AN ANALYSIS OF THE DEPENDENCY STRUCTURE BETWEEN A GILT'S PRE-BREEDING AND REPRODUCTIVE TRAITS

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CHAPTER I

INTRODUCTION

Increasing litter size offers a tremendous opportunity to increase the overall efficiency of swine production. The number of pigs born alive is determined by two parameters: number of ova shed per estrus (ovulation rate) and the proportion of eggs shed which are represented by live pigs at birth (embryo survival rate).

Bradford (1969) provided information on mice that suggests that ovulation rate and embryo survival rate are under genetic control and that they are at least partially independent. This research also indicates that there is a relatively high genetic correlation between ovulation rate and litter size. In addition, the number of eggs shed sets the upper limit on number of pigs born, thus forcing a phenotypic correlation between ovulation rate and litter size. These results suggest that one might increase litter size by increasing ovulation rate. Zimmerman and Cunningham (1975) reported a realized heritability of approximately .40 for ovulation rate which is considerably larger than the heritability normally found for litter size. Therefore, indirect selection for litter size by selecting on ovulation rate may be more effective than direct selection.

At this point, however, it is difficult and impractical for a commercial swine producer to determine ovulation rate on all females available for breeding. If certain traits measured before breeding can

be found which are highly correlated, both genetically and phenotypically, with ovulation rate, then selection for fertility would be more efficient.

This study was initiated to analyze the genetic and phenotypic dependency structures existing between traits measured on a gilt prior to breeding and her reproductive performance measured 30 days after breeding. In addition to the standard methods, this analysis will include the application of two multivariate techniques not normally used in the field of animal science.

CHAPTER II

REVIEW OF LITERATURE

This review of literature is divided into sections that deal with 1) the relationship between a female's pre-breeding characteristics and her subsequent reproductive performance and 2) the theory and application of principal component and canonical correlation analyses.

Relationship Between a Female's Pre-Breeding Characteristics and Her Subsequent Reproductive Performance

Genetic and phenotypic relationships among traits are of great importance in the prediction and description of genetic and phenotypic changes occurring in both selected and unselected traits. There are at least two ways by which ovulation rate at a given breeding age can be increased. One way is to decrease the age at puberty, thus allowing the female to have more heat periods by a given breeding age since ovulation rate appears to increase over the first few heat periods. Another way is to select those gilts which have the highest ovulation rate at a given heat period.

Warnick et al. (1951) studied the records of 205 gilts from five inbred lines to determine if weight at various ages was highly correlated with age at puberty, thus furnishing a basis for indirect selection for early sexual maturity. They found that as the age at which the weight

was taken increased so did the correlation between weight and age at puberty. The correlations were negative and significant at all ages. The correlations for weight at 56 days and 154 days with age at puberty were -.54 and -.58, respectively. The correlations of growth rates measured over various periods with age at puberty averaged around -.40. Robertson et al. (1951a, b) reported on two experiments designed to evaluate the relationship of weight at various ages with age at puberty using Chester White and Poland China gilts. They also found that as the age at which the weight was taken increased so did the correlation between weight and age at puberty. All correlations were negative and ranged from -.29 to -.38. These results indicate that faster growing gilts tend to reach puberty at an earlier age. These results are in good agreement with those reported by Phillips and Zeller (1943), Foote et al. (1956), Rio (1957), and Reutzel and Sumption (1968). Robertson et al. (1951b) also found that weight and age at puberty accounted for 13.0 and 3.6% of the variation in ovulation rate at the second heat period, respectively. This indicates that weight was a more important factor affecting ovulation rate than was age.

Several workers have indicated that the reproductive ability of gilts increases as they are allowed more heat periods before breeding. Warnick et al. (1951) found that the number of corpora lutea at the first, second and third heat periods were 10.0, 10.8 and 11.9, respectively. Robertson et al. (1951a, b) reported that ovulation rate increased by 1.4 and 2.0 eggs, respectively, from first to second heat periods. Similarily, Wiggins et al. (1950) observed that gilts that conceived at the second estrus farrowed 1.4 pigs more than those that conceived at the

second estrus. Those that conceived at the second estrus farrowed 2.5 pigs more than those that conceived at the first estrus.

