 3. HF \( \times \) Sb sired by Persian sires, and 4. B.S \( \times \) HF sired by Sahiwal sires) of corrected data were classified into eight classes with three months interval of age at first calving. The classes were 1. \( \leq 27.9 \) 2. 27.9-30.0 3. 30.0-33.0 4. 33.0-36.0 5. 36.0-39.0 6. 39.0-42.0 7. 42.0-45.0 and 8. \( \geq 45.1 \) months of age.
h. Body weight (at first calving) and first lactation yield relationship

The body weights at first calving were grouped into seven classes with 40 kg class difference. 1. $\leq 250$ 2. 251-290 3. 291-330 4. 331-370 5. 371-410 6. 411-450 and 7. $\geq 451$ kg body weight to find the effect of body weight (at first calving) on first lactation yield. The four sets of corrected data were used for the study.

't' test

To test the significance differences between means from non paired data, 't' test was used:

$$t = \frac{\bar{X} - \bar{Y}}{SE(\bar{X} - \bar{Y})}$$ with $(N_1 + N_2 - 2)$ degree of freedom

3.3.2. Genetic Estimates

Genetic study was made on all the corrected records of body weights, growth rates and production performance traits.

Sires with five or more than five daughters were included in this study. Heritability, genetic and phenotypic correlations were worked out by paternal half-sib unbalanced design (Becker, 1975).

a. Heritability ($h^2$) estimates

The model used is given below:

$$y_{ik} = u + s_i + e_{ik}$$

Where, $y_{ik} = k^{th}$ animal records of $i^{th}$ sire
\[ u = \text{common mean to all animals} \]

\[ S_i = \text{effect of } i^{\text{th}} \text{ sire common to all its daughters} \]

\[ e_{ik} = \text{uncontrolled environmental and genetic deviations attributable to individuals within sire groups.} \]

**Analysis of variance**

\[
\begin{array}{cccc}
\text{Source of Variation} & d.f. & SS & MS & \text{Df} \\
\hline
\text{Between sires} & S-1 & SS & MS & VW+V\bar{S} \\
\text{Progeny within sires} & S(n-1) & SS & MS & VW \\
\end{array}
\]

Where,

\[ S = \text{number of sires} \]

\[ n = \text{number of individuals within the } i^{\text{th}} \text{ sire.} \]

\[ k = \text{weighted average, number of progeny under each sire} \]

\[ VS = \text{the variance due to sire which contains } 1/4, \text{ the genetic variance plus a small fraction of epistatic variance} \]

\[ VW = \text{variance attributed within sires, which includes all the environmental variance plus } 3/4 \text{ the genetic variance, all of dominance and a major part of epistatic variance.} \]

\[
\begin{align*}
VS &= \frac{RS - MS}{k} \\
V^2 &= \frac{VS}{VW + VS} \times 4
\end{align*}
\]
\[
\bar{X} = \frac{\sum \bar{n}_i^2}{s-1} \left( n_i - \frac{n_i^2}{n} \right)
\]

Where,

- \( S \) = number of sires
- \( n_i \) = Total number of individuals under all sires (5)
- \( n_i^2 \) = Sum of squares of the progeny per sire.

**Standard error of \( h^2 \)**

The standard error of \( h^2 \) for unequal number of progeny per sire was estimated by Swiger et al. (1984) method:

\[
SE_{h^2} = \frac{4}{V(t)}
\]

Where,

\[
V(t) = \frac{4}{\bar{X}^2} \frac{2(n-1)(1-t)^2 \left[ 1 + (\bar{X}-1)t \right]^2}{(n-3)(3-t)}
\]

Where,

- \( t \) = intra class correlation
  \[
t = \frac{VS}{VS + VW}
\]
- \( n \) = Total number of progeny
- \( \bar{X} \) = weighted number of daughters' under each sire

**Estimation of correlations**

The components of covariances between two traits were calculated by Becker (1975) method for the estimation of genetic and phenotypic correlations.
Analysis of Covariance

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>Mean cross product (MCP)</th>
<th>Expected mean cross product (EMCP)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between sires</td>
<td>5-1</td>
<td>MCP_B</td>
<td>COV + ( \overline{K} ) COV_B</td>
</tr>
<tr>
<td>Pregeny within sires</td>
<td>n_y-5</td>
<td>MCP_y</td>
<td>COV_y</td>
</tr>
</tbody>
</table>

\( \overline{K} \) was estimated as in heritability estimate for unequal number of progeny per sire in the analysis of variance. The components of variance were derived as before in \( h^2 \) estimate.

Estimating covariance components

\[
\text{COV}_u = \text{MCP}_u
\]

\[
\text{COV}_s = \frac{\text{MCP}_s - \text{MCP}_u}{\overline{K}}
\]

b. Genetic correlation \( (r_g) \)

\[
r_g = \frac{\text{COV}_{(xy)}}{\sqrt{\text{VS}(x) \text{VS}(y)}}
\]

Where, \( x \) and \( y \) represents two characters in the same individual.

\( \text{COV}_{(xy)} \) = Covariance between two traits \( x \) and \( y \) due to sires.

