AN INVESTIGATION OF SELECTION INDEXES
IN SWINE POPULATIONS

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TABLE OF CONTENTS

TABLE OF CONTENTS (Continued)

LIST OF TABLES

LIST OF TABLES (Continued)

List of Figures

Figure | Page

CHAPTER I

INTRODUCTION

In most large animal and plant populations, the economic value of the organism is a function of more than one characteristic. It seems logical that each character contributing to the net merit of the individual should receive attention in selection. This would indicate that some type of index should be used.

In 1936, H. Fairfield Smith developed a discriminant function for plant selection which was designed to combine the information from several traits into an index. Hazel (1943) expanded on the theory developed by Smith from the genetic viewpoint and illustrated how selection indexes could be constructed for three swine traits. Prior to this, Hazel and Lush (1942) stated that selection for an index which gives proper weight to each trait is more efficient than selection for one trait at a time or for several traits simultaneously with an independent culling level for each trait. Almost three decades have passed since this theory of selection indexes was developed, but selection indexes have not been and are not now a commonly used method of selection. One might wonder as to why they have not been used more.

One explanation might be that the theory is not well enough understood to apply it to the development of new indexes. This does not seem likely due to the number of researchers who have written short mimeographed papers on the construction of selection indexes including the application of the method of least squares in their construction.

A second explanation might be the difficulty encountered in solving n simultaneous equations. This could definitely have been a deterent several years ago, but with the advent of the modern computer this problem should have been eleviated.

The third and probably the most plausible explanation is the problems involved in the estimation of the parameters used in the construction of the index. Hazel (1943) concludes that an index constructed from data taken on a herd in one locality may not be widely applicable. The reasons being:

1. Relative economic values for a trait may vary with the particular locality or nature of the enterprize.
2. The genetic constitution of herds may differ, especially where they are under distinctly non-random mating systems such as intense inbreeding.
3. Different managerial practices may cause the standard deviations for the traits to vary in different herds.
4. Few herds are large enough to provide data sufficient to make the sampling errors of the genetic constants small.

The primary objectives of this study were to (1) determine the proper method of weighting economic values when using the least squares method of construction, (2) compare the use of positive versus negative economic values for certain traits, (3) determine the economic values for different swine traits, (4) examine the effect of varying the estimates of the genetic and phenotypic correlations on the correlation between the index and the aggregate breeding value for a two and three trait index, (5) construct indexes involving various combinations of swine traits and (6) compare the indexes constructed with respect to their predictability of the aggregate breeding value.

CHAPTER II

SELECTION INDEXES

Construction

A selection index can be defined as an arithmetic device designed to combine information from different characters and from different sources into one value for each individual. The purpose of a selection index is to make selection more effective in terms of the total performance of the organism.

The phenotypic value, expressed as a deviation from the mean, for a particular trait can be defined as:

$$P_i - \bar{P}_i = a_i + e_i$$

where:

$P_i - \bar{P}_i$ = phenotypic value of trait i expressed as a deviation from the mean
a_i = breeding value for trait i
e_i = remainder (includes dominance, espistatic, and environmental deviations).

The breeding value and remainder are assumed to be independent.

If it can be assumed that the aggregate breeding value of an individual is a linear function of the individual breeding values for each trait, the aggregate breeding value of the j^{th} individual can be expressed as:

$$A_j = V_1a_1 + V_2a_2 + \dots + V_na_n = \sum_i V_ia_i$$

where the V_i represent the relative increase in net worth expected from one unit increase in trait i, independent of changes in the other traits (i.e. relative economic values) and the a_i are the breeding values for the various traits of the j^{th} individual.

However, only phenotypes of the individuals can be measured. Therefore, the index to be developed and used must be a linear function of the phenotypic values. The general form for the index would be:

$$I_j = b_1(P_1-\bar{P}_1) + b_2(P_2-\bar{P}_2) + \dots + b_n(P_n-\bar{P}_n) = \sum_i b_i(P_i-\bar{P}_i)$$

where the $P_i-\bar{P}_i$ denote the phenotypes of the various characters of individual j as deviations from the mean and the b_i the weights to be given the various phenotypic values. The b_i should be such that both:

1. the correlation between A and I is a maximum, and
2. the sum of squares of deviations, $\sum_j [A_j-I_j]^2$, is a minimum. This is essentially two ways of saying the same thing. The method of least squares can be used to minimize the sum of squares of deviations. The model is:

$$A_j = I_j - e_j$$

or

$$V_1a_1+V_2a_2+\dots+V_na_n = b_1(P_1-\bar{P}_1)+b_2(P_2-\bar{P}_2)+\dots+b_n(P_n-\bar{P}_n)+e_j.$$

The V's are constants, the P's and a's are variables and the b's are partial regression coefficients. To minimize

$\sum_j (A_j - I_j)^2$ the partial differential with respect to each b_i is taken and set equal to zero (i.e. $\frac{\partial \sum_j (A_j - I_j)^2}{\partial b_i}$). The summation is over the n individuals upon which the index is to be based. The resulting normal equations can be written in the following form by dividing every element by n-1.

$$
\begin{array}{l}
b_1 \hat{\sigma}_{P_1}^2 + b_2 \hat{\sigma}_{P_{12}} + \ldots + b_n \hat{\sigma}_{P_{1n}} = \hat{\sigma}_{P_1 A} \\
b_1 \hat{\sigma}_{P_{12}} + b_2 \hat{\sigma}_{P_2}^2 + \ldots + b_n \hat{\sigma}_{P_{2n}} = \hat{\sigma}_{P_2 A} \\
\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\
b_1 \hat{\sigma}_{P_{1n}} + b_2 \hat{\sigma}_{P_{2n}} + \ldots + b_n \hat{\sigma}_{P_n}^2 = \hat{\sigma}_{P_n A}
\end{array}
$$

The covariance between the n^{th} phenotypic value $(P_n - \bar{P}_n)$ and the aggregate breeding value can be expressed:

$$\hat{\sigma}_{P_n A} = \sum_i V_i \hat{\sigma}_{P_n a_i}$$

but,

$$P_n - \bar{P}_n = a_n + e_n$$

and it was assumed that breeding values and remainders were independent so,

$$\hat{\sigma}_{a_i e_n} = 0$$

which leads to the following result for $\hat{\sigma}_{P_n A}$.

$$\hat{\sigma}_{P_n A} = \sum_i V_i \hat{\sigma}_{a_n a_i}$$

This result leads to the following expression for the normal equations:

$$b_1\hat{\sigma}_{P_1}^2 + b_2\hat{\sigma}_{P_{12}} + \dots + b_n\hat{\sigma}_{P_{1n}} = V_1\hat{\sigma}_{a_1}^2 + V_2\hat{\sigma}_{a_{12}} + \dots + V_n\hat{\sigma}_{a_{1n}}$$

$$b_1\hat{\sigma}_{P_{12}} + b_2\hat{\sigma}_{P_2}^2 + \dots + b_n\hat{\sigma}_{P_{2n}} = V_1\hat{\sigma}_{a_{12}} + V_2\hat{\sigma}_{a_2}^2 + \dots + V_n\hat{\sigma}_{a_{2n}}$$

$$\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots$$

$$b_1\hat{\sigma}_{P_{1n}} + b_2\hat{\sigma}_{P_{2n}} + \dots + b_n\hat{\sigma}_{P_n}^2 = V_1\hat{\sigma}_{a_{1n}} + V_2\hat{\sigma}_{a_{2n}} + \dots + V_n\hat{\sigma}_{a_n}^2$$

where

$\hat{\sigma}_{P_i}^2$ = an estimate of the phenotypic variance for trait i.

$\hat{\sigma}_{P_{ij}}$ = an estimate of the phenotypic covariance between traits i and j.

$\hat{\sigma}_{a_i}^2$ = an estimate of the additive genetic variance for trait i.

$\hat{\sigma}_{a_{ij}}$ = an estimate of the additive genetic covariance between traits i and j.

V_i = economic value for trait i.

b_i = partial regression coefficients.

These are a symmetrical, non-singular (full rank) system of equations which can be solved by any appropriate method such as the Abbreviated Doolittle.

Since the normal equations are to be solved for the b_i, estimates must be obtained for:

1. the phenotypic variance for each trait
2. the phenotypic covariance or correlation between each pair of traits

$$\hat{\sigma}_{P_{ij}} = r_{P_{ij}}\,\hat{\sigma}_{P_i}\,\hat{\sigma}_{P_j}$$

3. the additive genetic variance or heritability for each trait

$$\hat{\sigma}_{a_i}^{2} = h_i^2 \, \hat{\sigma}_{P_i}^{2}$$

4. the additive genetic covariance or genetic correlation between each pair of traits

$$\hat{\sigma}_{a_{ij}} = r_{g_{ij}} \, \hat{\sigma}_{a_i} \, \hat{\sigma}_{a_j}$$

5. relative economic value for each trait.

An estimate of the correlation between the aggregate breeding value and the index can be determined as follows:

$$R_{AI} = \frac{\hat{\sigma}_{AI}}{\hat{\sigma}_I \, \hat{\sigma}_A}$$

where

$$\hat{\sigma}_A^2 = \sum_{ij} V_i \, V_j \, \hat{\sigma}_{a_{ij}} = \sum_i V_i^2 \, \hat{\sigma}_{a_i}^{2} + \sum_{\substack{ij \\ i \neq j}} V_i V_j \, \hat{\sigma}_{a_{ij}}$$

$$\hat{\sigma}_I^2 = \sum_{ij} b_i \, b_j \, \hat{\sigma}_{P_{ij}} = \sum_i b_i^2 \, \hat{\sigma}_{a_i}^{2} + \sum_{\substack{ij \\ i \neq j}} b_i b_j \, \hat{\sigma}_{P_{ij}}$$

$$\hat{\sigma}_{AI} = \sum_i b_i \, \hat{\sigma}_{P_i A}$$

The first set of normal equations illustrate that:

$$\hat{\sigma}_{P_i A} = \sum_j b_j \, \hat{\sigma}_{P_{ij}}$$

therefore,

$$\hat{\sigma}_{AI} = \sum_{ij} b_i b_j \, \hat{\sigma}_{P_{ij}} = \hat{\sigma}_I^{2}$$

so,

$$R_{AI} = \frac{\hat{\sigma}_I^2}{\hat{\sigma}_I \, \hat{\sigma}_A} = \frac{\hat{\sigma}_I}{\hat{\sigma}_A}$$

The correlation between the aggregate breeding value and the index turns out to be the ratio of the standard deviation of the index to the standard deviation of the aggregate breeding value. For an index involving only two traits, the variance of the aggregate breeding value and the index would be:

$$\hat{\sigma}_A^{\,2} = V_1^{\,2}\,\hat{\sigma}_{a_1}^{\,2} + V_2^{\,2}\,\hat{\sigma}_{a_2}^{\,2} + 2V_1V_2\,\hat{\sigma}_{a_{12}}$$

and

$$\hat{\sigma}_I^{\,2} = b_1^{\,2}\,\hat{\sigma}_{P_1}^{\,2} + b_2^{\,2}\,\hat{\sigma}_{P_2}^{\,2} + 2b_1b_2\,\hat{\sigma}_{P_{12}}$$

From this, Willham (1964) states that the heritability of the index would be as follows:

$$\begin{aligned} h_I^2 &= \hat{\sigma}_I^2/\hat{\sigma}_A^2 \\ &= R_{AI}^{\,2} \end{aligned}$$

Hazel (1943) states that for the special case where the traits are uncorrelated, R_{AI} is a maximum when each regression coefficient is equal to the product of the relative economic value and the heritability for each trait. This point can be illustrated by letting all $\hat{\sigma}_{P_{ij}}$ and $\hat{\sigma}_{a_{ij}}$ be zero in the normal equations. The normal equations then become:

$$\begin{aligned} b_1\,\hat{\sigma}_{P_1}^{\,2} &= V_1\,\hat{\sigma}_{a_1}^{\,2} \\ b_2\,\hat{\sigma}_{P_2}^{\,2} &= V_2\,\hat{\sigma}_{a_2}^{\,2} \\ &\cdots\cdots \\ b_n\,\hat{\sigma}_{P_n}^{\,2} &= V_n\,\hat{\sigma}_{a_n}^{\,2} \end{aligned}$$

and the solution to each of these equations is as follows:

$$b_i = V_i \hat{\sigma}_{a_i}^2 / \hat{\sigma}_{P_i}^2 = V_i h_i^2$$

Another interesting point is made by Kempthorne (1957) when he shows in the case where all economic values are zero except one, the index will still depend on the observed values for the other traits. The normal equations would become:

$$\begin{aligned}
b_1\hat{\sigma}_{P_1}^2 + b_2\hat{\sigma}_{P_{12}} + \ldots + b_n\hat{\sigma}_{P_{1n}} &= V_1\hat{\sigma}_{a_1}^2 \\
b_1\hat{\sigma}_{P_{12}} + b_2\hat{\sigma}_{P_2}^2 + \ldots + b_n\hat{\sigma}_{P_{1n}} &= V_1\hat{\sigma}_{a_{12}} \\
\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\
b_1\hat{\sigma}_{P_{1n}} + b_2\hat{\sigma}_{P_{2n}} + \ldots + b_n\hat{\sigma}_{P_n}^2 &= V_1\hat{\sigma}_{a_{1n}}
\end{aligned}$$

Solutions would exist for all the b_i if and only if genetic relationships existed between the traits. With solutions for all the b_i, then the phenotypic values for all the traits would appear in the index.

An index of the form given earlier where all the phenotypic values are expressed as deviations from their mean is cumbersome to use in practice. The index would be more conveniently used if it were expressed in terms of the observed phenotype. This could be accomplished by adding the sum of the products of the regression coefficients and the corresponding mean to the index value.

$$I + \sum_i b_i\bar{P}_i = b_1P_1 + b_2P_2 + \ldots + b_nP_n$$

In a selection index, it is not the absolute magnitude of the index values which is of real interest but rather the relative magnitude of the index values. Also, for a given population, $\sum_i b_i \bar{P}_i$ would be a constant for all individuals. Therefore, adding a constant to all index values does not impair the usefulness of the values. The index to be used in practice could then be written:

$$I' = b_1 P_1 + b_2 P_2 + \ldots b_n P_n$$

without changing its usefulness.