Stewart (1945) used the records of 749 inbred gilts to evaluate the effect of age and weight at breeding on the size of a gilt's first litter. As age at breeding increased, litter size increased in a curvilinear fashion with no further increase occurring after gilts reached 15 months of age. Most of the increase in litter size occurred between nine and twelve months. When the inbreeding of the dam and litter were held constant, the partial regression of total litter size at birth on age of dam in months was .61 pigs. These results agree with those reported by Johansson (1929), Olbrycht (1943) and Korkman (1947) which also suggest a progressive increase in litter size with an increase in age at first farrowing. Korkman (1947) obtained a smaller regression of .24 pigs at birth for each month increase in age of dam at breeding. However, his gilts farrowed first at 11 and 12 months. Olbrycht (1943) reported an average of 1.07 more pigs per litter for sows farrowing first at 17 months compared to those farrowing first at 12 months. In constrast to these workers, Ellinger (1921) and Krizenecky (1935) concluded that age at breeding had little effect upon the size of a gilt's first litter.

Squiers et al. (1952) studied the records of 278 gilts from three inbred lines, a Duroc line and crosses among the lines. All gilts were mated to unrelated boars and slaughtered 25 days after breeding. The number of ova shed at first estrus was significantly correlated with age at first estrus ($r = .31$). The simple correlation between growth rate and number of ova shed was .10, which they suggested would have been larger except for the rather strong tendency for faster growing gilts to be bred at an earlier age ($r = -.27$). When age was held constant, the

correlation between growth rate and ovulation rate was .20 and significant. Age at breeding was significantly correlated with litter size (r = .31). The number of ova shed accounted for only 22% of the variation in the number of embryos suggesting that factors controlling embryo mortality may be more important in determining number of embryos than is the number of ova shed.

Rathnasabapathy et al. (1956) used 42 gilts to evaluate the relationship of a gilt's growth performance with her reproductive performance measured 55 days after breeding. Weaning weight, 154-day weight and age at breeding were positively and significantly correlated with ovulation rate (r = .33, .34 and .32, respectively), but showed no significant relationship to litter size. Average daily gain and average backfat thickness showed positive correlations with ovulation rate and negative correlations with litter size with all values being small and nonsignificant. Ovulation rate accounted for only three percent of the variation in litter size indicating that factors other than ovulation rate are operating to limit litter size.

Reddy et al. (1958) utilizing data from 117 gilts slaughtered 55 days postbreeding found that weight at breeding and age at breeding were positively and significantly correlated with ovulation rate (r = .35 and .56, respectively). Age at breeding was also correlated with litter size (r = .41). However, this correlation was greatly reduced when ovulation rate was held constant, implying that the major effect of age at breeding on litter size is due primarily to its effect on ovulation rate. Weight at 154 days, average backfat thickness and average daily gain were not significantly correlated with either ovulation rate or litter size. The correlation between litter size and ovulation rate was .48 and significant.

Omtvedt et al. (1965) analyzed the breeding and farrowing records on 390 gilts from five breeding groups. Age at breeding, which ranged from 205 to 310 days, was positively correlated with litter size (r = .12) and breeding weight (r = .55). The correlation between breeding weight and litter size was .19. When breeding weight was held constant, the correlation between litter size and age at breeding was not significant indicating that the increase in litter size was due more to an increase in breeding weight than to an increase in breeding age.

Young and Omtvedt (1973) found that gilts farrowed in large litters tended to farrow fewer pigs than gilts farrowed in small litters (r = -.13) while the size of litter a gilt was weaned in was not associated with the size of her first litter. There was also a significant correlation of the size of a gilt's first litter with her birth weight (r = .16) and with her weaning weight (r = .10). Gilts that were younger at 200 lbs., thus being the faster growing gilts, farrowed larger litters than gilts which were older at 200 lbs. (r = -.13). These results are in general agreement with those reported by Young et al. (1974). They studied the records of 344 gilts to evaluate the relationship of various measures of performance with ovulation rate and number of embryos 30 days after breeding in gilts. No correlations were large, but those gilts which grew faster and were heavier at weaning and were heavier at breeding ovulated more eggs. No measurements were consistently correlated with the number of embryos.

