

EFFICIENCY OF FAMILY SELECTION

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1. INTRODUCTION

IN investigations on breeding programmes the chief aim is to study the possibility of improving the performance of the stock in respect of a given character and the alternative methods by means of which this can be achieved. The main tool the breeder has in his control is selection. "Causing or permitting some kinds of individuals to produce more offspring than other kinds do is selection" (Lush, *Animal Breeding Plans*). The primary effect of selection is to change the gene frequency and the frequency of gametes carrying certain gene combinations and its outward effect is to move the average of the population far from the original position. Even though genes are the units of inheritance, the animal is the smallest unit of selection. Selection may be resorted to between still larger units such as families, inbred line, breeds, etc.

In animal populations we generally encounter such as poultry, sheep, etc., the family classification is usually a hierarchal one, *viz.*, each sire is mated to a number of dams and each dam produces one or more offspring. In such a classification the procedures of selection may be any of the following:—

- (a) Selecting an individual on the basis of its own performance.
- (b) Selecting a group of individuals that constitute a full-sib family, on the basis of the average performance of such a family. Here half-sib family classification is disregarded.
- (c) Selecting a group of individuals constituting a paternal half-sib family (sire family) on the basis of the average performance of such a family. Here each family consists of a mixture of full-sibs and half-sibs.
- (d) Selecting an individual on the basis of an index with appropriate weights attached to its own performance and the average performance of the full-sib family to which it belongs.
- (e) Selecting an individual on the basis of an index with suitable weights attached to its own performance, the average

performances of the full-sib family and sire family to which it belongs.

Procedures (b) and (d) were discussed by Lerner (1950) and (c) and (e) by Osborne (1957). Lush (1947) discussed the relative merits of individual selection and family selection for traits of incomplete heritability. These authors have obtained the expressions for efficiency of the different selection procedures for the case of equal numbers of dams being mated to each sire and each dam producing equal number of offspring. But in actual practice such a condition is rarely satisfied. In this study the expressions for efficiency when unequal numbers are involved and when dominance is taken into consideration are obtained. A practical example is provided as an illustration.

2. NOTATION AND DEFINITIONS

We assume that the phenotypic differences among individuals are due to joint and independent effects of additive differences in genotype, the non-additive genotypic effect of dominance and environment. It is assumed that the interaction among non-allelic genes is negligible and the heredity-environment interaction is absent. If σ_p^2 denotes the phenotypic variance then

$$\sigma_p^2 = \sigma_a^2 + \sigma_d^2 + \sigma_e^2$$

where σ_a^2 , σ_d^2 and σ_e^2 are respectively the additive genetic, dominance and environmental components of variance. The proportion of additive genetic part to the total variance, viz., σ_a^2/σ_p^2 is denoted by h^2 and is termed as the coefficient of heritability. Heritability can be defined on a family basis as well. Let this be denoted by h_F^2 .

Let \bar{G}_S denote the average genotypic value of the selected lot and \bar{G} the average of the whole lot. Then the genetic advance is $(\bar{G}_S - \bar{G})$. The estimate of this genetic advance is given by the following relationship, assuming that the phenotype and the genotype are linearly related:

$$\text{Est } (\bar{G}_S - \bar{G}) = \beta_{G|I} (\bar{I}_S - \bar{I})$$

where $\beta_{G|I}$ is the regression of the genotype on phenotype, and \bar{I}_S and \bar{I} the average phenotypic values of the selected lot and whole population respectively. These phenotypic values may be individual performances or the family performances or the indices of selection. The genetic advance may also be denoted as $i\beta_{G|I}\sigma_I$ where i is the intensity of

selection in terms of the standard deviation units and σ_I the phenotypic standard deviation. The regression coefficient reduces to the coefficient of heritability when the index is the individual phenotypic value or the average performance of the family as the case may be.

The relative efficiency of alternative procedures of selection may be estimated by comparing the values of expected genetic advance accruing from adopting each one of them for the same intensity of selection. Accordingly, the efficiency of family selection relative to individual selection reduces to

$$\frac{h_F^2}{h^2} \cdot \frac{\sigma_F}{\sigma_p}$$

3. ESTIMATION OF VARIANCE COMPONENTS

In a population under consideration let there be s -sires, the i -th sire being mated to m_i dams and the j -th dam mated to the i -th sire giving rise to n_{ij} offspring.