Hazel (1943) illustrates the construction of selection indexes with n simultaneous equations involving correlations. The simultaneous equations appear as follows, using the notation of this chapter.

$$B_1 + B_2\, r_{p_{12}} + \ldots + B_n\, r_{p_{1n}} = r_{P_1 A}$$

$$B_1\, r_{p_{12}} + B_2 + \ldots + B_n\, r_{p_{2n}} = r_{P_2 A}$$

$$\cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot\ \cdot$$

$$B_1\, r_{p_{1n}} + B_2\, r_{p_{2n}} + \ldots + B_n = r_{P_n A}$$

where:

$B_i = b_i\, \hat{\sigma}_{P_i} / \hat{\sigma}_A$

$r_{P_i A}$ = the correlation between the aggregate breeding value and the i^{th} phenotypic value.

The correlation ($r_{P_i A}$) can be expressed in the following manner:

$$r_{P_i A} = r_{a_i P_i} [d_1\, r_{g_{1i}} + d_2\, r_{g_{2i}} + \ldots + d_n\, r_{g_{ni}}]$$

and,

$d_i = V_i\, \hat{\sigma}_{a_i} / \hat{\sigma}_A$

$r_{a_i P_i}$ = the correlation between the breeding value and phenotypic value for each trait. This is equal to the square root of the heritability (h_i).

$$r_{P_i A} = \frac{h_i}{\hat{\sigma}_A} [V_1 \hat{\sigma}_{a_1} r_{g_{1i}} + V_2 \hat{\sigma}_{a_2} r_{g_{2i}} + \ldots + V_n \hat{\sigma}_{a_n} r_{g_{ni}}]$$

The estimate of the standard deviation for the aggregate breeding value appears on both sides of each equation and, therefore, does not need to be estimated.

Henderson (1951) presents a procedure which allows the economic values to change without causing the index to be recalculated. The principle is to compute n indexes (I_1, I_2, ..., I_n) to predict the breeding values (a_1, a_2, ..., a_n) for each of the n characters under consideration.

The index for the i^{th} trait is:

$$I_i = b_{i1} P_1 + b_{i2} P_2 + \ldots + b_{in} P_n$$

where the P's represent the phenotypic values for the traits of interest and the b's represent the partial regression coefficients which maximize $R_{I_i a_i}$. The b's are obtained by solving the following simultaneous equations.

$$\begin{aligned}
b_{i1} \hat{\sigma}_{P_1}^2 + b_{i2} \hat{\sigma}_{P_{12}} + \ldots + b_{in} \hat{\sigma}_{P_{1n}} &= \hat{\sigma}_{a_i a_1} \\
b_{i1} \hat{\sigma}_{P_{12}} + b_{i2} \hat{\sigma}_{P_2}^2 + \ldots + b_{in} \hat{\sigma}_{P_{2n}} &= \hat{\sigma}_{a_i a_2} \\
\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\
b_{i1} \hat{\sigma}_{P_{1n}} + b_{i2} \hat{\sigma}_{P_{2n}} + \ldots + b_{in} \hat{\sigma}_{P_n}^2 &= \hat{\sigma}_{a_i a_n}
\end{aligned}$$

The n individual indexes are combined with the n economic values (V_1, V_2, ..., V_n) to give the total or overall index.

$$I = V_1I_1 + V_2I_2 + \dots + V_nI_n$$

A Numerical Example

Three traits will be used to numerically illustrate the construction of a selection index. The traits used will be weaning weight (P_1), average daily gain (P_2) and probe backfat (P_3). The desired form of the index is:

$$I = b_1P_1 + b_2P_2 + b_3P_3$$

where the b's represent partial regression coefficients and the P's are the phenotypic values for the above three traits. In this example, the aggregate breeding value which is being predicted will be defined as:

$$A = V_1a_1 + V_2a_2 + V_3a_3$$

where the a's are the breeding values of the respective traits and the V's are the corresponding economic values.

Construction of a selection index requires estimates of the phenotypic variances, economic values, heritabilities and genetic and phenotypic correlations. The estimates of the genetic correlations assumed in this example are 0.52 between weaning weight and average daily gain ($r_{g_{12}}$), -.05 between weaning weight and probe backfat ($r_{g_{13}}$) and -.18 between average daily gain and probe backfat ($r_{g_{23}}$). Corresponding estimates of the phenotypic correlations are 0.37 ($r_{p_{12}}$), -.22 ($r_{p_{13}}$) and -.02 ($r_{p_{23}}$). The remaining parameter estimates are summarized in Table I. All parameter esti-

TABLE I

PARAMETER ESTIMATES USED IN CONSTRUCTING AN EXAMPLE THREE TRAIT SELECTION INDEX

Trait	Economic Value[a]	$\hat{\sigma}_P$	$\hat{\sigma}^2_P$	h^2
P_1:Weaning weight, lb.	1.00	6.10	37.21	0.08
P_2:Average daily gain, lb./day	11.11	0.18	0.0324	0.33
P_3:Probe backfat, inch	-9.26	0.16	0.0256	0.40

[a] The determinations of the economic values are given in Chapter III.

mates except the economic values are based on a review of the literature. The economic values presented are on a relative basis.

The normal equations (in matrix notation) which are used to obtain the partial regression coefficients when the method of least squares is used are as follows for this example.

$$\begin{bmatrix} \hat{\sigma}^2_{P_1} & \hat{\sigma}_{P_{12}} & \hat{\sigma}_{P_{13}} \\ \hat{\sigma}_{P_{12}} & \hat{\sigma}^2_{P_2} & \hat{\sigma}_{P_{23}} \\ \hat{\sigma}_{P_{13}} & \hat{\sigma}_{P_{23}} & \hat{\sigma}^2_{P_3} \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix} = \begin{bmatrix} V_1\hat{\sigma}^2_{a_1} + V_2\hat{\sigma}_{a_{12}} + V_3\hat{\sigma}_{a_{13}} \\ V_1\hat{\sigma}_{a_{12}} + V_2\hat{\sigma}^2_{a_2} + V_3\hat{\sigma}_{a_{23}} \\ V_1\hat{\sigma}_{a_{13}} + V_2\hat{\sigma}_{a_{23}} + V_3\hat{\sigma}^2_{a_3} \end{bmatrix}$$

It is evident from the normal equations that estimates need to be obtained for the phenotypic covariances, additive genetic variances and additive genetic covariances. Estimates of these parameters can be obtained using the identities presented on page seven of this chapter.

$$\hat{\sigma}_{P_{12}} = r_{p_{12}} \hat{\sigma}_{P_1} \hat{\sigma}_{P_2} = 0.40626$$

$$\hat{\sigma}_{P_{13}} = r_{p_{13}} \hat{\sigma}_{P_1} \hat{\sigma}_{P_3} = -.21472$$

$$\hat{\sigma}_{P_{23}} = r_{p_{23}} \hat{\sigma}_{P_2} \hat{\sigma}_{P_3} = -.00058$$

$$\hat{\sigma}_{a_1}^2 = h_1^2 \, \hat{\sigma}_{P_1}^2 = 2.9768$$

$$\hat{\sigma}_{a_2}^2 = h_2^2 \, \hat{\sigma}_{P_2}^2 = 0.01069$$

$$\hat{\sigma}_{a_3}^2 = h_3^2 \, \hat{\sigma}_{P_3}^2 = 0.01024$$

$$\hat{\sigma}_{a_{12}} = r_{g_{12}} \hat{\sigma}_{a_1} \hat{\sigma}_{a_2} = 0.09277$$

$$\hat{\sigma}_{a_{13}} = r_{g_{13}} \hat{\sigma}_{a_1} \hat{\sigma}_{a_3} = -.00873$$

$$\hat{\sigma}_{a_{23}} = r_{g_{23}} \hat{\sigma}_{a_2} \hat{\sigma}_{a_3} = -.00188$$

Substituting these estimates and previous estimates results in the following normal equations:

$$\begin{bmatrix} 37.21 & 0.40626 & -.21472 \\ 0.40626 & 0.0324 & -.00058 \\ -.21472 & -.00058 & 0.0256 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix}$$

$$= \begin{bmatrix} 2.9786 + (11.11)(0.09277) + (-9.26)(-.00873) \\ 0.09277 + (11.11)(0.01069) + (-9.26)(-.00188) \\ -.00873 + (11.11)(-.00188) + (-9.26)(0.01024) \end{bmatrix}$$

which simplifies to the following:

$$\begin{bmatrix} 37.21 & 0.40626 & -.21472 \\ 0.40626 & 0.0324 & -.00058 \\ -.21472 & -.00058 & 0.0256 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix} = \begin{bmatrix} 4.08831 \\ 0.22894 \\ -.12444 \end{bmatrix}$$

The partial regression coefficients obtained by solving the above system of equations are:

$$b_1 = 0.00795$$

$$b_2 = 6.88328$$

$$b_3 = -4.63827$$

which yield the following selection index:

$$I = 0.00795\ P_1 + 6.88328\ P_2 - 4.63827\ P_3$$

The index constructed indicates that a one pound increase in weaning weight would increase the index value 0.00795 units. Similarly, a one pound per day increase in average daily gain would result in 6.88328 units increase in I. On a more realistic basis, a one-tenth pound per day increase in gain increases I by 0.688328 units. A one inch increase in probe backfat decreases the index value by 4.63827. However, a decrease of one-tenth inch in backfat (the desired direction of change) increases I by 0.463827 units. Therefore, the heavier a pig is at weaning, the faster his daily gain and the smaller his probe, the larger will be his index value.

Determining the correlation between the index and the aggregate breeding value (R_{AI}) requires estimates of the variance of the index and the variance of the aggregate breeding value. Estimates of these quantities can be obtained using the formulas given on page eight of this chapter.

$$\hat{\sigma}_I^2 = b_1^2\hat{\sigma}_{P_1}^2 + b_2^2\hat{\sigma}_{P_2}^2 + b_3^2\hat{\sigma}_{P_3}^2 + 2b_1b_2\hat{\sigma}_{P_{12}} + 2b_1b_3\hat{\sigma}_{P_{13}} + 2b_2b_3\hat{\sigma}_{P_{23}} = 2.18553$$

$$\hat{\sigma}_A^2 = V_1^2\hat{\sigma}_{a_1}^2 + V_2^2\hat{\sigma}_{a_2}^2 + V_3^2\hat{\sigma}_{a_3}^2 + 2V_1V_2\hat{\sigma}_{a_{12}} + 2V_1V_3\hat{\sigma}_{a_{13}} + 2V_2V_3\hat{\sigma}_{a_{23}} = 7.7842$$

$$R_{AI} = \frac{\hat{\sigma}_I}{\hat{\sigma}_A} = \sqrt{\frac{2.18553}{7.7842}} = 0.530$$

An index value of this magnitude indicates that the index value is not a good predictor of the aggregate breeding value. In terms of multiple regression, only about 28 percent of the variation in the aggregate breeding value is accounted for by the index. Also, the heritability of the index values is approximately 0.28 (R_{AI}^2). It must be remembered that even though I is not a good predictor of A, it is still the best available.

It should be apparent from the example that the partial regression coefficients are dependent upon the economic values, phenotypic variances, heritabilities and genetic and phenotypic correlations.

Review of the Literature for Swine Selection Indexes

The first indexes developed using swine traits were developed by Hazel (1943). The indexes involved combinations of three traits, 180 day weight, market score and sow productivity. The relative economic values used were 1/3, 1 and 2 for weight, score and productivity, respectively. Sow productivity was measured in the following manner:

$$P = N_0 + N_{21} + N_{56} + \frac{W_{21}}{10} + \frac{W_{56}}{30}$$

The N's refer to number of live pigs in the litter at farrowing, 21 and 56 days and the W's refer to litter weights at 21 and 56 days. The estimates of productivity are for the litter in which the pig was born.

The first index constructed involved only 180 day weight and score.

$$I_1 = 0.137\ W - .268\ S$$

The second index contained all three traits.

$$I_2 = 0.136\ W - .232\ S + 0.164\ P$$

The third index included all three traits plus the average weight and score of the litter as a fourth and fifth variable. The regression coefficients for productivity, litter weight and litter score were dependent upon the size of the litters. For a litter size of five pigs the index was:

$$I_3 = 0.098\ W - .165\ S + 0.166\ P + 0.088\ \overline{W} - .197\ \overline{S}$$

The correlations between the index and the aggregate breeding value were 0.363, 0.395 and 0.404 for indexes 1, 2 and 3, respectively. Index 2 was 8.8 percent and index 3 was 11.3 percent more efficient than the first index. Hazel concludes that the second would almost certainly be preferable to the first. The third might also be chosen over the second, since genetic progress could still be increased, and the amount of labor required would only be in computing and using the litter averages from data already taken.

Bernard et al. (1954) present four indexes using combinations of four swine traits. The four traits were number of pigs per litter at birth (X_1), number of pigs per litter at 154 days (X_2), litter weight at 154 days (X_3) and individual pig weight at 154 days (X_4). Litter records are for the litter in which the pig was born. The indexes were constructed using the method presented by Hazel (1943) with some modifications suggested by Henderson (1951). The four indexes presented are as follows:

$$I_a = 0.950\ X_2 + 0.103\ X_4$$

$$I_b = -.070\ X_1 + 0.990\ X_2 + 0.103\ X_4$$

$$I_c = 1.33\ X_2 - .003\ X_3 + .103\ X_4$$

$$I_d = -.102\ X_1 + 1.459\ X_2 - .004\ X_3 + 0.103\ X_4$$

The corresponding correlations are 0.394, 0.395, 0.397 and 0.399. Based on the magnitudes of the correlations, they recommended using index d. They stated, however, that probably little would be gained by using index d in preference to index a. In order to make the indexes more useful, they modified them by multiplying by a constant and rounding off the coefficients, resulting in the following indexes.

$$I_a' = 4.5\ X_2 + 0.5\ X_4$$

$$I_d' = -.5\ X_1 + 7\ X_2 - .02\ X_3 + 0.5\ X_4$$

These are the indexes which they recommended for practical use.

A selection index was used by Christian (1957) as the selection criteria in an experiment where selection was carried out under two nutritional environments with swine. The two nutritional environments were a high energy diet and a low (70 percent of the high) energy diet. The index used as the selection criteria was:

$$I = B + 2W + 35G$$

where B refers to number of pigs born alive and W to number of pigs weaned in the litter in which the individual was born, and G to rate of gain from weaning to 150 pounds. The coefficients in the index were determined by the method of path coefficients.

Five generations of selection indicated that no increase had been made in number of pigs born alive or number of pigs weaned. Gain did show an increase after five generations of selection. The high energy line increased from 1.21 to 1.48 pounds per day, an increase of 0.27 pounds per day, and the low line increased from 0.77 to 1.02 pounds per day, an increase of 0.25 pounds per day. This indicated that selection based on the index was effective in increasing rate of gain, but ineffective in increasing either number born or number weaned.