Hetzer and Miller (1970) evaluated the influence of selection for high and low fatness on reproductive performance of swine. The correlation between backfat thickness and litter size at any age was essentially

zero. However, they did find a high relationship of litter size with breeding age and breeding weight.

Revelle and Robison (1973), using 1,078 two-generation and 710 three-generation pedigrees, noted a negative relationship between the size of litter a gilt came from and the size of her first litter. They noted a high, low, high oscillation for litter size in the three generation pedigree. These results indicate that gilts from large litters were prevented from expressing their genetic superiority by the stress of being reared in large litters. Further evidence for the delay in maturation due to competition in large litters was noted in that gilts from litters of six to twelve pigs reached puberty at about the same age while gilts from litters of more than twelve pigs were progressively older at puberty. Engle et al. (1973) also found that female rats selected from large litters reached puberty later than females from small litters principally because of the higher growth rate of the latter group.

In general, the research in swine indicates that gilts which grow faster and are heavier at any given age or at breeding tend to ovulate more eggs and farrow larger litters. A considerable amount of research has been done in mice to evaluate reproductive performance and its relationship to growth rate and weight at various ages.

MacArthur (1949) reported the results of an experiment on selection for large and small body size in mice. After 22 generations, a large and a small body size line had been successfully developed. However, the small race of mice developed slowly, bred a little later, ovulated half as many eggs and produced fewer young per litter than did the large race. Falconer (1953) evaluated the correlated response of reproduction in a line selected for large six week weight and a line selected for

small six week weight through eleven generations of selection. Litter size increased in the large line only through the first half of the experiment. The small line showed little change in litter size up to the fifth generation but litter size declined rapidly thereafter. After eleven generations, the litter size for the large and small lines were 7.8 and 4.0 mice, respectively. Falconer and King (1953) concluded from their experiment that there is a genetic correlation between litter size and body weight; however, it operates over a limited weight range. This suggests the presence of an optimum body weight with regards to the size of litter produced by the female. Above the maximum weight of the above range, no increase in litter size would occur but the maintenance cost of the female would continue to increase as weight increased. Fowler and Edwards (1960) evaluated the ovulation rate of mice selected for either large or small body size. The lines selected for large body size ovulated about six more eggs than lines selected for small body size. In addition, the number of eggs ovulated was positively correlated with body weight within each line although the correlation was not significant. These results are in agreement with those reported by Elliot et al. (1968).

All of the above authors selected on body weight at a given age. Rahnefeld et al. (1966) selected for postweaning growth rate in mice. The realized genetic correlation between litter size and growth rate was .89 resulting in a total increase in litter size of 2.5 mice after 29 generations of selection. This correlated response is qualitatively comparable to that reported by MacArthur (1949) and Falconer (1953) when then selected for large body size. However, in their experiments the correlated response in litter size ceased after about six generations. This was probably due to differences in selection criterion. The effect

of litter size was less on postweaning growth than on 42-day weight. The largest females at 42 days were probably found in the smallest litters resulting in selection for small litter size. In disagreement with Rahnefeld, Bradford (1971) found that mean litter size did not increase in a line of mice selected for gain. The gain line showed a decline in fertility had irregular estrus cycles and longer gestation periods. The gain line also tended to have litters which were either very large or very small with few in between. Frahm and Brown (1973) found that lines of mice selected for weaning weight or average daily gain from 21-42 days had significantly larger litters than the control line after 14 generations of selection. However, the percentage of females exposed for breeding that produced litters was significantly reduced in the average daily gain line.