Let

$$\sum_{i=1}^{m_i} n_{ij} = N_{ij}, \quad \sum_{j=1}^s N_{ij} = N \quad \text{and} \quad \sum_{i=1}^s m_i = M.$$

Let y_{ijk} denote the phenotypic value of the character under study, observed on the k -th progeny obtained by mating the j -th dam to the i -th sire. Then we may express,

$$y_{ijk} = \mu + s_i + d_{ij} + e_{ijk}$$

where,

μ = effect common to all individuals

s_i = ,, ,, to progeny of the i -th sire

d_{ij} = ,, ,, to progeny of the j -th dam and i -th sire

e_{ijk} = a random deviation.

Let these effects be independent and

$$E(s_i) = 0; \quad E(s_i^2) = \sigma_s^2;$$

$$E(d_{ij}) = 0; \quad E(d_{ij}^2) = \sigma_m^2 \quad \text{and} \quad E(e_{ijk}) = 0; \quad E(e_{ijk}^2) = \sigma_e^2$$

where E denotes expectation.

Let

$$\bar{y}_{ij} = \sum_{k=1}^{n_{ij}} \frac{y_{ijk}}{n_{ij}}$$

$$\bar{y}_{i..} = \sum \frac{n_{ij}\bar{y}_{ij}}{N_i} = \sum_{j=1}^{m_i} \sum_{k=1}^{n_{ij}} \frac{y_{ijk}}{N_i}$$

and

$$\bar{y}_{...} = \sum_{i=1}^s \frac{N_i \bar{y}_{i..}}{N} = \sum_{i=1}^s \sum_{j=1}^{m_i} \sum_{k=1}^{n_{ij}} \frac{y_{ijk}}{N}$$

Then the variation between the N individuals can be partitioned into components as given in the following table (Sastry, 1956).

Analysis of variance table

Source of variation	Degrees of freedom	Sum of squares	M.S.	E (M.S.)
Between sires	$s-1$	$\sum_i N_i (\bar{y}_{i..} - \bar{y}_{...})^2$	A	$\sigma^2 + \lambda_2 \sigma_m^2 + \lambda_3 \sigma_s^2$
Between dams within sires	$\sum_i (m_i - 1)$	$\sum_i \sum_j n_{ij} (\bar{y}_{ij.} - \bar{y}_{i..})^2$	B	$\sigma^2 + \lambda_1 \sigma_m^2$
Within dams within sires	$\sum_i \sum_j (n_{ij} - 1)$	$\sum_i \sum_j \sum_k (y_{ijk} - \bar{y}_{ij.})^2$	C	σ^2
TOTAL	$N-1$	$\sum_i \sum_j \sum_k (y_{ijk} - \bar{y}_{...})^2$		

where,

$$\lambda_1 = \frac{1}{\sum_i (m_i - 1)} \left\{ N - \sum_i \left(\frac{\sum_j n_{ij}^2}{N_i} \right) \right\}$$

$$\lambda_2 = \frac{1}{s-1} \left\{ \sum_i \left(\sum_j \frac{n_{ij}^2}{N_i} - \sum_i \sum_j \frac{n_{ij}^2}{N} \right) \right\}$$

and

$$\lambda_3 = \frac{1}{s-1} \left\{ N - \sum_i \frac{N_i^2}{N} \right\}.$$

From the analysis of variance given above the estimates of σ_a^2 , σ_d^2 and σ_e^2 could be obtained by noting the following relations:—

$$\sigma_s^2 = \frac{1}{4} \sigma_a^2$$

$$\sigma_m^2 = \frac{1}{4} \sigma_a^2 + \frac{1}{4} \sigma_d^2$$

$$\sigma^2 = \frac{1}{2} \sigma_a^2 + \frac{3}{4} \sigma_d^2 + \sigma_e^2.$$

4. INDIVIDUAL SELECTION

The expectation of the mean square between the N individuals estimates the phenotypic variation $\sigma_{p_1}^2$ among them and is given by