An index for boars of the Iowa Swine Testing Station, Hazel (1956), was constructed giving equal weight to growth rate and feed efficiency but emphasizing fatness twice as much. All genetic and phenotypic correlations were assumed to be zero.

$$I = 260 + 35 \text{ Gain} - 40 \text{ Feed} - 75 \text{ Fatness}$$

where gain is the boar's rate of gain per day, fatness is measured by backfat probe and feed is feed required per pound of gain and is based on a pen of three pigs. The constant of 260 was added in order to give the index values a mean of about 100. This index has since been modified (deBaca, 1962). The resulting indexes are:

Index = 117+(50Xgain)-(50Xfeed eff.)-(40Xprobe)+(3X H-L%)

and

Index = 240 + (50 X gain) - (50 X eff.) - (50 X probe)

for boars with full-brother barrows and half-brother barrows, respectively. The term H-L% refers to the percent ham and loin of the chilled carcass for full-brother barrows.

Robison et al. (1960) used phenotypic information available on the parents to predict the aggregate phenotypic value of the progeny. The aggregate phenotypic value of the progeny was expressed as $V = \sum_i A_i X_i$ where the A's are the relative economic values and the X's are the phenotypic values of the progeny. The progeny phenotypic values of concern were 154 day weight, percent lean cuts and litter size at 154 days with relative economic values of 1, 2.67 and 20, respectively. Four different indexes including various combinations of parental traits were constructed. The traits involved were individual 154 day weight (X_1), depth of chest (X_2), width behind the shoulders (X_3), length of foreleg (X_4), backfat at the shoulders (X_5), backfat at the loin (X_6). Data on the litter in which the dam was raised were number of pigs in the litter at farrowing (X_7), number of pigs in the litter at 154 days (X_8) and weight of the litter at 154 days (X_9). The resulting indexes were:

$$I_a = 0.062\ X_1 + 0.243\ X_2 - .314\ X_3 - .407\ X_4 - 1.805\ X_5 - 2.564\ X_6 + 0.127\ X_7 - .154\ X_8 - 0.000\ X_9$$

$$I_b = 0.072\ X_1 - .238\ X_3 - .446\ X_4 - 4.408\ X_6 + 0.107\ X_7 - .156\ X_8$$

$$I_c = 0.047\ X_1 - .162\ X_3 - 3.383\ X_6 + 0.064\ X_7 - .109\ X_8$$

$$I_d = 0.054\ X_1 - .403\ X_4 - 4.334\ X_6 + 0.123\ X_7 - .204\ X_8$$

Correlations of 0.34, 0.33, 0.28 and 0.32 were obtained for the respective indexes. Based on these correlations, the authors recommended using index d modified for easier use.

$$I_d' = 164 + 0.5\ X_1 - 4X_4 - 43.3\ X_6 + 1.2\ X_7 - 2X_8$$

CHAPTER III

ECONOMIC VALUES

Weighting of Economic Values

Economic values play an important role in the construction of a selection index. The methods by which these economic values are determined and incorporated into the index varies. It is not the value itself which is of interest at present, but the method by which it is incorporated into the index.

A regression coefficient in the index should have units of measure which are the reciprocal of the units of measure of the phenotypic value to which it corresponds in order to make the index value unitless. To illustrate this, assume the following index.

$$I = b_1P_1 + b_2P_2$$

If the units of measure for phenotypic value P_1 is U_1 and the units of measure for P_2 is U_2, then the units of measure for b_1 and b_2 should be $1/U_1$ and $1/U_2$, respectively.

One method which has been described for incorporating economic values into a selection index is to determine the value of one unit change in the traits, multiply each value by the corresponding standard deviation to place all values on a comparable basis (i.e. each is unitless), and then generally the smallest value is divided into the rest to place all values on a relative basis. These relative values are what are used in the normal equations when the method of least squares is used to determine the regression coefficients. Table II is used to illustrate this procedure using average daily gain and weaning weight as the two traits involved. The units of measure for average daily gain is pounds per day and for weaning weight it is pounds.

TABLE II

ONE METHOD OF DETERMINING RELATIVE ECONOMIC VALUES

Trait	Economic Value	σ	E.V. X σ	Relative Economic Value	h^2
Gain	\$3.00	0.18	0.54	1.00	0.33
Weight	\$0.27	6.10	1.647	3.05	0.08

The index which would result from using the relative economic values of Table II and assuming both the genetic and phenotypic correlation to be zero would be

$$I = 1.35 \text{ Gain} + 1.00 \text{ Weight}$$

The index indicates that a one pound increase in weaning weight would add one unit to the index value and a one pound per day change in average daily gain would add only 1.35

units to the index. The validity of this could surely be questioned.

The inappropriateness of this method of determining relative economic values can be illustrated by solving the normal equations just using the units of measure of the appropriate terms in the equations. It should be noted that when only units of measure are used that $U_1 - U_1$ is equal to U_1 and not equal to zero. The system of equations can be solved using the Abbreviated Doolittle Technique.

$$\begin{array}{cc|c}
U_1^2 & U_1U_2 & U_1(U_1+U_2) \\
 & U_2^2 & U_2(U_1+U_2) \\
\hline
U_1^2 & U_1U_2 & U_1(U_1+U_2) \\
1 & U_2/U_1 & (U_1+U_2)/U_1 \\
\hline
 & U_2^2 & U_2(U_1+U_2) \\
 & 1 & (U_1+U_2)/U_2
\end{array}$$

Therefore, the units of measure for b_1 are $(U_1+U_2)/U_1$ and for b_2 are $(U_1+U_2)/U_2$. Based on these results, the index would have units of measure which are a combination of the units of measure of the traits involved. This leads to the conclusion that these particular relative economic values are inappropriate when the least squares method is used to determine the regression coefficients.

The question now becomes, what are the appropriate economic values to use? It seems reasonable to consider the values given in Table II under economic value (i.e. \$3.00

and \$0.27). Units of measure are associated with these values and are the reciprocals of the units of measure of the standard deviations. The normal equations can be set up again using these terms as the economic values. If just the normal equations of the units of measure are considered, they will appear as follows, and this system can be solved to determine the units of measure on the regression coefficients.

$$\begin{array}{cc|c} U_1^2 & U_1U_2 & U_1{}^* \\ & U_2^2 & U_2 \\ \hline U_1^2 & U_1U_2 & U_1 \\ 1 & U_2/U_1 & 1/U_1 \\ \hline & U_2^2 & U_2 \\ & & 1/U_2 \end{array}$$

*In terms of units of measure $V_1\sigma^2_{a_1} + V_2\sigma_{a_{12}} = 1/U_1 \cdot U_1^2 + 1/U_2 \cdot U_1U_2 = U_1$

The units of measure for b_1 and b_2 are $1/U_1$ and $1/U_2$, respectively. These are the reciprocals of the units of measure for the two traits and will lead to a unitless index.

This leads to the conclusion that the economic values should not be multiplied by the standard deviation to remove the units of measure. For the regression coefficients to have the proper units of measure, to yield a unitless index, the units of measure should be left on the economic values if the method of least squares is used to determine the regression coefficients.

It should be noted that the economic values used can be placed on a relative basis by dividing all values by the magnitude of the smallest value. Dividing by a constant does not change the units of measure associated with each value.

Positive Versus Negative Economic Values

With some traits such as probe backfat and age at 200 pounds, the smaller the phenotypic value the more desirable is the individual animal. Therefore, selection pressure should be exerted to decrease the phenotypic values for these traits. If the selection criteria is a selection index value, it would be desirable for the regression coefficients corresponding to these traits to have a negative sign. This could be accomplished in at least two ways: (1) the economic value of the trait could be taken as negative, thereby causing the calculated regression coefficient to generally be negative, or (2) using the economic value as positive, which would generally make the regression coefficient positive, but giving it negative emphasis in the index. The problem arising here is that the magnitudes of the regression coefficients will change depending on how the economic values are incorporated into the construction of the index.

If the relative economic value is defined as the increase in profit expected to result from one unit change in a trait, it would seem that all values should be positive. However, it also seems reasonable to measure the unit change the same for all traits. Either the unit change is a unit increase or a unit decrease in all traits. This would give some traits a negative economic value since a unit increase might result in a loss of profit. Thus, method 1 above would appear to be the most valid method.

In order to obtain some insight into which method would be preferred, sample indexes could be constructed using both positive and negative estimates of the economic values. The correlation between the aggregate breeding value and the index (R_{AI}) will be used as the criteria for comparison.

To obtain some idea of what happens in a three trait selection index, indexes were constructed involving weaning weight (P_1), average daily gain (P_2) and probe backfat (P_3). The economic values of the three traits were assumed to be \$0.30, \$2.80 and \$2.20, respectively. On a relative basis the values were 1.00 (V_1), 9.33 (V_2) and 7.33 (V_3). The basic parameters used in the construction are presented in Table III.

TABLE III

PHENOTYPIC VARIANCES, STANDARD DEVIATIONS AND HERITABILITIES ASSUMED IN THE CONSTRUCTION OF THE THREE TRAIT SELECTION INDEX

Trait	$\hat{\sigma}_P^2$	$\hat{\sigma}_P$	h^2
P_1:Weaning weight	72.25	8.5	0.12
P_2:Average daily gain	0.04	0.20	0.28
P_3:Probe backfat	0.0225	0.15	0.45

In addition, the genetic and phenotypic correlations between weaning weight and average daily gain used were 0.45 and 0.50, respectively, for all indexes calculated using these three traits. The correlations between the index and the aggregate breeding value, for the sixteen pairs of indexes calculated, are presented in Table IV. The right four columns indicate the values for the remaining parameter estimates which were used. All sixteen possible combinations of positive and negative estimates of the parameters are represented. The left two columns show the correlations (R_{AI}) obtained when the economic value of probe backfat was incorporated into the normal equations as a negative value (V_3 negative) and when it was incorporated as a positive value (V_3 positive). The asterisk indicates the correlation of a pair with the largest magnitude.

It is apparent that with certain indexes, a larger correlation (R_{AI}) can be obtained by using the economic value as positive, but with other indexes the negative economic value yields the largest correlation. The correlation with the largest magnitude ($r_{g_{13}}$ in this example) appears to be the determining factor. When the genetic correlation ($r_{g_{13}}$) is positive, the largest correlation (R_{AI}) is obtained with a positive economic value. With a negative genetic correlation between weaning weight and probe, the largest correlation is obtained using a negative economic value.

It might seem that the theory is not valid since two indexes calculated with the same estimates of the genetic

TABLE IV

A COMPARISON OF USING A POSITIVE VERSUS NEGATIVE ECONOMIC VALUE FOR PROBE BACKFAT IN A THREE TRAIT SELECTION INDEX[a]

Index No.	R_{AI} when Economic Value is:		Correlation Coefficient[b]			
	Negative	Positive	$r_{p_{13}}$	$r_{p_{23}}$	$r_{g_{13}}$	$r_{g_{23}}$
1.	0.394	0.445*	0.12	0.20	0.30	0.10
2.	0.405	0.440*	0.12	0.20	0.30	-.10
3.	0.525*	0.416	0.12	0.20	-.30	0.10
4.	0.533*	0.407	0.12	0.20	-.30	-.10
5.	0.397	0.504*	0.12	-.20	0.30	0.10
6.	0.408	0.493*	0.12	-.20	0.30	-.10
7.	0.478*	0.402	0.12	-.20	-.30	0.10
8.	0.480*	0.392	0.12	-.20	-.30	-.10
9.	0.392	0.480*	-.12	0.20	0.30	0.10
10.	0.402	0.478*	-.12	0.20	0.30	-.10
11.	0.493*	0.408	-.12	0.20	-.30	0.10
12.	0.504*	0.397	-.12	0.20	-.30	-.10
13.	0.407	0.533*	-.12	-.20	0.30	0.10
14.	0.416	0.525*	-.12	-.20	0.30	-.10
15.	0.440*	0.405	-.12	-.20	-.30	0.10
16.	0.445*	0.394	-.12	-.20	-.30	-.10

[a] $r_{p_{12}} = 0.50$ and $r_{g_{12}} = 0.45$ for all indexes.

[b] Subscript one refers to weaning weight, two to average daily gain and three to probe backfat.

and phenotypic parameters do not yield the same results. However, it must be remembered that when the sign on the economic value is changed, the dependent variable (A) is also changed. There are really two different sets of normal equations involved.

The question is, what is the economic value which should be used?. The positive correlation between weaning weight and probe ($r_{g_{13}} = 0.30$) indicates that some of the genes which affect weaning weight also affect probe. The positive sign indicates that if these genes act to increase weaning weight, they would also act to increase probe and this is not the desirable situation. The desirable situation would be to increase weaning weight and decrease probe. If this is the true relationship, then the greatest progress from selection could be made by selecting to increase both traits. If an increase is desirable for both traits, the economic value for probe backfat would definitely be positive and the correlation between the index and the aggregate breeding value would be higher than if a decrease is desired because greater progress could be made in both traits due to the positive genetic relationship. If a decrease is desired in probe backfat, then selection for both traits simultaneously would result in less progress in both traits due to the positive genetic correlation between the two traits. Therefore, it seems reasonable that selection on an index would result in a smaller correlation between the index and the aggregate breeding value when a decrease is desired in one trait and an increase is desired in the other with a positive genetic relationship existing between the two traits. Therefore, the smaller correlation (R_{AI}) when the economic value for probe is used as negative appears reasonable.

The expected result when the genetic correlation between the two traits is negative would be that the correlation (R_{AI}) would be higher when the economic value for probe was used as negative. The results of Table IV bear this out. Due to this negative genetic relationship, selection would result in desirable change in both traits.

The correlation with the largest magnitude appears to be the factor that determines which economic value will yield the largest (R_{AI}). In order to further investigate this point, another sixteen pairs of indexes were constructed, only this time the genetic correlation between weaning weight and probe was reduced in magnitude from 0.30 to 0.05. The resulting correlations are presented in Table V.