Crane et al. (1972) evaluated the relation of reproductive performance to age and weight at puberty in two lines of mice selected for 42-day weight. In this case, a female was considered to reach puberty when the first estrus was observed, therefore, puberty could be considered a threshold character. The authors concluded that selection for weight had increased growth to the point that the minimum weight necessary for onset of puberty was reached before the minimum necessary age at which puberty could occur. The correlations for weight with reproductive measures were larger ($r = .24$ to $.38$) than the correlations for age with reproductive measures ($r = -.11$ to $-.35$).

Meyer and Bradford (1974) found that lines of mice selected for ovulation rate had ovulation rates higher than controls but lower than a line selected for gain. Land (1970), using mice, found genetic and

phenotypic correlations of about .40 between body weight at six weeks and ovulation rate.

Bateman (1966) successfully selected a strain of mice for large litter size and a strain for small litter size. After twelve generations of selection, the litter size was 11.1 and 5.5 mice for the large and small litter size strains, respectively. The females of each line were of approximately equal weights indicating that litter size can be changed without changing body weight. In contrast to this study, Dalton and Bywater (1963), after 14 generations of selection, were not able to change litter size in a line selected for small litter size at weaning or a line selected for large litter size at weaning. The difference in the results of these two experiments probably resulted from different selection criteria. Bateman selected on litter size at birth while Dalton and Bywater selected on litter size at weaning.

Bradford (1969) tried to increase litter size by selecting for ovulation rate, embryo survival or litter size. Direct response to selection occurred in the lines selected for ovulation rate and embryo survival; however, only the latter line showed an increase in litter size. The line that was successfully selected for increased litter size showed an increase in ovulation rate but not in embryo survival. These results suggest that litter size may be increased by increasing ovulation rate or embryo survival.

In general, the correlations between growth traits and reproductive traits have been small and variable. The largest and most consistent correlations were found for average daily gain, breeding age and breeding weight with ovulation rate. The correlations of performance traits with litter size were generally smaller than their correlations with ovulation

rate. The size of litter a gilt was born or weaned in did not seem to be related to her ovulation rate or the size of her litter.

Theory and Application of Principal Component and Canonical Correlation Analyses

General

The derivation of principal components and canonical correlations result from direct usage of the theory of characteristic roots and the corresponding characteristic vectors of a square matrix.

Given an n x n matrix, A, the problem is to determine simultaneously a non-zero vector X and a scalar λ such that

$$AX = \lambda X$$

This can be rewritten as

$$(A - \lambda I)X = 0$$

which is a system of linear homogeneous equations. The determinant of $(A - \lambda I)$ must be zero for there to be a non-trivial solution for X. Any λ which satisfies this requirement is a characteristic root of A. If A is n x n, there are n characteristic roots. The characteristic vector, X_i, associated with a given characteristic root λ_i, can be found by solving the following for X:

$$(A - \lambda_i I)X = 0$$

If A is symmetric, then the characteristic vectors corresponding to distinct roots (roots which have different values) are pairwise orthogonal and linearly independent.

Principal Components

Principal component analysis is a method for reducing p correlated measurement variables to a smaller set of statistically independent linear combinations of the original measurements which have unique properties. The first principal component is that weighted combination of the several original variables which accounts for the maximum amount of the total variation represented in the complete set of original variables. The second principal component is that weighted combination of the original variables, which of all possible weighted combinations uncorrelated with the first principal component, accounts for the maximum amount of the remaining variation. The r^{th} principal component is that weighted combination which, of all possible weighted combinations uncorrelated with the first r - 1 principal components, accounts for a maximum amount of the remaining variation among the original p-variates (Overall and Klett, 1972).