$$\begin{aligned} \sigma_{p_1}^2 &= E \frac{1}{N-1} \sum_i \sum_j \sum_k (y_{ijk} - \bar{y}_{...})^2 \\ &= \frac{1}{N-1} \{ (s-1) (\sigma^2 + \lambda_2 \sigma_m^2 + \lambda_3 \sigma_s^2) + (M-s) \\ &\quad \times (\sigma^2 + \lambda_1 \sigma_m^2) + (N-M) \sigma^2 \} \\ &= \sigma^2 + A_1 \sigma_m^2 + A_2 \sigma_s^2 \\ &= \frac{1}{4} (2 + A_1 + A_2) \sigma_a^2 + \frac{1}{4} (3 + A_1) \sigma_d^2 + \sigma_e^2 \end{aligned}$$

where,

$$A_1 = \frac{1}{N-1} \left\{ N - \sum_i \sum_j \frac{n_{ij}^2}{N} \right\}$$

and

$$A_2 = \frac{1}{N-1} \left\{ N - \sum_i \frac{N_i^2}{N} \right\}.$$

The additive genetic variance is $\frac{1}{4} (2 + A_1 + A_2) \sigma_a^2$ and the heritability on an individual basis is

$$h_1^2 = \frac{\frac{1}{4} (2 + A_1 + A_2) \sigma_a^2}{\sigma_{p_1}^2}$$

and the gain from individual selection is $ih_1^2 \sigma_{p_1}$.

5. FULL-SIB FAMILY SELECTION

The mean square between unrelated full-sib families estimate.

$$\begin{aligned}\sigma_{p_2}^2 &= E \frac{1}{M-1} \sum_i \sum_j (\bar{y}_{ij} - \bar{y}_{...})^2 \\ &= B_1 \sigma^2 + B_2 \sigma_m^2 + B_3 \sigma_a^2 \\ &= \frac{1}{4} (2B_1 + B_2 + B_3) \sigma_a^2 + \frac{1}{4} (3B_1 + B_2) \sigma_d^2 + B_1 \sigma_e^2\end{aligned}$$

where

$$\begin{aligned}B_1 &= \frac{1}{M-1} \left\{ \sum_i \sum_j \frac{1}{n_{ij}} - \frac{M}{N} \right\} \\ B_2 &= \frac{1}{M-1} \left\{ (M-2s) + \frac{M}{N^2} \sum_i \sum_j n_{ij}^2 \right. \\ &\quad \left. + \frac{2}{N} \sum_i \frac{N-N_i}{N_i^2} \cdot m_i \sum_j n_{ij}^2 \right\}\end{aligned}$$

and

$$B_3 = \frac{1}{M-1} \left\{ M + \frac{M}{N^2} \sum_i N_i^2 - \frac{2}{N} \sum_i m_i N_i \right\}.$$

The additive genetic component of variance is $\frac{1}{4} (2B_1 + B_2 + B_3) \sigma_a^2$ and the heritability on full-sib family basis is

$$h_2^2 = \frac{\frac{1}{4} (2B_1 + B_2 + B_3) \sigma_a^2}{\sigma_{p_2}^2}.$$

The gain by selection on the basis of the average performance of the full-sib family is $ih_2^2 \sigma_{p_2}$. The efficiency of full-sib family selection relative to individual selection is

$$\frac{h_2^2 \sigma_{p_2}}{h_1^2 \sigma_{p_1}} = \frac{2B_1 + B_2 + B_3}{2 + A_1 + A_2} \cdot \frac{\sigma_{p_1}}{\sigma_{p_2}}.$$