With the exception of pairs eight and nine, the correlation (R_{AI}) with the largest magnitude is determined by the phenotypic correlation between average daily gain and probe. However, the sign of the phenotypic correlation and the maximum R_{AI} value for a pair are exactly opposite from the first example. This would appear to contradict the results previously presented. However, if one line of the normal is examined,

$$b_1 r_{p_{12}} \hat{\sigma}_{P_1} \hat{\sigma}_{P_2} + b_2 \hat{\sigma}_{P_2}^2 + b_3 r_{p_{23}} \hat{\sigma}_{P_2} \hat{\sigma}_{P_3} = V_1 \hat{\sigma}_{a_{12}} + V_2 \hat{\sigma}_{a_2}^2 + V_3 \hat{\sigma}_{a_{23}}$$

TABLE V

ANOTHER COMPARISON OF USING A POSITIVE VERSUS NEGATIVE ECONOMIC VALUE FOR PROBE BACKFAT IN A THREE TRAIT SELECTION INDEX[a]

Index No.	R_{AI} when Economic Value of backfat is:		Correlation Coefficient[b]			
	Negative	Positive	$r_{p_{13}}$	$r_{p_{23}}$	$r_{g_{13}}$	$r_{g_{23}}$
1.	0.427*	0.402	0.12	0.20	0.05	0.10
2.	0.438*	0.394	0.12	0.20	0.05	-.10
3.	0.450*	0.395	0.12	0.20	-.05	0.10
4.	0.460*	0.386	0.12	0.20	-.05	-.10
5.	0.396	0.439*	0.12	-.20	0.05	0.10
6.	0.404	0.427*	0.12	-.20	0.05	-.10
7.	0.412	0.420*	0.12	-.20	-.05	0.10
8.	0.418*	0.408	0.12	-.20	-.05	-.10
9.	0.408	0.418*	-.12	0.20	0.05	0.10
10.	0.420*	0.412	-.12	0.20	0.05	-.10
11.	0.427*	0.404	-.12	0.20	-.05	0.10
12.	0.439*	0.396	-.12	0.20	-.05	-.10
13.	0.386	0.460*	-.12	-.20	0.05	0.10
14.	0.395	0.450*	-.12	-.20	0.05	-.10
15.	0.394	0.438*	-.12	-.20	-.05	0.10
16.	0.402	0.427*	-.12	-.20	-.05	-.10

[a] $r_{p_{12}} = 0.50$ and $r_{g_{12}} = 0.45$ for all indexes.

[b] Subscript one refers to weaning weight, two to average daily gain and three to probe backfat.

it can be noted that $r_{p_{23}}$ is on the left of the equal sign and V_3 is on the right. In order to see how one variable affects the other, both should be on the same side of the equal sign. When this is done the sign of one of the variables must be changed and the results would then be the same as previously stated.

The reason that pairs eight and nine do not conform to the theory is not known. The magnitude of the differences in the correlations is not very great. It would be advantageous to attribute this nonagreement to round off errors associated with the various values used, but there is really no evidence to support this conclusion. One reason might be that phenotypic correlations are not directly multiplied by economic values so their effect may not be as great. Also, all the genetic and phenotypic correlations are small so the effects may not be very great.

The correlation with the largest magnitude is the determining factor due to the fact that it has the greatest affect on the normal equations. The larger the magnitudes of the correlations, the larger will be the difference in the R_{AI} values.

Based on these results, the economic value for a trait for which a decrease is desirable should always be used as negative. The genetic and phenotypic relationships will determine how large the association is between the index and the aggregate breeding value. If the genetic relationship between two traits, one in which an increase is desired and one in which a decrease is desired, is positive this association will be lower than if the relationship is negative.

Determination of Economic Values for Swine Traits

The determination of economic values depends on the size and nature of the operation as well as current prices. Economic values which are calculated in this study are based on average figures and are presented in Table VI. All traits presented are assumed to be of importance in the overall operation.

Litter Size

The economic value of litter size at weaning is a function of average litter size of the herd. Based on present management recommendations, sows will consume an average of five pounds of feed per day during the pregestation and gestation periods (125 days) and approximately 12 pounds of feed daily during the lactation and reconditioning period (56 days). This results in a total feed consumption of 1330 pounds. If average litter size is six pigs, increasing to seven pigs results in a savings of $\frac{1300}{6} - \frac{1300}{7}$ or 31 pounds of feed per pig weaned. Assuming sow feed costs of \$0.03 per pound, the economic value of litter size is \$0.93. If the average litter size is four pigs, the economic value would be $\frac{1300}{4} - \frac{1300}{5}$ times \$0.03 or \$1.95. Values for other litter sizes are presented in Table VI. The following simple relationship can be used to determine the economic values for litter sizes between three and 10 pigs weaned with a

TABLE VI

ECONOMIC VALUES FOR SWINE TRAITS

Trait	Units	Economic Value	Relative Economic Value
Litter size at weaning	pig		
Ave. = 2		$6.50	46.43
Ave. = 4		$1.95	13.93
Ave. = 6		$0.93	6.64
Ave. = 8		$0.54	3.86
Pig weaning weight	lb.	$0.27	1.93
Average daily gain	lb./day	$3.00	21.43
Age at 200 pounds	day	$0.14	1.00
Probe backfat	inch	$2.50	17.86
Feed efficiency	$\frac{\text{lb. feed}}{\text{lb. gain}}$	$4.88	34.86
% lean cuts	%	$0.30	2.14
Carcass backfat	inch	$2.50	17.86
Loin eye area	< 4.00 sq. in.	$0.75	5.36

fair degree of accuracy.

$$E.V. = \frac{27 + X}{X^2}$$

where X represents the average number of pigs weaned.

Weaning Weight

If a feeder pig is worth $18 and weighs 50 pounds, he is worth $0.36 per pound. If the overhead costs to get a pig to weaning are $0.09, then the economic value of weaning weight is $0.27 per pound. Based on current feeder pig pricing structure, a pound of weaning weight is worth one and one-half times the market price. Therefore, the value of $0.27 per pound is valid if the market price is $18 a hundred weight (approximate 10 year average for Oklahoma City).

Growth Rate

Growth rate is measured both as postweaning average daily gain and age at 200 pounds. A pig that gains one pound per day will require 150 days to gain 150 pounds, while if he gains two pounds per day the time required is only 75 days. Therefore, one unit change in daily gain results in 75 days less time to reach 200 pounds. With postweaning overhead costs of $0.04 per pig per day, the economic value of daily gain is $3.00 per pound per day.

Figuring overhead costs at $0.04 per day per pig and feed costs at $0.10 per day for maintenance (3.0 pounds of feed at $0.0325 per pound), the total cost would be $0.14 per day for each day extra that a pig requires to reach 200 pounds. Therefore, the economic value of age at 200 pounds is approximately $0.14 per day.

Backfat Thickness

The economic value of probe backfat at 200 pounds can be determined by dividing the difference in price of number one and two market hogs by the range in fatness. If the price differential is $1.25 and the fat differential is 0.5 inches, the economic value of probe backfat would be $2.50

per inch. The economic value of carcass backfat can be assumed to be the same as the value for probe backfat.

Feed Efficiency

A pig that requires one less pound of feed per pound of gain (3.0 pounds of feed per pound of gain versus 4.0 pounds of feed per pound of gain) would require 150 pounds less feed to produce 150 pounds of gain. If the price of feed is $0.0325 per pound, the economic value of feed efficiency, measured as pounds of feed per pound of gain, would be $4.88 per pound of feed per pound of gain.

Lean Cut Yield

Robison *et al*. (1960) reported the difference in value of lean cuts and all other parts of the dressed carcass to be approximately $0.20 per pound. Assuming a carcass weight of 150 pounds, a one percent increase in lean cuts would result in 1.5 pounds more lean cuts. The economic value of percent lean cuts, on a carcass weight basis, would be 1.5 pounds X $0.20 per pound or $0.30 per percent.

Loin Eye Area

Wilson and Company receives $0.05 per pound premium if 90 percent of the loin is greater than four square inches. Therefore, the economic value of loin eye area would be $0.75 if loins are assumed to weigh 15 pounds. This economic value only applies to increasing the loin eye area from below four square inches to above four square inches. A different economic value would probably need to be determined if percent lean cuts was not included.

CHAPTER IV

PARAMETER ESTIMATES

As was stated earlier, it is necessary to have estimates of the phenotypic variances or standard deviations, phenotypic and genetic correlations and the heritabilities of the various traits in order to construct a selection index. Estimates to be used in this study are estimates obtained from a review of the literature.

A summary of the results from many sources is presented in Tables VII through X. Table VII contains a summary of the phenotypic standard deviations, Table VIII the phenotypic correlations, Table IX the genetic correlations and Table X the heritability estimates.

Each table consists of a column for the trait or traits involved, the number of estimates obtained, the range of the estimates, the simple average of the estimates, the "best estimate" and the references from which the estimates were taken. The column headed best estimate indicates the value which the author felt was probably the most accurate estimate of the parameter. In most cases, it agrees with the simple average; but in a few instances where an extreme estimate greatly affects the simple average, the value that represents the majority of the estimates was used.

TABLE VII

PHENOTYPIC STANDARD DEVIATIONS

Trait	Number Estimates	Range	Simple Average	Best Estimate	References
Number pigs weaned	4	2.33-2.72	2.50	2.50	25, 59, 67, 86
Pig weaning weight, lb.	7	4.60-8.42	6.10	6.10	19, 25, 67, 75, 81, 87, 91
Average daily gain, lb./day	12	0.05-0.25	0.15	0.18	6, 25, 35, 41, 48, 52, 73, 75, 77, 78, 81, 91
Feed efficiency, $\frac{\text{lb. feed}}{\text{lb. gain}}$	6	0.11-0.35	0.23	0.23	6, 25, 35, 41, 77, 78
Age at 200 pounds, days	3	8.50-15.6	12.00	12.00	2, 33, 66
Probe backfat, in.	13	0.09-0.23	0.16	0.16	2, 25, 38, 41, 49, 59, 66, 70, 71, 73, 75, 81, 91
Carcass length, in.	15	0.28-1.27	0.84	0.84	2, 25, 31, 33, 35, 45, 49, 52, 55, 66, 69, 70, 77, 78, 84
Carcass backfat, in.	21	0.10-0.25	0.16	0.16	2, 6, 25, 31, 33, 35, 45, 46, 48, 49, 50, 52, 55, 66, 69, 70, 71, 77, 78, 84
Loin eye area, sq. in.	15	0.32-0.61	0.48	0.52	2, 6, 25, 31, 33, 45, 49, 50, 55, 66, 69, 70, 71, 78, 84
% lean cuts (carcass)	12	1.40-2.90	2.24	2.24	2, 6, 45, 48, 49, 50, 66, 69, 70, 71, 84, 91

TABLE VIII

PHENOTYPIC CORRELATIONS

Traits Correlated	Number Estimates	Range	Simple Average	Best Estimates	References
Number pigs weaned and:					
Pig weaning weight	1			-.51	67
Pig weaning weight and:					
Average daily gain	6	0.17 to 0.44	0.35	0.37	19, 29, 75, 88, 91
Feed efficiency	1			-.19	29
Age at 200 pounds	1			-.52	66
Probe backfat	3	-.29 to -.12	-.22	-.22	66, 75, 91
Average daily gain and:					
Feed efficiency	8	-.84 to -.24	-.62	-.62	6, 7, 29, 35, 52, 77, 78, 85
Probe backfat	3	-.34 to 0.21	-.02	-.02	75, 85, 91
Carcass length	6	-.56 to 0.13	-.08	-.02	15, 28, 35, 52, 77, 78
Carcass backfat	8	-.14 to 0.37	0.03	0.03	6, 7, 15, 28, 35, 52, 77, 78
Loin eye area	4	-.10 to 0.24	0.03	0.03	6, 15, 77, 78
% lean cuts	4	-.19 to -.06	-.14	-.17	6, 7, 15, 28
Feed efficiency and:					
Age at 200 pounds	1			0.51	33
Probe backfat	2	0.00 to 0.12	0.06	0.12	85, 91
Carcass length	6	-.16 to 0.01	-.05	-.04	28, 33, 35, 52, 77, 78
Carcass backfat	8	-.15 to 0.26	0.16	0.20	6, 7, 28, 33, 35, 52, 77, 78
Loin eye area	4	-.16 to 0.04	-.07	-.07	6, 33, 77, 78
% lean cuts	3	-.26 to 0.03	-.08	-.08	6, 7, 28

TABLE VIII (Continued)

Age at 200 pounds and:					
Probe backfat	3	-.18 to -.13	-.16	-.16	2, 66
Carcass length	3	-.16 to 0.09	-.06	-.10	2, 33, 66
Carcass backfat	4	-.19 to -.03	-.14	-.14	2, 33, 66
Loin eye area	3	0.06 to 0.16	0.11	0.11	2, 33, 66
% lean cuts	2	0.31 to 0.45	0.38	0.38	2, 66
Probe backfat and:					
Carcass length	4	-.45 to -.28	-.37	-.37	2, 27, 66, 70
Carcass backfat	6	0.55 to 0.71	0.62	0.62	2, 27, 48, 66, 70
Loin eye area	6	-.45 to -.08	-.25	-.25	2, 27, 49, 66, 70, 71
% lean cuts	8	-.79 to -.22	-.54	-.54	2, 27, 48, 49, 66, 70, 71, 91
Carcass length and:					
Carcass backfat	15	-.66 to -.11	-.35	-.35	2, 3, 27, 31, 33, 35, 45, 52, 55, 62, 66, 77, 78, 79, 84
Loin eye area	13	-.29 to 0.38	0.01	0.00	2, 3, 31, 33, 45, 49, 55, 62, 66, 69, 77, 78, 84
% lean cuts	8	-.08 to 0.57	0.24	0.24	2, 14, 45, 49, 62, 66, 69, 84
Carcass backfat and:					
Loin eye area	15	-.57 to 0.27	-.16	-.16	2, 6, 27, 31, 33, 49, 50, 55, 66, 69, 70, 77, 78, 79, 84
% lean cuts	13	-.80 to -.29	-.56	-.56	2, 6, 14, 27, 45, 48, 49, 50, 66, 68, 70, 79, 84
Loin eye area and:					
% lean cuts	11	0.37 to 0.66	0.51	0.51	2, 6, 14, 15, 45, 49, 50, 66, 70, 79, 84

TABLE IX

GENETIC CORRELATIONS

Traits Correlated	Number Estimates	Range	Simple Average	Best Estimates	References
Number pigs weaned and:					
Pig weaning weight	2	-.25 to 0.13	-.06	-.25	89
Average daily gain	2	0.04 to 0.07	0.06	0.06	89
Feed efficiency	1			-.08	89
Loin eye area	2	0.02 to 0.20	0.11	0.11	89
Pig weaning weight and:					
Average daily gain	8	0.20 to 0.87	0.52	0.52	29, 75, 81, 87, 88, 89
Feed efficiency	2	-.77 to -.54	-.66	-.66	29, 75
Probe backfat	2	-.05 to 0.61	0.28	?	81
Average daily gain and:					
Feed efficiency	9	-.92 to -.22	-.67	-.67	7, 29, 35, 52, 68, 74, 77, 78, 87
Probe backfat	4	-.98 to 0.70	-.18	-.18	75, 81, 91
Carcass length	5	0.06 to 0.19	0.11	0.11	28, 35, 52, 77, 78
Carcass backfat	8	-.26 to 1.34	0.24	-.08	7, 9, 28, 35, 52, 77, 78, 89
Loin eye area	3	-.38 to -.04	-.18	-.25	77, 78, 89
% lean cuts	2	-.61 to 0.44	-.10	?	7, 28