\( \text{VS}(x) \) = Variance of \( x \) trait due to sires

\( \text{VS}(y) \) = Variance of \( y \) trait due to sires

In an analysis of half-sib families the component of covariance between sire estimate 1/4 additive genetic covariance, 1/16 Cov AA and 1/64 Cov AAA (Decker, 1979).
Standard error (SE) of genetic correlation ($r_g$)

Standard error of the genetic correlation was estimated by Reeve (1958) and Robertson (1959) method:

$$SE. r_g = \frac{1 - r_g^2}{\sqrt{2}} \times \frac{SE(h_1^2) \times SE(h_2^2)}{h_1^2 \times h_2^2}$$

Where, $h_1^2$ and $h_2^2$ were the heritabilities of $x$ and $y$ traits used for $r_g$.

b. Phenotypic correlation ($r_p$)

Phenotypic correlation coefficient was estimated as outlined by Searle (1961) and Becker (1975):

$$r_p = \frac{COV_x(x,y) + COV_y(x,y)}{VS(x) + WW(x) \times VS(y) + WW(y)}$$

Where,

$COV_x(x,y)$ = Covariance between $x$ and $y$ traits within sires.

$COV_y(x,y)$ = The additive genetic covariance for $x$ and $y$ traits between sires.

$VS(x)$ = Sire component of variance for $x$ trait

$VS(y)$ = Sire component of variance for $y$ trait

$WW(x)$ = Environmental component of variance for $x$ trait

$WW(y)$ = Environmental component of variance for $y$ trait.
Standard error (SE) of phenotypic correlation

Standard error of phenotypic correlation was estimated as given by Penrose and Sukhatme (1967):

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

Where,

- \( r_p(xy) \) = phenotypic correlation coefficient between x and y character in the same individual.
- \( n-2 \) = degree of freedom

3.3.3. Construction of Selection Index

From the adjusted data the following estimates were derived to construct selection indexes by Hazal (1943) method and assumptions.

Genetic estimates

The following genetic estimates were calculated by paternal half-sib correlation method:

(a) Heritability of each trait.
(b) Genetic correlation between traits.

Phenotypic estimates

(a) Phenotypic correlations.
(b) Phenotypic standard deviation of traits.

Relative economic value for each trait

In the present study the economic value reported by Kuber Ram and Kulwant Singh (1975) were used to work out
relative economic value for each trait.

The rate of body weight at six, 12 months and weight at first calving will be same as for age at respective intervals. The economic values of the traits for Friesian crossbreeds were considered equal to Brown Swiss crossbred animals. The sale price of milk is ₹1.40 per kg, with 3.5% fat was taken. It was corrected on the basis of fat content produced by the cow (Ghuluk and Mishra, 1976).

Relative economic values of some traits of $Sx$, $BS x S$, $HF x S$ and $S x HF$ cattle are given below:

<table>
<thead>
<tr>
<th>Traits</th>
<th>$S$</th>
<th>$BS x S$</th>
<th>$HF x S$</th>
<th>$S x HF$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Body weight at 6 month age</td>
<td>0.459</td>
<td>0.366</td>
<td>0.416</td>
<td>0.436</td>
</tr>
<tr>
<td>Body weight at 12 month age</td>
<td>0.464</td>
<td>0.382</td>
<td>0.409</td>
<td>0.412</td>
</tr>
<tr>
<td>Body weight at 1st calving</td>
<td>0.654</td>
<td>0.389</td>
<td>0.490</td>
<td>0.560</td>
</tr>
<tr>
<td>Age at 1st calving (mths)</td>
<td>5.606</td>
<td>4.332</td>
<td>4.628</td>
<td>5.128</td>
</tr>
<tr>
<td>Average peak yield (kg)</td>
<td>1.429</td>
<td>1.491</td>
<td>1.437</td>
<td>1.420</td>
</tr>
<tr>
<td>First milking average (kg)</td>
<td>1.000</td>
<td>1.000</td>
<td>1.000</td>
<td>1.000</td>
</tr>
</tbody>
</table>
Index equations (Hazel, 1945)

1. \[ b_1 x_1 x_1 + b_2 x_1 x_2 + \cdots + b_n x_1 x_n = r_{x_1} \frac{d_1 r_{G_1} G_1 + d_2 r_{G_2} G_2 + \cdots + d_n r_{G_n} G_n}{G_H} \]

2. \[ b_1 x_2 x_1 + b_2 x_2 x_2 + \cdots + b_n x_2 x_n = r_{x_2} \frac{d_1 r_{G_1} G_1 + d_2 r_{G_2} G_2 + \cdots + d_n r_{G_n} G_n}{G_H} \]

3. \[ b_1 x_n x_1 + b_2 x_n x_2 + \cdots + b_n x_n x_n = r_{x_n} \frac{d_1 r_{G_1} G_1 + d_2 r_{G_2} G_2 + \cdots + d_n r_{G_n} G_n}{G_H} \]

Where,

\( b_n \) are the regression coefficients calculated to maximize the correlation between Index I and additive genetic value (G) for a trait which in turn maximize the value of \( R_{IH} \).

\( r_{x_n} \) = Phenotypic correlation between two traits.

\( \frac{r_{G_n} G_n}{G_H} \) = Genotypic correlation between two traits.

\[ d_n = s_1 \frac{G_n}{G_H} \text{ where } s_1 = \text{relative economic value of a trait.} \]

Genetic standard deviation (\( G^2 G \)) = \( h^2 \text{ x } G^2 \) of each trait.

\[ r_{G_n} G_n = \sqrt{h^2} \text{ The efficiency of selection index was measured in terms of } R_{IH} (\text{Hazel, 1945}). \]