6. SIRE FAMILY SELECTION

The mean square between sire families has expectation

$$\begin{aligned}\sigma_{p_3}^2 &= E \frac{1}{s-1} \sum_{i=1}^s (\bar{y}_{i..} - \bar{y}_{...})^2 \\ &= C_1 \sigma^2 + C_2 \sigma_m^2 + C_3 \sigma_s^2 \\ &= \frac{1}{4} (2C_1 + C_2 + C_3) \sigma_a^2 + \frac{1}{4} (3C_1 + C_2) \sigma_d^2 + C_1 \sigma_e^2\end{aligned}$$

where,

$$\begin{aligned}C_1 &= \frac{1}{s-1} \left(\sum_i \frac{1}{N_i} - \frac{s}{N} \right), \\ C_2 &= \frac{1}{s-1} \left\{ \sum_i \frac{1}{N_i^2} \sum_j n_{ij}^2 - \frac{2}{N} \sum_i \frac{1}{N_i} \sum_j n_{ij}^2 \right. \\ &\quad \left. + \frac{s}{N^2} \sum_i \sum_j n_{ij}^2 \right\}\end{aligned}$$

and

$$C_3 = \frac{1}{s-1} \left\{ (s-2) + \frac{s}{N^2} \sum_i N_i^2 \right\}.$$

The additive genetic variance is $\frac{1}{4} (2C_1 + C_2 + C_3) \sigma_a^2$ and the heritability is

$$h_3^2 = \frac{\frac{1}{4} (2C_1 + C_2 + C_3) \sigma_a^2}{\sigma_{p_3}^2}.$$

The gain by selection on the basis of sire family selection is $ih_3^2 \sigma_{p_3}$ and the efficiency relative to individual selection is

$$\frac{h_3^2 \sigma_{p_3}}{h_1^2 \sigma_{p_1}} = \frac{2C_1 + C_2 + C_3}{2 + A_1 + A_2} \frac{\sigma_{p_3}}{\sigma_{p_1}}.$$

7. SELECTION INDEX

Next we proceed to obtain an index of selection for an individual taking into account its own performance, the average performance of

the full-sib family to which it belongs and that of the corresponding sire family. Our object is to construct an index I_{ijk} given by

$$I_{ijk} = W_1' y_{ijk} + W_2' \bar{y}_{ij.} + W_3' \bar{y}_{i..}$$

where y_{ijk} , $\bar{y}_{ij.}$ and $\bar{y}_{i..}$ are the values of the performance of the k -th individual, the (i, j) -th full-sib family and the i -th sire family to which the k -th individual belongs and W_1' , W_2' and W_3' are respectively the appropriate weights to be attached to them. Without loss of generality this can be written as

$$I_{ijk} = W_1 (y_{ijk} - \bar{y}_{ij.}) + W_2 (\bar{y}_{ij.} - \bar{y}_{i..}) + W_3 (\bar{y}_{i..} - \bar{y}_{...})$$

where $\bar{y}_{...}$ is the population mean.

Let G_{ijk} denote the genotypic value of the k -th individual we are considering. The deviation of the same from the population value ($G_{ijk} - \bar{G}_{...}$) say, M_{ijk} can be written as

$$M_{ijk} = (G_{ijk} - \bar{G}_{...}) = (G_{ijk} - \bar{G}_{ij.}) + (\bar{G}_{ij.} - \bar{G}_{i..}) + (\bar{G}_{i..} - \bar{G}_{...})$$

The purpose of selection is to make the genetic advance maximum, viz., $i\beta_{GI}\sigma_I$ maximum.

The value of the regression coefficient is

$$\begin{aligned} & \beta_{GI} \\ = & \frac{\text{Cov}(M_{ijk}, I_{ijk})}{\sigma_{I_{ijk}}^2} \\ = & \frac{W_1 \text{Cov}\{(G_{ijk} - \bar{G}_{ij.}), (y_{ijk} - \bar{y}_{ij.})\} + W_2 \text{Cov}\{(\bar{G}_{ij.} - \bar{G}_{i..}), (\bar{y}_{ij.} - \bar{y}_{i..})\} + W_3 \text{Cov}\{(\bar{G}_{i..} - \bar{G}_{...}), (\bar{y}_{i..} - \bar{y}_{...})\}}{W_1^2 V(y_{ijk} - \bar{y}_{ij.}) + W_2^2 V(\bar{y}_{ij.} - \bar{y}_{i..}) + W_3^2 V(\bar{y}_{i..} - \bar{y}_{...})} \end{aligned}$$