TABLE IX (Continued)

Feed efficiency and:					
Age at 200 pounds	1			0.37	33
Probe backfat	1			-.46	91
Carcass length	6	-.25 to 0.27	-.04	-.10	28, 33, 35, 52, 77, 78
Carcass backfat	9	-.58 to 0.27	0.03	0.20	1, 7, 28, 33, 35, 52, 77, 78, 89
Loin eye area	4	-.34 to -.13	-.24	-.24	33, 77, 78, 89
% lean cuts	2	0.25 to 0.67	0.46	?	7, 28
Age at 200 pounds and:					
Probe backfat	1			-.20	2
Carcass length	2	-.15 to 0.97	0.41	?	2, 33
Carcass backfat	2	-.60 to 0.00	-.30	-.30	2, 33
Loin eye area	2	-.45 to 0.10	-.18	-.18	2, 33
% lean cuts	1			0.27	2
Probe backfat and:					
Carcass length	1			-.53	2
Carcass backfat	1			0.83	2
Loin eye area	1			-.24	2
% lean cuts	1			-.58	2
Carcass length and:					
Carcass backfat	8	-.72 to 0.19	-.33	-.33	2, 31, 33, 35, 52, 57, 77, 78
Loin eye area	5	-.51 to 0.08	-.16	-.16	2, 31, 33, 77, 78
% lean cuts	1			0.30	2

TABLE IX (Continued)

Carcass backfat and:					
Loin eye area	6	-.37 to 0.10	-.16	-.16	2, 31, 33, 50, 77, 78
% lean cuts	2	-.81 to -.58	-.70	-.70	2, 50
Loin eye area and:					
% lean cuts	2	0.49 to 0.77	0.63	0.63	2, 50

TABLE X

HERITABILITIES

Trait	Number Estimates	Range	Simple Average	Best Estimates	References
Number pigs weaned	12	-.09 to 0.32	0.14	0.14	5, 10, 17, 21, 22, 24, 34, 58, 59, 61, 63, 86
Pig weaning weight	16	-.18 to 0.24	0.08	0.08	4, 12, 13, 17, 19, 23, 29, 34, 56, 63, 81, 88, 89, 91
Average daily gain	26	0.15 to 0.77	0.33	0.33	7, 8, 9, 12, 19, 21, 22, 28, 29, 30, 34, 35, 42, 51, 52, 57, 60, 64, 68, 73, 77, 78, 81, 88, 89, 91
Feed efficiency	16	0.12 to 0.59	0.38	0.38	1, 6, 7, 21, 22, 28, 29, 33, 34, 35, 52, 68, 77, 78, 89, 91
Age at 200 lbs.	6	-.07 to 0.68	0.39	0.50	2, 12, 33, 51, 65, 83
Probe backfat	16	0.15 to 0.87	0.40	0.40	2, 20, 36, 37, 38, 46, 47, 58, 59, 72, 73, 81, 91
Carcass length	18	0.20 to 0.73	0.51	0.51	1, 2, 12, 22, 28, 31, 33, 34, 35, 51, 52, 57, 60, 65, 77, 78, 83
Carcass backfat	21	0.12 to 0.69	0.46	0.46	1, 2, 6, 9, 12, 22, 28, 31, 33, 34, 35, 50, 51, 52, 54, 57, 60, 77, 78, 83, 89
Loin eye area	10	0.35 to 0.82	0.53	0.53	2, 6, 22, 31, 33, 34, 50, 77, 78, 89
% lean cuts (carcass)	5	0.29 to 0.64	0.45	0.45	2, 6, 22, 28, 50

CHAPTER V

EFFECTS OF GENETIC AND PHENOTYPIC PARAMETERS ON SELECTION INDEXES

As was noted earlier, it is necessary to have estimates of the phenotypic variances, phenotypic correlations, genetic correlations and heritabilities of the various traits in order to construct selection indexes involving these traits. Changes in these estimates will affect the partial regression coefficients of the index. The amount of change that can be made in the estimate of a parameter without greatly affecting the predictability of the index is not definitely known. However, the task of examining this by varying one estimate at a time while holding all others constant is for all practical purposes impossible. It should be possible to precisely estimate the phenotypic variances for a given population, and obtain estimates of heritabilities with relatively small standard errors. In addition, heritabilities for most economically important traits have been estimated by many different workers from many different types of populations such that the magnitudes of the estimates are fairly well determined. Therefore, for purposes of this study, only the genetic and phenotypic correlations will be varied. Also, only a two and a three trait selection index will be examined, since any definite patterns which exist should be present in these simpler indexes.

It would be desirable to obtain some simple relationship between the genetic and phenotypic correlations which would indicate the predictive value of a given index compared to an index using different estimates of the correlations without actually computing the indexes.

Two Trait Selection Index

The two trait selection index to be examined will involve average daily gain and probe backfat. Estimates of the economic values, phenotypic variances and heritabilities assumed are presented in Table XI. These estimates were constant for all 14 indexes constructed.

TABLE XI

CONSTANT PARAMETERS USED IN THE CONSTRUCTION OF A SELECTION INDEX INVOLVING AVERAGE DAILY GAIN AND PROBE BACKFAT

Trait	Economic Value	σ_P^2	h^2
P_1:Average daily gain	1.20	0.0324	0.33
P_2:Probe backfat	-1.00	0.0256	0.40

The 14 indexes constructed are presented in Table XII. In order to make comparisons among the indexes easier, the regression coefficient corresponding to average daily gain (b_1) was given the value one for all indexes. Also, the indexes are arranged so that the index with the smallest correlation between the index and the aggregate breeding value is presented first and the index with the largest correlation is presented last.

First note that index seven has a correlation (R_{AI}) which is approximately in the middle of the 14 correlations. In fact, the numerical average of all 14 R_{AI} values is 0.597. Index seven was constructed assuming the genetic and phenotypic correlations were zero, so the regression coefficients were simply the heritabilities times the economic values. This illustrates that unless confidence can be placed in the estimates of the genetic and phenotypic correlations, it is probably safer to assume they are zero. This would prevent placing too much emphasis on either of the traits. If the estimates are correct, then less progress would be made by assuming them to be zero than by using the estimates. However, if the estimates were incorrect, then greater progress could be made using index seven than by using the index constructed from the estimates. It is essentially using a mean value rather than individual values if all these possible combinations are present in swine populations.

The magnitude of the correlation (R_{AI}) appears to be associated with the difference between the genetic and pheno-

TABLE XII

THE EFFECT OF DIFFERENT ESTIMATES OF THE GENETIC AND PHENOTYPIC CORRELATIONS ON A SELECTION INDEX INVOLVING AVERAGE DAILY GAIN AND PROBE BACKFAT

Index No.	b_1(ADG)	b_2(Probe)	R_{AI}	r_p	r_g	$r_g - r_p$
1.	1.0	- .496	0.409	-.34	0.40	0.74
2.	1.0	- .749	0.470	-.34	0.18	0.52
3.	1.0	- .871	0.517	0.20	0.40	0.20
4.	1.0	- .915	0.536	-.02	0.18	0.20
5.	1.0	- .930	0.547	0.02	0.18	0.16
6.	1.0	-1.026	0.563	-.34	-.18	0.16
7.	1.0	-1.010	0.598	0	0	0
8.	1.0	- .986	0.604	0.20	0.18	-.02
9.	1.0	-1.146	0.614	-.34	-.40	-.06
10.	1.0	-1.073	0.645	-.02	-.18	-.16
11.	1.0	-1.077	0.658	0.02	-.18	-.20
12.	1.0	-1.096	0.671	0	-.25	-.25
13.	1.0	-1.092	0.728	0.20	-.18	-.38
14.	1.0	-1.132	0.795	0.20	-.40	-.60

typic correlation ($r_g - r_p$) used in the index construction. The larger the magnitude of this difference, the greater is the deviation of the R_{AI} value from the R_{AI} value for index seven. In all cases when $r_g - r_p$ was positive, the R_{AI} value was less than 0.598 (the R_{AI} value for index 7); and when $r_g - r_p$ was negative, the R_{AI} value was greater than 0.598. In Chapter III it was discussed that the phenotypic and genetic correlations are on opposite sides of the equal sign in the normal equations. To determine the effect of both correlations together, they would need to be put on the same side. This is essentially what has been done by examining $r_g - r_p$. If an antagonistic relationship exists between the two traits, the R_{AI} value would be expected to be less than 0.598, since simultaneous selection for both traits would result in less progress for both traits than if they were independent. The degree to which the R_{AI} values are different would depend on the magnitude of the antagonism. If there is a nonantagonistic relationship between the two traits, the R_{AI} value would be expected to be greater than 0.598, since simultaneous selection would result in greater progress for both traits than if they were independent. This point appears to be indicated in the difference between the genetic and phenotypic correlations ($r_g - r_p$) for the present example. If the difference is positive, an antagonistic relationship exists; and if the difference is negative, a nonantagonistic relationship exists. The results in Table XII would tend to substantiate this conclusion. The degree of antagonism or nonantagonism is probably not just simply the difference between the genetic and phenotypic correlations, but the difference appears to be a good indicator of the amount of antagonism or nonantagonism. One might hypothesize that the true relationship might be the genetic correlation minus some factor times the phenotypic correlation. The R_{AI} values of indexes three and four or five and six indicate this factor should probably be less than one. These results indicate that if the magnitude of the difference $(r_g - r_p)$ is large and positive, selection on an index will be less effective than if the difference is large and negative.

Another interesting point can be made by considering the relationship between the phenotypic, genetic and environmental correlations. The relationship between these correlations is presented in Falconer (1960) and can be rearranged thusly:

$$r_e = \frac{r_p - h_i h_j r_g}{\sqrt{(1-h_i^2)(1-h_j^2)}}$$

This relationship illustrates that the greater the magnitude of the difference between the phenotypic and genetic correlations, the greater the magnitude of the environmental correlation. For example, index one would have an environmental correlation associated with it of -.77 and for index fourteen the value of r_e would be 0.54 compared to the environmental correlation associated with index seven of zero. If the difference between the genetic and phenotypic correlations becomes too large, the environmental correlation will be greater than one or less than minus one which is theoretically impossible. For example, if $r_p = -.50$ and $r_g = 0.50$ for these two traits, r_e will equal -1.07. This indicates that large differences between the estimates of the phenotypic and genetic correlations should probably be questioned with respect to their accuracy. Also, indexes developed from estimates of this type are probably inaccurate.

The R_{AI} values for indexes six, eight and nine indicate that the predictability of these indexes is changed only slightly by either increasing or decreasing the genetic and phenotypic correlations as long as both correlations are increased or decreased by approximately the same amount. In other words, as long as the magnitude of the difference between the genetic and phenotypic correlations is close to zero, the predictability of the index is not changed. However, the regression coefficients for probe backfat (b_2) for indexes six, eight and nine do not conform to the pattern established by the other eleven indexes. Although there is no apparent reason for this discrepancy, it may possibly be due to the fact that even though the difference between the correlations ($r_g - r_p$) is small, the actual magnitudes of these correlations are relatively large. In fact, the phenotypic correlations used were the extremes of the estimates obtained from the literature. In addition, the sign of both correlation coefficients is the same within each of the three pairs. Table XIII contains four indexes constructed with extreme values of the genetic and phenotypic correla-

TABLE XIII

INDEXES FOR AVERAGE DAILY GAIN AND PROBE BACKFAT RESULTING WHEN EXTREME ESTIMATES OF THE GENETIC AND PHENOTYPIC CORRELATIONS ARE USED IN THE CONSTRUCTION

Index	b_1(ADG)	b_2(Probe)	R_{AI}	r_p	r_g
1	1.0	- .945	0.592	0.50	0.50
2	1.0	-1.225	0.602	-.50	-.50
3	1.0	- .923	0.581	0.75	0.75
4	1.0	-1.816	0.605	-.75	-.75

tions. The difference ($r_g - r_p$) is zero in all cases and the R_{AI} values are essentially the same, but the magnitudes of the regression coefficients are quite different. Greater differences in the regression coefficients are present when both the genetic and phenotypic correlations are negative. This agrees with the results obtained for index nine in the previous example. These results seem to indicate that extreme estimates of the correlations, in the same direction, tend to give inconsistent results. The R_{AI} values are essentially the same, but this is not reflected in the regression coefficients. However, it must be remembered that the predictability of any of these indexes is only moderate ($R^2<0.40$). Some different individuals would be selected using these indexes, but the overall change in the herd might be essentially the same due to the moderate predictability of the three indexes.

To help in the understanding of why the regression coefficients are different, but the R_{AI} values are essentially the same for indexes six, eight and nine in Table XII, the general solution for the regression coefficients in a two trait selection index can be obtained.

$$b_1 = V_1 h_1^2 - V_2 h_2^2 \frac{\hat{\sigma}_{P_2}}{\hat{\sigma}_{P_1}} r_p + V_2 h_1 h_2 \frac{\hat{\sigma}_{P_2}}{\hat{\sigma}_{P_1}} r_g - V_1 h_1 h_2 r_p r_g$$

$$b_2 = V_2 h_2^2 - V_1 h_1^2 \frac{\hat{\sigma}_{P_1}}{\hat{\sigma}_{P_2}} r_p + V_1 h_1 h_2 \frac{\hat{\sigma}_{P_1}}{\hat{\sigma}_{P_2}} r_g - V_2 h_1 h_2 r_p r_g$$

It should be noted that if $V_1 = V_2$, $h_1^2 = h_2^2$ and $\hat{\sigma}_{P_1} = \hat{\sigma}_{P_2}$. changes in b_1 and b_2 would depend solely on r_p and r_g. If these assumptions are true, then regardless of what the genetic and phenotypic correlations are the ratio of the regression coefficients (b_1/b_2) would always be the same and, in fact, would equal one. Therefore, if the two traits involved have equal heritabilities, phenotypic variances and economic values, any estimates, equal or unequal, of the genetic and phenotypic correlations will yield equal results for b_1 and b_2. In other words, if the above assumptions are met, b_1 would equal b_2 and on a relative basis the values would be independent of the genetic and phenotypic correlations. If the above assumptions are not met, it is difficult to say just what the ratio (b_1/b_2) would be.