Assume a sample is taken from a population and measurements X_1, X_2, . . ., X_p are taken on each element in the sample. The first principal component of the complex of sample values of the responses X_1, X_2, . . ., X_p is the linear compound

$$Y_1 = a_{11} X_1 + a_{12} X_2 + \ldots + a_{1p} X_p$$

whose coefficients, a_{1i}, are the elements of the characteristic vector associated with the greatest characteristic root, λ_1, of the sample correlation matrix R. The a_{1i} are unique up to a multiple by a scalar. If they are scaled such that $a'_1 a_1 = 1$, the characteristic root λ_1 is interpreted as the sample variance of Y_1. Similarily, the j^{th} principal component is the linear compound

$$Y_j = a_{j1} X_1 + a_{j2} X_2 + \ldots + a_{jp} X_p$$

whose coefficients are the elements of the characteristic vector associated with the j^{th} largest characteristic root, λ_j, of the sample correlation matrix, R. The total variance of all possible principal components derived from a given R matrix is

$$\sum_i \lambda_i = \text{trace } R = p$$

where p is the dimension of R. The relative value of the i^{th} principal component can be measured by

$$\frac{\lambda_i}{\text{trace } R} = \frac{\lambda_i}{p}$$

The correlation matrix is normally used because the measurements are generally taken in a large variety of units. If these units differ widely, linear compounds of the original quantities would have little meaning. Therefore, the standardized variates and correlation matrix are normally employed. For a more complete discussion of principal components, characteristic roots and characteristic vectors see Anderson (1958), Morrison (1967) and Overall and Klett (1972).

The usefulness of these new variates called principal components can be illustrated as follows. If a researcher took 10 measurements on each individual and calculated all possible simple correlations, he would have 45 correlations. To try to think about all these correlations simultaneously is very difficult if the aim is to generalize about the extent of the interrelationships of the 10 measurements. Suppose that the first principal component is derived and it accounts for 90 percent of the total variation in the system of 10 measurements. It would appear then that almost all of the variation in the system could be expressed along a single line rather than in a 10 dimensional space. The relative importance of the 10 variables in explaining the variation accounted for by that

principal component can be determined by the relative magnitude of the coefficients.

The following example was adapted from Morrison (1967):

The lengths of the humerus (M_1), ulna (M_2), tibia (M_3) and femur (M_4) bones of 276 leghorn fowl were found to have the following correlation matrix:

$$\begin{array}{c} M_1 \\ M_2 \\ M_3 \\ M_4 \end{array} \begin{bmatrix} 1.00 & .94 & .88 & .88 \\ & 1.00 & .88 & .89 \\ & & 1.00 & .92 \\ & & & 1.00 \end{bmatrix}$$

In order to derive the coefficients for the principal components, the following system of equations must be solved for the non-zero vector X and the scalar λ.

$$\begin{bmatrix} 1.00 & .94 & .88 & .88 \\ .94 & 1.00 & .88 & .89 \\ .88 & .88 & 1.00 & .92 \\ .88 & .89 & .92 & 1.00 \end{bmatrix} \begin{bmatrix} x_1 \\ x_2 \\ x_3 \\ x_4 \end{bmatrix} = \lambda \begin{bmatrix} x_1 \\ x_2 \\ x_3 \\ x_4 \end{bmatrix}$$

or

$$\begin{bmatrix} 1.00-\lambda & .94 & .88 & .88 \\ .94 & 1.00-\lambda & .88 & .89 \\ .88 & .88 & 1.00-\lambda & .92 \\ .88 & .89 & .92 & 1.00-\lambda \end{bmatrix} \begin{bmatrix} x_1 \\ x_2 \\ x_3 \\ x_4 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

The determinant of the left matrix must be zero for there to be a nontrivial solution for X. There are four distinct λ's or characteristic roots which will make the determinant zero. They are:

$$\lambda_1 = 3.69$$

$$\lambda_2 = .17$$

$$\lambda_3 = .08$$
$$\lambda_4 = .06$$

Now find the characteristic vector, X_1, associated with greatest characteristic root, λ_1. X_1 is the solution vector to the following system of equations.