Noting that the regression of genotype on phenotype provides an estimate of heritability, the regression value β_{GI} reduces to

$$\frac{W_1 h_1'^2 \sigma_1'^2 + W_2 h_2'^2 \sigma_2'^2 + W_3 h_3'^2 \sigma_3'^2}{W_1^2 \sigma_1'^2 + W_2^2 \sigma_2'^2 + W_3^2 \sigma_3'^2}$$

where $h_1'^2$, $h_2'^2$ and $h_3'^2$ are what may be termed as effective heritabilities, for individuals within full-sib families, between full-sib family averages within sire families and between sire families respectively and $\sigma_1'^2$, $\sigma_2'^2$

and $\sigma_3'^2$ the corresponding phenotypic variances. These are obtained as follows:—

$$\begin{aligned} \sigma_1'^2 &= E \frac{1}{M-1} \sum_t \sum_j \frac{1}{n_{tj}-1} \sum_k (y_{tk} - \bar{y}_{tj})^2 \\ &= \sigma^2 \\ &= \frac{1}{2} \sigma_a^2 + \frac{3}{4} \sigma_d^2 + \sigma_e^2 \\ h_1'^2 &= \frac{\frac{1}{2} \sigma_a^2}{\sigma_1'^2} \end{aligned}$$

$$\begin{aligned} \sigma_2'^2 &= E \frac{1}{s-1} \sum_{i=1}^s \frac{1}{m_i-1} \sum_{j=1}^{m_i} (\bar{y}_{ij} - \bar{y}_{i..})^2 \\ &= K_1 \sigma^2 + K_2 \sigma_m^2 \\ &= \frac{1}{4} (2K_1 + K_2) \sigma_a^2 + \frac{1}{4} (3K_1 + K_2) \sigma_d^2 + K_1 \sigma_e^2 \\ h_2'^2 &= \frac{\frac{1}{4} (2K_1 + K_2) \sigma_a^2}{\sigma_2'^2} \end{aligned}$$

where

$$K_1 = \frac{1}{s-1} \left\{ \sum_{i=1}^s \frac{1}{m_i-1} \sum_j \frac{1}{n_{ij}} - \sum_i \frac{1}{N_i} \right\}$$

and

$$K_2 = \frac{1}{s-1} \left[\sum_{i=1}^s \frac{1}{m_i-1} \left\{ (m_i - 2) + \frac{m_i}{N_i^2} \sum_{j=1}^{m_i} n_{ij}^2 \right\} \right]$$

$$\begin{aligned} \sigma_3'^2 &= E \frac{1}{s-1} \sum_{i=1}^s (\bar{y}_{i..} - \bar{y}_{...})^2 \\ &= C_1 \sigma^2 + C_2 \sigma_m^2 + C_3 \sigma_s^2 \\ h_3'^2 &= \frac{\frac{1}{4} (2C_1 + C_2 + C_3) \sigma_a^2}{\sigma_3'^2} \end{aligned}$$

where C_1 , C_2 and C_3 are as defined in Section 6.

The weights are to be so chosen that $\beta_{G/I\sigma_I} (= K, \text{ say})$

$$= \frac{W_1 h_1'^2 \sigma_1'^2 + W_2 h_2'^2 \sigma_2'^2 + W_3 h_3'^2 \sigma_3'^2}{\sqrt{W_1^2 \sigma_1'^2 + W_2^2 \sigma_2'^2 + W_3^2 \sigma_3'^2}}$$

is maximum. Differentiating with respect to W_1 , W_2 and W_3 equating $\partial K/\partial W_1$, $\partial K/\partial W_2$ and $\partial K/\partial W_3$ to zero respectively, we obtain

$$W_1 = \frac{h_1'^2 \cdot D}{K^2}, \quad W_2 = \frac{h_2'^2 \cdot D}{K^2} \quad \text{and} \quad W_3 = \frac{h_3'^2 \cdot D}{K^2}$$

where

$$D = W_1 h_1'^2 \sigma_1'^2 + W_2 h_2'^2 + W_3 h_3'^2 \sigma_3'^2.$$

As we are interested in the proportional weights only we can take

$$W_1 = h_1'^2, \quad W_2 = h_2'^2 \quad \text{and} \quad W_3 = h_3'^2.$$

Thus the index of optimum selection is

$$I_{ijk} = h_1'^2 (y_{ijk} - \bar{y}_{ij.}) + h_2'^2 (\bar{y}_{ij.} - \bar{y}_{i..}) + h_3'^2 (\bar{y}_{i..} - \bar{y}_{...})$$

or

$$I_{ijk} = x_1 + \frac{h_2'^2 - h_1'^2}{h_1'^2} \cdot x_2 + \frac{h_3'^2 - h_2'^2}{h_1'^2} \cdot x_3$$

where x_1 , x_2 and x_3 are the deviations of the individual phenotypic value, full-sib family average and sire family average respectively from the population mean. Let this index be called I_e .