The solutions for b_1 and b_2, in terms of the genetic and phenotypic correlations, for the example involving average daily gain and probe backfat, are:

$$b_1 = 0.396 + 0.356\ r_p - .323\ r_g - .436\ r_p r_g$$

$$b_2 = -.400 - .446\ r_p + 0.490\ r_g + 0.363\ r_p r_g$$

With indexes six, eight and nine, the sign of both the genetic and phenotypic correlations is the same, so the quantity $r_p r_g$ would always be positive. Notice that for b_1 the coefficient for r_p is larger than for r_g, but the reverse is true for b_2. Also, the coefficient for $r_p r_g$ is considerably larger for b_1 than b_2. With index nine, the genetic correlation is larger than the phenotypic correlation (-.40 versus -.34). The large coefficient on $r_p r_g$ causes b_1 to be less than b_2; thus, giving the large coefficient for b_2. When the magnitudes are not as large (indexes six and eight), the change in the ratio of the regression coefficients is not as pronounced. However, these nonconforming regression coefficients would appear to be due to the fact that the coefficients of r_p, r_g and $r_p r_g$ in the general solution for b_1 and b_2 are different in this case, and the values of the genetic and phenotypic correlations are large and have the same sign.

The reason that the correlation (R_{AI}) is essentially the same is due to the fact that the difference in the correlations ($r_g - r_p$) is small. With a small difference ($r_g - r_p$), the effect on $\hat{\sigma}_I$ and $\hat{\sigma}_A$ ($R_{AI} = \hat{\sigma}_I/\hat{\sigma}_A$) should be essentially the same regardless of the magnitudes of the estimates.

Three Trait Selection Index

Weaning weight (P_1), average daily gain (P_2) and probe backfat (P_3) are the three traits used in the three trait selection index to be examined. Similar to the two trait selection index, the economic values, phenotypic variances and heritabilities used were constant for all indexes. A summary of these parameter estimates is presented in Table XIV.

TABLE XIV

CONSTANT PARAMETERS USED IN THE CONSTRUCTION OF A SELECTION INDEX INVOLVING WEANING WEIGHT, AVERAGE DAILY GAIN AND PROBE BACKFAT

Trait	Economic Value	σ_p^2	h^2
P_1:Weaning weight	1.00	37.21	0.08
P_2:Average daily gain	11.00	0.0324	0.33
P_3:Probe backfat	-9.26	0.0256	0.40

The seventeen indexes constructed are presented in Table XV. The regression coefficient for average daily gain (b_2) is given the value one for all indexes to facilitate comparison of the indexes. The indexes are arranged so that the index with the smallest correlation between the index and the aggregate breeding value is listed first, and the

TABLE XV

EFFECT OF DIFFERENT ESTIMATES OF THE GENETIC AND PHENOTYPIC CORRELATIONS ON AN INDEX INVOLVING WEANING WEIGHT, AVERAGE DAILY GAIN AND PROBE BACKFAT

Index	b_1(W.Wt.)	b_2(ADG)	b_3(Probe)	R_{AI}	$r_{p_{12}}$	$r_{p_{13}}$	$r_{p_{23}}$	$r_{g_{12}}$	$r_{g_{13}}$	$r_{g_{23}}$	$r_{g_{12}}-r_{p_{12}}$	$r_{g_{13}}-r_{p_{13}}$	$r_{g_{23}}-r_{p_{23}}$	K^a
1.	0.0063	1.0	- .4753	0.353	0.37	-.22	0	0	0.28	0	-.37	0.50	0	0.87
2.	0.0211	1.0	- .1136	0.356	0	-.22	-.02	0	0.28	0.18	0	0.50	0.20	0.70
3.	0.0218	1.0	-1.0103	0.445	0	0	0	0	0	0	0	0	0	0
4.	0.0263	1.0	-2.3371	0.446	-.37	-.22	-.02	-.52	-.05	-.18	-.15	0.17	-.16	0.16
5.	0.0202	1.0	- .3868	0.447	0	0.22	0	0.25	0.28	0.18	0.25	0.06	0.18	-.01
6.	0.0052	1.0	- .3874	0.479	0.37	-.22	-.34	0.52	-.05	-.18	0.15	0.17	0.16	0.18
7.	0.0032	1.0	- .2799	0.493	0.37	-.22	-.34	0.52	0.28	-.18	0.15	0.50	0.16	0.51
8.	0.0008	1.0	- .3460	0.514	0.37	-.22	-.02	0.52	0.28	-.18	0.15	0.50	-.16	0.19
9.	0.0011	1.0	- .6740	0.530	0.37	-.22	-.02	0.52	-.05	-.18	0.15	0.17	-.16	-.14
10.	-.0046	1.0	- .6741	0.530	0.50	-.25	-.02	0.50	-.05	-.18	0	0.20	-.16	0.04
11.	0.0047	1.0	- .6680	0.530	0.25	-.25	-.02	0.50	-.05	-.18	0.25	0.20	-.16	-.21
12.	0.0036	1.0	- .4160	0.530	0.25	-.25	0	0.50	0.25	-.25	0.25	0	-.25	-.50
13.	-.0056	1.0	- .4492	0.534	0.50	-.25	0	0.50	0.25	-.25	0	0	-.25	-.25
14.	0.0036	1.0	- .6614	0.545	0.25	-.25	0	0.50	0	-.25	0.25	0.25	-.25	-.25
15.	-.0056	1.0	- .6644	0.548	0.50	-.25	0	0.50	0	-.25	0	0.25	-.25	0
16.	-.0024	1.0	- .5665	0.559	0.37	-.22	0.20	0.52	0.28	-.18	0.15	0.50	-.38	-.03
17.	-.0029	1.0	- .8129	0.641	0.37	-.22	0.20	0.52	0.28	-.18	0.15	0.50	-.38	-.03

[a] $K = r_{g_{13}} + r_{g_{23}} - r_{g_{12}} - r_{p_{13}} - r_{p_{23}} + r_{p_{12}}$

index with the largest correlation (R_{AI}) is listed last.

Index three, in which all traits are assumed to be genetically and phenotypically independent, is not near the middle of the indexes as the corresponding index was for the two trait selection indexes. Part of the reason for this is that for twelve of the indexes, a relatively large nonantagonistic relationship is assumed between weaning weight and average daily gain. Indexes one and two indicate that when the correlations between weaning weight and daily gain are small, the correlation (R_{AI}) is less than the 0.445 for index three. However, index four illustrates that an antagonistic relationship between weight and gain is, by itself, not sufficient to cause the R_{AI} value to be lower than 0.445. Apparently an antagonistic relationship in weight and gain would need to be coupled with an antagonistic or close to independent relationship in the other traits. Independence in the relationship between weight and gain coupled with antagonistic relationships in the other traits (index two) causes the correlation (R_{AI}) to be less than 0.445. It should be remembered that the greater the relationship, the greater will be its effect on the resultant regression coefficients. Therefore, if all possible indexes were constructed using both positive and negative estimates of the genetic and phenotypic correlations, the R_{AI} value for index three would probably be essentially the mean.

Since $r_g - r_p$ appeared to be a good indicator of the magnitude of the R_{AI} values for the two trait selection index, then $\Sigma\, r_{g_{ij}} - \Sigma\, r_{p_{ij}}$ would be expected to be an indicator for the three trait indexes. The traits are such that a nonantagonistic relationship between weaning weight and average daily gain, as indicated by $r_{g_{ij}} - r_{p_{ij}}$, is a positive value; but for weaning weight with probe backfat and average daily gain with probe, a nonantagonistic relationship is a negative value. Therefore, to place all traits on the same basis, the following relationship is used. It will be defined as K to simplify its use in the discussion.

$$K = (r_{g_{13}} - r_{p_{13}}) + (r_{g_{23}} - r_{p_{23}}) - (r_{g_{12}} - r_{p_{12}}) = r_{g_{13}} + r_{g_{23}} - r_{g_{12}} - r_{p_{13}} - r_{p_{23}} + r_{p_{12}}$$

The pattern established by the K values is not as clear as $r_g - r_p$ was for the two trait selection indexes. However, it should be noted that in all indexes, which do not conform to the hypothesized pattern, at least one of the simple correlation coefficients is an extreme or antagonistic value (index 4: $r_{p_{12}} = -.37$, $r_{g_{12}} = -.52$; index 6: $r_{p_{23}} = -.34$; index 7: $r_{p_{23}} = -.34$, $r_{g_{13}} = 0.28$; index 8: $r_{g_{13}} = 0.28$). Also, there is generally one difference $(r_{g_{ij}} - r_{p_{ij}})$ which is relatively large and generally the difference is of an antagonistic nature. The failure of the indexes to fit the pattern nicely would indicate that there is some type of interaction between the simple correlations for the three traits which might be a function of the magnitudes of the phenotypic variances or heritabilities of the traits. Also, it might indicate that simple sums and differences of the genetic and phenotypic correlations are not a sufficient indicator.

The magnitude of the R_{AI} values indicate that none of the indexes are very good predictors of the aggregate breeding value (A) defined in terms of these three traits ($0.12<R^2<0.42$). However, the R_{AI} values do indicate that the changes which were made in the genetic and phenotypic correlations do not greatly affect the predictability of the indexes. In general, less change in the R_{AI} values is present with the three trait selection indexes than was seen for the two trait selection indexes when the estimates of the genetic and phenotypic correlations are varied. This indicates that the more traits which are involved in an index, the less sensitive the index is to changes in one or two of the estimates.

With index three (all traits independent), the partial regression coefficients for average daily gain (b_2) and probe backfat (b_3) are approximately equal. For most of the other sixteen indexes the regression coefficient for probe is less than the coefficient for daily gain. With almost all of these indexes, there is a positive relationship between weaning weight and gain. When the relationship between weight and gain is negative (index four), the regression coefficient for probe is over twice as large as the coefficient for gain. This indicates that even though a trait has a low heritability and contributes little to the index value, fairly high genetic and phenotypic relationships between this trait and other traits can greatly affect the regression coefficients of all traits involved in the index.

There is some difference in the coefficients of the seventeen indexes even though the R_{AI} values are not greatly different. However, the predictability of the indexes is such that the mean of the selected individuals for all indexes would probably be roughly the same for all three traits.

CHAPTER VI

SELECTION INDEXES INVOLVING VARIOUS COMBINATIONS OF SWINE TRAITS

The ideal selection index would be one which maximizes the correlation between the index and the aggregate breeding value, is composed of traits for which measurements are easily obtained and contains as few traits as possible. Theoretically, an index which satisfies all three of these ideals simultaneously is impossible to obtain. Multiple regression theory illustrates that the addition of new variables to a multiple regression equation never decreases the multiple correlation coefficient; and if the dependent variable is to some extent dependent on these additional variables, the multiple correlation coefficient will be increased. Therefore, the greater the number of traits, which affect the aggregate breeding value, included in a selection index, the larger will be the correlation between the index and the aggregate breeding value. Also, a trait such as feed efficiency has a large economic value, but is difficult to measure. The purpose of this chapter is to construct indexes involving various combinations of swine traits and to compare the predictive value (R_{AI}) of these indexes. If the addition of a certain trait to an index increases the predictive value of the index only slightly, it might be excluded from the index, especially if it is a trait which is difficult to measure. Some characteristics such as carcass traits are difficult and sometimes expensive to measure, so they must increase the predictive value of the index enough to compensate for this increased labor and cost.

Average daily gain and age at 200 pounds are both measures of growth rate. Therefore, it does not seem necessary to include both traits in the same selection index. Two sets of indexes will be constructed: one using average daily gain as a measure of growth rate and the other using age at 200 pounds as the measure of growth rate. A similar situation exists for probe backfat and carcass backfat since both are a measure of fatness. The phenotypic variances and economic values are the same for both of these traits and the heritabilities, phenotypic and genetic correlations are not different enough to warrant construction of two sets of indexes. Therefore, only one measure of fatness will be included in any index. Both measures could be included and approximately half the emphasis for fatness would be given to each trait. The regression coefficient obtained can be used as either probe backfat or carcass backfat depending upon which measurement is available. It must be remembered that if the coefficient is used for carcass backfat, it must be weighted by the appropriate factor depending on the relationship to the individual in question.

Parameter Estimates Used

The estimates of the economic values, heritabilities and phenotypic variances used in construction of the various indexes are presented in Table XVI. The estimates of the heritabilities and phenotypic variances used were obtained from a review of the literature. The estimates of the economic values were derived in Chapter III and presented in Table VI. No satisfactory economic value could be obtained for carcass length, so it was assigned the value one on a relative basis. Estimates of the genetic and phenotypic correlations used are presented in Table XVII. They also represent estimates obtained from a review of the literature.

TABLE XVI

ESTIMATES OF ECONOMIC VALUES, HERITABILITIES AND PHENOTYPIC VARIANCES USED IN THE CONSTRUCTION OF SELECTION INDEXES

Trait	Economic Value	$\hat{\sigma}_P^2$	h^2
Number of pigs weaned	6.64	6.25	0.14
Pig weaning weight, lb.	1.93	37.21	0.08
Average daily gain, lb./day	21.43	0.0324	0.33
Feed efficiency, $\frac{\text{lb. feed}}{\text{lb. gain}}$	-34.86	0.0529	0.38
Probe backfat, in.	-17.86	0.0256	0.40
Carcass length, in.	1.00	0.7056	0.51
Loin eye area, sq. in.	5.36	0.2704	0.53
% lean cuts	2.14	5.0176	0.45
Age at 200 pounds, days	-1.00	144.0	0.50

TABLE XVII

ESTIMATES OF GENETIC AND PHENOTYPIC CORRELATIONS USED IN THE CONSTRUCTION OF SELECTION INDEXES[a]

	No. Weaned	W.Wt.	ADG	Age	F.Eff.	Probe	Carcass Length	L.E.A.	% Lean
Number pigs weaned		-.51	0	0	0	0	0	0	0
Pig weaning weight	-.25		0.37	-.52	-.19	-.22	0	0	0
Average daily gain	0	0.52		---	-.62	-.02	-.02	0.03	-.17
Age at 200 pounds	0	0	--		0.51	-.16	-.10	0.11	0.38
Feed efficiency	0	-.66	-.67	0.37		0.12	-.04	-.07	-.08
Probe backfat	0	-.05	-.18	-.20	0.20		-.37	-.20	-.55
Carcass length	0	0	0.11	-.15	-.10	-.33		-.01	0.24
Loin eye area	0	0	-.25	-.18	-.24	-.16	-.16		0.51
% lean cuts	0	0	0	0.27	0.46	-.58	0.30	0.63	

[a] Phenotypic correlations above main diagonal, genetic correlations below.