$$\begin{bmatrix} (1.00 - 3.69) & .94 & .88 & .88 \\ .94 & (1.00 - 3.69) & .88 & .89 \\ .88 & .88 & (1.00 - 3.69) & .92 \\ .88 & .89 & .92 & (1.00 - 3.69) \end{bmatrix} \begin{bmatrix} x_{11} \\ x_{12} \\ x_{13} \\ x_{14} \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

or

$$\begin{bmatrix} -2.69 & .94 & .88 & .88 \\ .94 & -2.69 & .88 & .89 \\ .88 & .88 & -2.69 & .92 \\ .88 & .89 & .92 & -2.69 \end{bmatrix} \begin{bmatrix} x_{11} \\ x_{21} \\ x_{31} \\ x_{41} \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

The solution is: $X'_1 = (.961 \quad .964 \quad .957 \quad .960)$. The coefficient vector a'_1 for the coefficients of the first principal component are to be scaled such that $a'_1 a_1 = 1$. To do this, divide each of the elements of X'_1 by $(.961)^2 + (.964)^2 + (.957)^2 + (.960)^2$. Then $a'_1 = (.5004 \quad .5018 \quad .4980 \quad .4997)$.

To find the coefficients for the second, third, and fourth principal components follow the same procedure using the second, third and fourth largest characteristic roots, respectively.

The first principal component was:

$$Y_1 = .5004M_1 + .5018M_2 + .4980M_3 + .4997M_4$$

and accounted for 92.25 percent of the total variation in the original bone lengths $92.25 = 3.69/(3.69 + .17 + .08 + .06)$. The coefficients for each bone length are about equal, indicating that Y_1 is a measure of

overall size. The second principal component was

$$Y_2 = -.5195M_1 - .4774M_2 + .5299M_3 + .4707M_4$$

and it accounted for 4.35 percent of the total variation. Inspection shows that the coefficients for leg bones were negative and those for wing bones were positive but all were of about equal magnitude. This principal component contrasts leg and wing measurements. These components indicate that the major source of variation in the bone measurements is due to differences in body size and a considerably less amount is due to the relative differences between leg and wing measurements.

Canonical Correlation

Suppose a researcher has n observations from a p + q variate population and the variates fall into two natural subdivisions. For example, the first p variates may be measures of gilt's growth performance and the last q variates are measures of her reproductive performance. Let X_p and X_q denote the matrix of observations for the p and q variates, respectively. The task of the researcher is to evaluate the relationship of the p-variates with the q-variates. In the normal case the researcher would calculate the pq simple correlations. Again, it would be very difficult to evaluate the extent and nature of the interrelationships simply by looking at pq simple correlations. One method of evaluating the interrelationship existing between variables of two distinct groups is by the use of canonical correlations. This process develops two sets of linear combinations of the original variables. One set is derived for the p-variates (call it $U_i = a'_i X_p$) and one set is derived for the q-variates (call it $V_j = b'_j X_q$) subject to the following restrictions:

1. U_i and U_j are uncorrelated for $i \neq j$
2. V_i and V_j are uncorrelated for $i \neq j$
3. U_i and V_j are uncorrelated for $i \neq j$
4. U_1 and V_1 are the pair of linear compounds of X_p and X_q, respectively, which have the highest possible correlation.
5. U_2 and V_2 are the pair of linear compounds of X_p and X_q, respectively, with the next highest possible correlation subject to restrictions 1, 2 and 3.
6. Etc.

In order to derive the canonical variates, one must use either the covariance or correlation matrix including all p + q variates. The correlation matrix and standardized variates are normally used when units of measurement are different for different variates. Construct the symmetric correlation matrix, R, with order p + q and subdivide it as follows:

$$R = \left[\begin{array}{c|c} R_{11} & R_{12} \\ \hline R_{21} & R_{22} \end{array}\right]$$

where R_{11} contains the correlations among the elements of the p-variates and R_{22} contains the correlations among the elements of the q-variates. The correlations of the elements of the p-variates with the elements of the q-variates are contained in R_{12} and $R_{12} = R'_{21}$. The characteristic roots, λ_i, of the matrix

$$\left[R^{-1}_{11} R_{12} R^{-1}_{22} R_{21}\right]$$

are the squares of the canonical correlations. The coefficient vectors, a_i and b_i, corresponding to each λ_i are obtained as solutions to the following:

$$\left[R_{12}\, R^{-1}_{22}\, R_{21} - \lambda_i\, R_{11}\right] a_i = 0$$

$$\left[R_{21}\, R^{-1}_{11}\, R_{12} - \lambda_i\, R_{22}\right] b_i = 0$$

For a more indepth discussion of canonical correlation analysis see Morrison (1967) and Anderson (1958).