On similar lines we obtain an index based on the individual performance and the full-sib family performance to which it belongs. Let this index be denoted by I_d and is given by

$$I_d = x_1 + \frac{h_2''^2 - h_1''^2}{h_1''^2} \cdot x_2$$

where x_1 and x_2 are the deviations of the individual and full-sib family average phenotypic performances from the population mean and $h_1''^2$ and $h_2''^2$ are the effective heritabilities within full-sib families respectively and these are given by

$$h_1''^2 = h_1'^2 \quad \text{and} \quad h_2''^2 = h_2'^2$$

and the respective phenotypic variances are

$$\sigma_1''^2 = \sigma_1'^2 \quad \text{and} \quad \sigma_2''^2 = \sigma_p^2.$$

8. EFFICIENCY OF SELECTION BASED ON THE INDEX

The efficiency of selection based on the index I , relative to individual selection, as we have already seen in Section 2, is

$$\frac{\beta_{GI} \sigma_I}{h^2 \sigma_p} = \frac{\text{Cov}(G, I)}{\sigma_I} \cdot \frac{1}{h^2 \sigma_p} = \frac{R}{h^2} \cdot \frac{\sigma_a}{\sigma_p} = \frac{R}{h}$$

where R is the correlation between G and I .

This correlation R can also be viewed as the multiple correlation coefficient between the genotype G and the mutually independent parts $(y_{ijk} - \bar{y}_{ij.})$, $(\bar{y}_{ij.} - \bar{y}_{i..})$ and $(\bar{y}_{i..} - \bar{y}_{...})$.

$$R^2 = b_1'^2 \frac{\sigma_1'^2}{\sigma_a^2} + b_2'^2 \frac{\sigma_2'^2}{\sigma_a^2} + b_3'^2 \frac{\sigma_3'^2}{\sigma_a^2}$$

where b_1' , b_2' and b_3' are regression coefficients of the genotype over the three phenotypes and therefore

$$b_1' = h_1'^2, b_2' = h_2'^2 \text{ and } b_3' = h_3'^2.$$

Then the efficiency of selection on the basis of the index I_e relative to individual selection is

$$\sqrt{\frac{(h_1'^2)^2 \sigma_1'^2}{h^2 \sigma_a^2} + \frac{(h_2'^2)^2 \sigma_2'^2}{h^2 \sigma_a^2} + \frac{(h_3'^2)^2 \sigma_3'^2}{h^2 \cdot \sigma_a^2}}$$

Similarly for the index I_d the efficiency is

$$\sqrt{\frac{(h_1''^2)^2}{h^2} \cdot \frac{\sigma_1''^2}{\sigma_a^2} + \frac{(h_2''^2)^2}{h^2} \cdot \frac{\sigma_2''^2}{\sigma_a^2}}$$

9. ILLUSTRATION

Data relating to the sheep breeding scheme conducted at the Government Livestock Farm, Hissar, during 1936-47, were used to illustrate the applications of the procedures developed in the present investigation. The birth-weights and wool-yields (first clip yield and the total of first two clip yields) of the non-inbred females were considered for the purpose of this study. The total number of ewes considered was 510 and they came from 365 dams and 22 sires.

The estimates of additive genetic, dominance and the environmental components of variance as obtained by the method given in Section 3, for the different characters considered are given in Table I.

TABLE I

Character	$\hat{\sigma}_a^2$	$\hat{\sigma}_d^2$	$\hat{\sigma}_e^2$
Birth Weight ..	0.1951	1.1315	— (0.3447)
First Clip Yield ..	13.8206	12.9881	11.9486
Total of First two Clips	36.7207	36.1610	26.8289

In Table II, the estimates of heritability for the individual performance, the average performances of the full-sib family and the sire family for different characters are given.