The phenotypic correlations are given above the main diagonal and the genetic correlations are listed below the main diagonal. Most of the estimates of the genetic and phenotypic parameters are the "best estimate" presented in Tables VII through X.

Information Based on Collateral Relatives

Traits involving carcass measurements are impossible to measure on the breeding animal. Carcass information on collateral relatives must, therefore, be relied on to furnish some indication of the breeding value of the breeding animal. Since the information is not obtained from the animal directly, but from a collateral relative, it is not as reliable an indicator of the individual's breeding value as if the information were from the individual himself. If information from enough collateral relatives can be obtained, then this mean value may be as reliable an indicator of the individual's breeding value as if the information were obtained directly from the individual. The number of collateral relatives required depends upon the type of collateral relatives involved (i.e. full-sibs, half-sibs, etc.).

For purposes of a selection index, it would be desirable to have some method of utilizing information from collateral relatives. The nature of the method needs to be relatively simple and preferably would involve only the regression coefficients of the index. This would allow for the use of information from different types and numbers of collateral relatives without causing recalculation of the entire index. Even if the method is not completely accurate, it would be much more practical and, if the bias is small, almost as reliable.

Figure 1 is a path coefficient diagram which illustrates the relationship between collateral relatives. The A_i and P_i refer to the breeding and phenotypic value, respectively, for the i^{th} trait of the individual of interest. The A_{1i}, A_{2i} and A_{ni} are the breeding values for trait i for collateral relatives one, two and n. The P_{1i}, P_{2i} and P_{ni} refer to the corresponding phenotypic values of the collateral relatives. The degree of relationship between the collateral relatives is indicated by the correlation coefficient r and h represents the square root of the heritability for trait i.

The correlation between the individual's breeding value (A_i), what is trying to be predicted; and his own phenotypic value, what is observed, can be represented as follows:

$$R_{A_iP_i} = h$$

The correlation between the individual's breeding value and the mean phenotypic value of the collateral relatives is equal to:

$$R_{A_i\bar{P}_{\cdot i}} = nrhp$$

$$p = \sqrt{\frac{1}{n[1+(n-1)t]}}$$

$$R_{A_i\bar{P}_{\cdot i}} = rh\sqrt{\frac{n}{1+(n-1)t}}$$

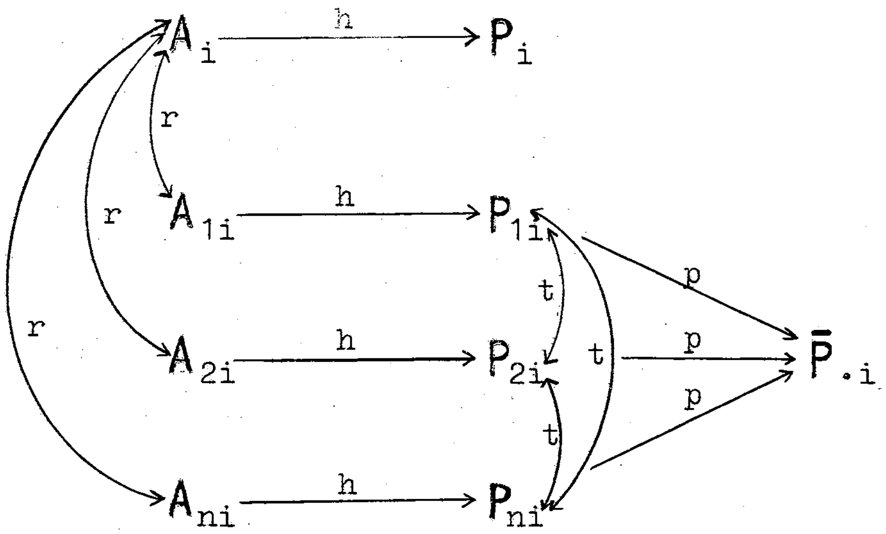

Figure 1. Path Coefficient Diagram Illustrating the Relationship Between Collateral Relatives

For traits such as carcass traits, the mean phenotypic value for the collateral relatives will be used instead of the individual's phenotypic value. Thus, it seems reasonable to weight the regression coefficients for the carcass traits by the ratio of the above two correlations.

$$\frac{R_{A_i\bar{P}\cdot i}}{R_{A_iP_i}} = \frac{rh\sqrt{\frac{n}{1+(n-1)t}}}{h} = r\sqrt{\frac{n}{1+(n-1)t}}$$

where r = the relationship between collateral relatives

n = the number of collateral relatives

t = the phenotypic intra-class correlation between collateral relatives.

If the collateral relative information is obtained from full-sibs, r would be equal to one-half assuming no inbreeding. Also, if the phenotypic intra-class correlation (t) is due to genetic causes (i.e. no common environment effect), which is reasonable for carcass traits, t can be represented in terms of known quantities. From the path diagram:

$$t = r^2h^2$$

If the collateral relatives are full-sibs ($r = \frac{1}{2}$) and for simplicity, the heritabilities of all carcass traits are assumed to equal one-half, then

$$t = 1/8$$

and

$$\frac{R_{A_i\bar{P}\cdot i}}{R_{A_iP_i}} = \sqrt{\frac{2N}{7 + N}}$$

It can easily be obtained by setting the above ratio equal to one that it would require seven full-sibs to have as much information as if the information were from the individual itself. If carcass data is available on only one full-sib, the regression coefficients corresponding to carcass information should be multiplied by one-half; and for two full-sibs, the value is two-thirds.

All regression coefficients presented in the remainder of this chapter for carcass traits will be equivalent to the regression coefficient for seven full-sibs or information on the individual itself. Therefore, to utilize any of the indexes presented, these regression coefficients would need to be multiplied by the appropriate fraction.

Selection Indexes Involving Average Daily Gain As a Measure of Growth Rate

The aggregate breeding value for all indexes constructed in this section was defined as follows:

$$A = V_1a_1 + V_2a_2 + V_3a_3 + V_4a_4 + V_5a_5 + V_6a_6 + V_7a_7 + V_8a_8$$

where

a_1 = number of pigs weaned

a_2 = pig weaning weight

a_3 = average daily gain

a_4 = feed efficiency

a_5 = probe backfat

a_6 = carcass length

a_7 = loin eye area

a_8 = percent lean cuts

V_i = corresponding economic values

Eighteen different indexes were constructed involving average daily gain as the measure of growth rate and containing various combinations of traits. The partial regression coefficients obtained and the correlation between the index and the aggregate breeding value (R_{AI}) for each index are presented in Table XVIII. Average daily gain was present in all indexes except index 18, so the partial regression coefficient for gain was given the value one in all indexes, except index 18 in which the coefficient for probe was given the value one, to simplify comparison of the various indexes.

As was expected, the index containing all eight traits had the largest correlation (R_{AI}). However, there was only 0.187 difference between the largest and smallest R_{AI} values. For correlations of the magnitudes obtained for the various indexes, there is probably not a great deal of difference in the predictive value of the sixteen indexes. Index one is 45.8 percent more efficient than index eighteen (probe, carcass length, loin eye area and percent lean) and, thus, may be worth the extra time and expense involved in obtaining the measurements.

Indexes two and four, three and five, seven and eight, nine and ten, and twelve and thirteen indicate that the addition of weaning weight to a selection index does not increase the predictive value of the index. This is also reflected to some degree in the magnitudes of the regression coeffi-

TABLE XVIII

PARTIAL REGRESSION COEFFICIENTS AND R_{AI} VALUES FOR SELECTION INDEXES INVOLVING AVERAGE DAILY GAIN AS A MEASURE OF GROWTH RATE

Index	No. Weaned	W. Wt.	A.D.G.	F. Eff.	Probe	Carcass Length[a]	L.E.A.[a]	% Lean[a]	R_{AI}
1.	0.221	0.054	1.0	-2.987	-2.755	0.264	1.244	-.092	0.595
2.			1.0		- .992				0.454
3.			1.0		- .793	0.055	0.271	-.007	0.516
4.		-.004	1.0		- .974				0.457
5.		-.002	1.0		- .796	0.052	0.262	-.007	0.517
6.			1.0	-1.356	-1.844				0.504
7.			1.0	-1.623	-1.895	0.131	0.690	-.055	0.560
8.		-.002	1.0	-1.570	-1.861	0.126	0.669	-.054	0.560
9.			1.0	-1.848					0.429
10.		0.010	1.0	-2.112					0.431
11.	0.122	0.027	1.0	-1.567	-1.387	0.096		0.050	0.546
12.			1.0		- .641	0.032		0.028	0.469
13.		-.003	1.0		- .650	0.029		0.027	0.471
14.			1.0	-1.095	-1.225	0.059		0.033	0.511
15.			1.0			0.084	0.231	0.022	0.483
16.	0.036		1.0		- .992				0.484
17.	0.034		1.0			0.084	0.231	0.022	0.512
18.					-1.0	0.055	0.333	-.036	0.408

[a] Regression coefficients for carcass traits are equivalent to information from seven full-sibs.

cients for weaning weight. The absence of any increase in the R_{AI} value when weaning weight is added to an index is probably partially due to the low heritability and relatively small economic value for weaning weight. In addition, the genetic and phenotypic relationships between weaning weight and the other traits involved in the index could be responsible for the lack of importance for weaning weight, although none of the relationships appear to be antagonistic. The low heritability for weaning weight can not be the complete cause since number of pigs weaned, which also has a low heritability, is considerably more important than weaning weight. Indexes two and sixteen and fifteen and seventeen illustrate that the inclusion of number of pigs weaned does increase the predictive value of an index slightly. The higher economic value for number weaned and its assumed independence of all traits except weaning weight indicate that the economic value of weaning weight or the genetic and phenotypic relationships involving weaning weight account for the failure of weaning weight to increase the predictive value of an index. Irregardless of the exact cause, weaning weight would not need to be included in selection indexes constructed using the estimates of the parameters used in this study and involving this same group of traits.

In all indexes in which feed efficiency is not included with average daily gain and probe backfat, the partial regression coefficient for probe is less than the coefficient for gain. When feed efficiency is included in addition to gain and probe, the regression coefficient for probe is larger than the coefficient for gain. The genetic and phenotypic correlations between gain and feed efficiency are high ($r_g = -.67$, $r_p = -.62$), while between feed efficiency and probe they are low ($r_g = 0.20$, $r_p = 0.12$). Also, the economic value for feed efficiency is extremely high. This would indicate that feed efficiency is reducing the emphasis placed on gain due to the high genetic and phenotypic relationships, but due to the low relationships with probe, feed efficiency has little effect on the regression coefficient for probe.

The partial regression coefficients for percent lean cuts are negative in indexes one, three, five, seven, eight and eighteen. This would appear undesirable since an increase in percent lean cuts is desired. However, percent lean cuts and loin eye area are fairly highly related genetically ($r_g = 0.63$) and phenotypically ($r_p = 0.51$). In addition, both traits are to a certain extent a measure of the same quantity. Therefore, it would probably be better to consider both traits together when examining the indexes. This point can partially be illustrated by examination of indexes eleven, twelve, thirteen and fourteen. When loin eye area was excluded from the indexes, the regression coefficients for percent lean became positive as desired. However, it is probably not entirely the relationship between loin eye area and percent lean which is causing the negative coefficients for percent lean. This is illustrated in indexes fifteen and sixteen where both the coefficient for loin eye area and percent lean are positive. However, feed efficiency and probe backfat are not present in either of these indexes and both are fairly highly related to percent lean genetically (r_g = 0.46 for feed efficiency and r_g = -.58 for probe backfat). These two traits could be partially contributing to the negative regression coefficient for percent lean in some indexes. Index eighteen indicates the negative coefficient may be due more to the relationship with probe than with feed efficiency. It would appear that with the parameters assumed in this study, loin eye area is a more desirable measure for predicting the aggregate breeding value than percent lean.

Selection Indexes Involving Age at 200 Pounds As a Measure of Growth Rate

The aggregate breeding value (A) for indexes constructed in this section was defined the same as it was in the last section using average daily gain as the measure of growth rate except that age at 200 pounds was substituted for gain.

The ten indexes constructed using age at 200 pounds as the measure of growth rate are presented in Table XIX. The regression coefficient for age at 200 pounds was given the value one for all indexes.

The most noticable difference between the indexes constructed using age at 200 pounds as a measure of growth rate and those using average daily gain is the higher correlations

TABLE XIX

PARTIAL REGRESSION COEFFICIENTS AND R_{AI} VALUES FOR SELECTION INDEXES INVOLVING AGE AT 200 POUNDS AS A MEASURE OF GROWTH RATE

Index	No. Weaned	W. Wt.	Age	F. Eff.	Probe	Carcass Length[a]	L.E.A.[a]	% Lean[a]	R_{AI}
19.	-.229	-.999	-1.0	-6.719	-31.105	0.559	13.766	-.485	0.703
20.			-1.0		-35.730				0.527
21.			-1.0		-25.408	2.564	19.183	-.887	0.650
22.		-.955	-1.0		-37.176				0.593
23.		-.917	-1.0		-29.592	0.275	12.567	-.236	0.700
24.			-1.0	-23.476	-37.480				0.549
25.			-1.0	-24.623	-29.589	4.354	25.734	-2.010	0.666
26.		-.946	-1.0	-7.673	-31.024	0.762	14.405	-.566	0.703
27.			-1.0	-35.951					0.513
28.		-.764	-1.0	-25.912					0.534

[a] Regression coefficients for carcass traits are equivalent to information from seven full-sibs.

between the indexes and the aggregate breeding value for the indexes involving age at 200 pounds. The reason for this is the higher heritability assumed for age at 200 pounds than was assumed for gain. The heritability of an index (R^2_{AI}) should be some function of the heritabilities of the traits included in the index, and the only difference in the two sets of indexes was in the trait used as a measure of growth rate. One might think that using age at 200 pounds instead of average daily gain will increase the predictive value of an index. This will be true only if the parameter estimates are accurate. The heritability for age is based on relatively few estimates and is, therefore, less reliable than the heritability for average daily gain. In addition, since age is a measure of growth rate, the heritability would appear to be higher than expected. Therefore, before too much can be said about the higher predictive value of indexes involving age at 200 pounds compared to indexes involving average daily gain, more estimates of the heritability for age at 200 pounds are needed.

With indexes involving age at 200 pounds, including number of pigs weaned does not increase the predictive value of the index (index 19 versus index 26). However, including pig weaning weight increased the R_{AI} value of the index (indexes 20 and 22, 21 and 23, 25 and 26, and 27 and 28). This is contrary to what was observed with the indexes involving average daily gain. The reason for the differences is not readily apparent, but is involved with the estimates of the parameters used. Whether it is economic values, variances, genetic or phenotypic correlations causing the differences is not known. The negative sign on the partial regression coefficients for weaning weight might be due to the fact that the genetic correlation between age and weaning weight was assumed to be zero since no estimates were available. If an estimate of the correlation were known, the right hand sides of the normal equations would be changed due to the large variance for both weaning weight and age; thus, causing the coefficient to possibly be positive.

Similarly, to the indexes involving average daily gain, the partial regression coefficients for percent lean cuts were negative for the indexes involving age. However, the regression coefficients for loin eye area were positive as before, so the overall value of carcass meatiness would be positive. As was suggested earlier, the interrelationship between percent lean cuts, loin eye area, feed efficiency and probe backfat is probably the major cause for the negative signs. No specific parameter estimates can be pointed to as the entire cause.

Indexes Constructed with Loin Eye Area Omitted From the Definition of Aggregate Breeding Value

To try and gain some insight into what was causing the negative sign on the partial regression coefficient for percent lean, a set of indexes was constructed eliminating loin eye area both from the index and the definition of aggregate breeding value (A). The aggregate breeding value was defined identically to the one given in the section on average daily gain indexes except loin eye area was omitted. The indexes constructed are presented in Table XX. The regression coefficient for average daily gain was again given the value one for ease of comparison.

The regression coefficients for percent lean were generally positive when loin eye area was omitted, but the magnitudes of the coefficients were small. This further illustrates that it is not entirely the high genetic and phenotypic relationship between loin eye area and percent lean which is causing the deemphasis of percent lean cuts. The relationship of percent lean to both probe backfat and feed efficiency are probably also involved.

As was true with the other indexes involving average daily gain, the addition of weaning weight did not increase the predictive value of a given index. Also, number weaned did increase the predictive value of an index as was true earlier. The regression coefficient for probe was again less in absolute magnitude than the regression coefficient for average daily gain when feed efficiency was not included in the index, but greater when feed efficiency was included. The regression coefficients for carcass length were smaller in the above indexes than they were with the previous average daily gain indexes. The interrelationship between loin eye area, carcass length and the other traits would almost certainly be the cause, but the exact cause is not evident.

TABLE XX

PARTIAL REGRESSION COEFFICIENTS AND R_{AI} VALUES FOR SELECTION INDEXES CONSTRUCTED WITH LOIN EYE AREA OMITTED FROM THE DEFINITION OF AGGREGATE BREEDING VALUE

Index	No. Weaned	W. Wt.	A.D.G.	F. Eff.	Probe	Carcass Length[a]	% Lean[a]	R_{AI}
29.	0.086	0.017	1.0	-.954	-1.173	0.109	0.025	0.564
30.			1.0		- .869			0.490
31.			1.0		- .681	0.050	0.009	0.499
32.		-.004	1.0		- .857			0.493
33.		-.004	1.0		- .691	0.046	0.008	0.501
34.			1.0	-.755	-1.271			0.522
35.			1.0	-.739	-1.100	0.080	0.000	0.529
36.		-.004	1.0	-.688	-1.082	0.073	-.001	0.530
37.			1.0	-1.010				0.447
38.		0.004	1.0	-1.074				0.448

[a] Regression coefficients for carcass traits are equivalent to information from seven full-sibs.

The regression coefficients for feed efficiency are considerably smaller when loin eye area is omitted from the definition of aggregate breeding value (A). However, the genetic and phenotypic correlations between loin eye area and feed efficiency are small. This would indicate that the relationship between loin eye area and the other traits involved is what is causing the reduction in the partial regression coefficients for feed efficiency.

Another interesting point needs to be made with respect to the two sets of indexes involving average daily gain. When loin eye area is omitted from A, indexes not including carcass traits have a higher correlation (R_{AI}) than when loin eye area is included. This seems reasonable since these non-carcass traits can account for more of the variation in A when loin eye area is omitted. On the other hand, indexes including carcass traits have lower R_{AI} values than they previously had. This indicates that loin eye area adds to the predictive value of an index. As a trait, loin eye area probably accounts for more variation in A than either of the other two carcass traits. This indicates that loin eye area should definitely be included in the carcass traits.

R_{AI} Values When Carcass Data is From Full-Sibs

The correlations (R_{AI}) presented in Tables XVIII, XIX and XX reflect the predictive value of an index if all measurements were obtained from the individual itself. In the case of carcass measurements, data from seven full-sibs would be equivalent. How much will the predictive value of an index be reduced if carcass data were available on only one or two full-sibs? The R_{AI} values obtained when it was assumed that carcass data was available on only one or two full-sibs are listed in Table XXI. Probe backfat was assumed to be carcass backfat in index 18; thus, all four traits in index 18 are carcass traits.

The amount the R_{AI} value is reduced depends upon the number of traits involved in the index and the number of carcass traits involved. Indexes 11 through 13 and 29 through 36 contain only two carcass traits, and, thus, the reduction is less than in the other indexes in which there were three or four carcass traits. Loin eye area was the trait omitted from all these indexes, so this could be an indication of the importance of loin eye area in a selection index using the parameters assumed in this study. Also, the greater the number of traits included in the index, which can be measured on the individual, the smaller is the reduction in the R_{AI} values. Index 18 demonstrates the greatest reduction and is composed of only the four carcass traits. Index 15 exhibits the next greatest reduction and the only non-carcass trait in index 15 is average daily gain. All other indexes contain at least one other non-carcass trait. This indicates that smaller numbers of sibs could be used with indexes containing greater numbers of non-carcass traits without greatly affecting the predictive value of the

TABLE XXI

CORRELATIONS (R_{AI}) WHEN CARCASS DATA IS AVAILABLE ON SEVEN, TWO AND ONE FULL-SIB

Index	Seven Full-Sibs	Two Full-Sibs	One Full-Sib
1.	0.595	0.550	0.537
3.	0.516	0.467	0.446
5.	0.517	0.468	0.448
7.	0.560	0.519	0.503
8.	0.560	0.520	0.503
11.	0.546	0.531	0.525
12.	0.469	0.448	0.439
13.	0.471	0.450	0.441
14.	0.511	0.497	0.490
15.	0.483	0.415	0.389
17.	0.512	0.452	0.424
18.	0.408	0.272	0.204
19.	0.703	0.645	0.622
21.	0.650	0.577	0.549
23.	0.700	0.642	0.621
25.	0.666	0.592	0.562
26.	0.703	0.643	0.620
29.	0.564	0.554	0.549
31.	0.499	0.485	0.479
33.	0.501	0.488	0.482
35.	0.529	0.519	0.515
36.	0.530	0.520	0.516

index.

With almost all of the indexes, there does not appear to be sufficient reduction in predictability by having carcass data on only one full-sib to recommend exclusion of carcass data from the index. However, it should be noted that in all indexes, using gain as the measure of growth rate, the correlation (R_{AI}) for an index with carcass data from only one full-sib is lower than the R_{AI} value for the corresponding index excluding the carcass traits. Indexes two and three illustrate this ($R_{AI} = 0.454$ for index two and $R_{AI} = 0.446$ for index three with one full-sib). This is theoretically impossible and could possibly just be rounding error since it was not true for the indexes involving age. It could, however, indicate that the fraction one-half is not the correct factor to multiply the regression coefficient by for carcass data on one full-sib. The R_{AI} values are only slightly less and coupled with slightly larger R_{AI} values for the age indexes, the bias associated with the factor one-half is probably not sufficient to overcome its practicality. The extreme closeness of the R_{AI} values for indexes with one full-sib to the corresponding index with no carcass data does indicate that if carcass data is available on only one full-sib, it is not extremely valuable in predicting the aggregate breeding value of an individual. If carcass data from one full-sib is available, it should be used; but if it is difficult to obtain and can only be obtained on one full-sib for each individual, its value could certainly be questioned.

Summary

The first and probably most important point which needs to be made concerns contributing the differences in two indexes to one or two specific parameter estimates. It could certainly be true and probably is that these specific parameter estimates are the major reason for the changes observed in the regression coefficients, but it must be remembered that it is the interrelationship among all parameter estimates which determines the magnitude of the regression coefficients.

The changes which were observed in the various indexes illustrate the need for accurate estimates of the parameters. This is especially true of genetic correlations for which accurate estimates are not available. Erroneous estimates of a genetic correlation could have a large effect on the resulting regression coefficients. However, there was not a great deal of difference in the predictive value of the indexes constructed. This indicates that even though the regression coefficients are different, causing different individuals to be selected, the mean genetic change using any of the indexes would probably not be greatly different. There would be some differences between the index containing only a few traits to one containing a large number, but the addition or deletion of one trait does not affect the predictive value greatly.

It is difficult to recommend specific indexes since this would depend on the measurements available in a particular operation. The amount of time, labor and expense required to obtain a particular measurement for a specific operation would need to be determined before deciding if the measurement is worth obtaining. The indexes involving age should probably be questioned until the heritability of age at 200 pounds is more accurately determined. Also, the additional information gained from carcass data on only one full-sib is questionable; and if it is expensive or difficult to obtain, it should probably be omitted providing probe is evaluated.

CHAPTER VII

CONCLUSIONS

A selection index is a mathematical tool which, if proper weight is given to each trait, is more efficient than selection for one trait at a time or for several traits with an independent culling level for each trait (Hazel and Lush, 1942). In order to give the proper weight to each trait, it is necessary to obtain accurate estimates of the parameters involved in the construction of the index.

In the present study, the correlation between the index and the aggregate breeding value (R_{AI}) was used as the criteria for comparing indexes constructed using different estimates of the parameters and indexes involving various combinations of traits. A selection index is essentially a multiple regression equation and it is the multiple correlation coefficient which indicates the predictive value of a given equation. The R_{AI} value is the multiple correlation coefficient for a given index.

Results of this study indicate that the economic values of the traits considered may be placed on a relative basis by dividing one of the economic values into the rest prior to incorporation into the normal equations. The relative magnitudes, not the absolute magnitudes, of the resultant regression coefficients are of primary interest; therefore, dividing all economic values by a constant will not affect the relative magnitudes of the regression coefficients. However, the economic values should not be multiplied by the standard deviation of the trait to which they correspond before placing them on a relative basis since the least squares procedure, where the normal equations are composed of variance and covariance estimates, adjusts for differences in variability of the traits involved (see Chapter III).

The economic value of a trait is defined as the increase in profit expected to result from one unit change in that trait. However, a decrease is the desired direction of change for certain traits such as probe backfat, feed efficiency and age at 200 pounds. Thus, these traits would have a negative economic value. It was demonstrated in Chapter III that higher correlations between the index and the aggregate breeding value (R_{AI}) can be obtained using positive economic values for traits in which a decrease is desired if antagonistic relationships exist between this trait and other traits in the index. This is to be expected since selection to increase this trait would result in more rapid progress due to the antagonistic relationship. If selection were to increase this trait, then the economic value would be positive, not negative. If the relationships are compatible, greater progress can be made by selecting to increase certain traits and decrease others. The R_{AI} value will be higher in this case using negative economic values for the traits for which the decrease is desired. Since the desired improvement is to increase some traits and decrease others, negative economic values should be used for all the traits in which a decrease is desired.

In order to evaluate selection indexes involving different parameter estimates without actually calculating the indexes, it is necessary to determine some relationship between the parameters involved which indicates the magnitude of the criteria used to compare the indexes. In this study, since R_{AI} was used as the criteria, some simple relationship between the genetic and phenotypic correlations (since the phenotypic variances, heritabilities and economic values were not varied) was desired which would indicate the magnitude of R_{AI} for each index. In order to have much practical utility, the relationship needed to be simple.

Fourteen indexes were constructed in Chapter V, involving average daily gain and probe backfat, to try and determine what effect varying the correlations had on R_{AI} and to try and find, if possible, a simple relationship between the genetic and phenotypic correlations which would give an indication of the magnitudes of R_{AI}. The magnitude of the correlation (R_{AI}) appeared to be associated with the difference between the genetic and phenotypic correlations ($r_g - r_p$) used in the construction. The larger the magnitude of this difference, the larger or smaller the correlation (R_{AI}) depending on the traits involved. If an increase is desired in one trait and a decrease in the other, a positive difference ($r_g - r_p$) would indicate a smaller R_{AI} value than if the difference were negative. With the indexes involving average daily gain and probe backfat, the smallest R_{AI} value (0.409) was associated with the largest positive difference (0.74), while the largest R_{AI} value (0.795) was associated with the largest negative difference (-.60). If an increase were desired in both traits, the reverse should be true; small R_{AI} values should be associated with large negative differences and large R_{AI} values with large positive differences. The difference ($r_g - r_p$) was not a perfect indicator. The results indicated that a more accurate indicator would have been r_g minus some factor times r_p. The factor involved was not able to be determined except that it should be less than one.

The pattern established by using the sum of the genetic correlations minus the sum of the phenotypic correlations was not as clear an indicator of the magnitude of the R_{AI} value in a three trait selection index as it was in a two trait index. However, less change was present in the R_{AI} values for the three trait indexes when the estimates of the genetic and phenotypic correlations were varied. This indicated that the more traits involved in an index, the less sensitive the index is to changes in one or two of the parameter estimates.

It was illustrated in Chapter VI that the correlation between the index and the aggregate breeding value (R_{AI}) does not differ greatly for indexes constructed from various combinations of swine traits (range in R_{AI} values was 0.408 to 0.595). Certain traits (average daily gain, feed efficiency, probe backfat and loin eye area) increase the predictive value of an index more than other traits (number of pigs weaned, weaning weight, carcass length and percent lean). Even though indexes composed of different combinations of traits do not differ greatly in predictive value, the amount of emphasis for each trait (magnitudes of the partial regression coefficients) varied among the indexes. Changes in the partial regression coefficients from index to index could be explained, for the most part, by specific genetic and phenotypic correlations as the major cause. It was evident, however, that it is the interrelationship of all variables involved which determine the magnitudes of the regression coefficients. Failure of the regression coefficients to be similar from index to index should not affect the mean genetic change expected in a population if the correlations between the index and the aggregate breeding value are similar. To a certain extent, different individuals would be selected using different indexes, but with identical R_{AI} values the mean genetic change in a population should be the same for both indexes.

The particular traits which should be included in a selection index depend on the nature of a particular operation. The amount of time, labor and expense involved in obtaining particular measurements must be weighed against the increase in predictive value expected. The inclusion of carcass traits in a selection index is warranted if suitable numbers of collateral relatives are evaluated. The number of collateral relatives required depends on the relationship between the individual and the relatives. It is questionable, unless emphasis is entirely on meatiness, whether information from one full-sib is sufficient to overcome the difficulties involved in obtaining the measurements.

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