TABLE II

Character	Estimate of heritability of		
	Individual value	Full-sib family average	Sire family average
Birth Weight ..	0.1452	0.1513	0.4208
First Clip Yield ..	0.3531	0.3703	0.7089
Total of First two Clips	0.3648	0.3815	0.7182

Let E_b , E_c , E_d and E_e denote the percentage efficiencies of full-sib family selection, sire family selection, selection based on I_d and I_e respectively relative to individual selection. These efficiencies are tabulated in Table III for the different characters considered.

TABLE III

Character	E_b	E_c	E_d	E_e
Birth Weight ..	97.9	95.7	100.1	119.0
First Clip Yield	98.2	79.8	100.2	109.0
Total of First two Clips ..	98.1	78.9	100.2	108.0

In Table IV, the indices of selection I_d and I_e for the traits considered are given.

TABLE IV

Character	I_d	I_e
Birth Weight ..	$x_1 + 0.46x_2$	$x_1 + 0.12x_2 + 2.95x_3$
First Clip Yield ..	$x_1 + 0.53x_2$	$x_1 + 0.25x_2 + 1.69x_3$
Total of First two Clips ..	$x_1 + 0.50x_2$	$x_1 + 0.23x_2 + 1.60x_3$

10. DISCUSSION

The expressions for efficiencies of family selection relatively to individual selection given in Sections 5 and 6 can be seen to be functions of the coefficient of variation for the character considered, heritability of the character and the size of the families and their number. In particular, when there is no dominance and $n_{ij} = n$ (*viz.*, each dam produces equal number of offspring), $m_i = m$ (*viz.*, each sire is mated to the same number of dams) and when s , the number of sires used is large the expressions reduce to

$$\frac{n + 1}{\sqrt{2n \{2 + (n - 1) h^2\}}}$$

in the case of full-sib family selection and

$$\frac{2 + n(1 + m)}{\sqrt{4mn [4 + \{n(1 + m) - 2\} h^2]}}$$

for sire family selection. The former expression was obtained by Lerner (1950) and the latter by Osborne (1957). The expressions obtained by these authors have their own limitations as the assumptions involved would seldom hold in practical situations.

The results obtained in the illustration indicate that selecting families as a whole is not more efficient than individual selection in the case of wool yield and birth weight in sheep for which the estimates of heritability are not so low as obtained for poultry characters (*e.g.*, 0.045 for production index) by Lerner and others where family selection could be usefully practised as suggested by Lush. However, the results indicate comparatively greater efficiency of sire family selection for birth weight than for wool yield which is in consonance with the fact that birth weight is less heritable than wool yield. In this connection it may be added that the additive genetic variance constitutes a smaller fraction of the total phenotypic variance for birth weight than wool yield. It is interesting to note, however, that if heritability is defined in the broad sense to include dominance variance, the value for birth weight is extremely high whereas for wool yield the value on the basis of first clip is as high as 0.69 and for the total of first two clips is 0.73.

The results show that selecting an individual on the basis of its own performance and the average performances of the full-sib family and the sire family to which it belongs is more efficient than individual selection showing an increase to the extent of 9% and 19% respectively

for wool yield and birth weight. Index based on the individual performance and that of the corresponding full-sib family performance does not lead to increase in efficiency. This may be partly ascribed to small average size of the full-sib family (about 1.4 individuals per family). This is also seen from Table II, where no great difference between individual heritability and full-sib family heritability is noticed.

The indices indicate that less importance need be given to full-sib family averages and greater weights should be attached to the sire family averages, about three times the individual performance in selecting for birth weight and about two times in the case of wool yield.

11. SUMMARY

The expressions for the efficiency of full-sib family and sire family selection are obtained when unequal numbers of dams are mated to each sire and each dam produces unequal number of offspring. Selection indices are obtained when individual performance, the average performances of the full-sib and the paternal half-sib families to which the individual belongs are taken into account. The results thus obtained are illustrated by an example.

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