The following example was adapted from Morrison (1967).

In an investigation of the relation of age to the Wechsler Adult Intelligence Scale the following matrix of correlations was obtained among the digit span, vocabulary subtest, chronological age and number of years of formal education.

$$R = \begin{bmatrix} 1.00 & .45 & -.19 & .43 \\ & 1.00 & -.02 & .62 \\ & & 1.00 & -.29 \\ & & & 1.00 \end{bmatrix}$$

The researcher was interested in evaluating the relationship of the first two variates with the second two. The first set of canonical variates derived from this matrix was

$$U_1 = .26 \text{ (digit span)} + 1 \text{ (vocabulary)}$$

$$V_1 = .20 \text{ (age)} + 1 \text{ (years of education)}$$

and the correlation between U_1 and V_1 was .65. The second set of canonical variates derived from this matrix was

$$U_2 = 1 \text{ (digit span)} - .64 \text{ (vocabulary)}$$

$$V_2 = 1 \text{ (age)} + .10 \text{ (years of education)}$$

The canonical variate U_1 places four times as much emphasis on vocabulary score as on digit span score. Similarily, the variate V_1, places about five times as much emphasis on years of education as on age. Thus, the major link between these two groups of variates is based on the vocabulary-education link. As education increases so does vocabulary. The

second set of variates seem to compare the chronological age with a weighted comparison of digit span and vocabulary scores. If the small coefficient for education is disregarded, the second pair of canonical variates would reflect the widening gap between accumulated knowledge and performance skills with advancing age.

CHAPTER III

GENETIC AND PHENOTYPIC CORRELATIONS OF PRE-BREEDING TRAITS WITH REPRODUCTIVE TRAITS IN GILTS

Summary

This study involved the records of 339 purebred Duroc, Hampshire and Yorkshire gilts and 192 two-breed gilts resulting from matings among the three breeds. Heritability was estimated for all traits and in general the estimates were somewhat higher than those normally reported. All measures of growth were favorably and moderately to highly correlated, genetically, to ovulation rate with the relationship being stronger for traits measured late in growth as compared to traits measured early in growth. The sire component of variance was negative for number of embryos and embryos per corpora lutea thus preventing estimating genetic correlations for these traits. Only the genetic correlations of corpora lutea per embryo with birth weight (r_g = -.90), weaning weight (r_g = .91) and weaning weight deviated from the litter average (r_g = .72) were large.

None of the phenotypic correlations between pre-breeding traits and reproductive traits were large and only eight of the 68 correlations were significant. Gilts which grew faster, were younger at 100 kg, were heavier at breeding and had more days from 100 kg to breeding also had

higher ovulation rates. Gilts which were heavier and older at breeding and had more days from 100 kg to breeding also had more embryos.

A stepwise regression procedure was used to find the "best" model to predict ovulation rate (CL), number of embryos (EMB), embryo per corpora lutea (E/CL) and corporea lutea per embryo (CL/E). The "best" model accounted for only 15%, 18%, 9% and 6% of the variation in CL, EMB, E/CL and CL/E, respectively.

Introduction

Increasing litter size offers a tremendous opportunity to increase the overall efficiency of swine production. Basically the number of pigs born alive is determined by two parameters: number of ova shed per estrus (ovulation rate) and the proportion of eggs shed which are represented by live pigs at birth (embryo survival rate).

Bradford (1969) provided information from mice which suggests that ovulation rate and embryo survival rate are under genetic control and that they are at least partially independent. Direct response to selection occurred in lines selected for ovulation rate and embryo survival rate; however, only the latter line showed an increase in litter size. A line successfully selected for increased litter size showed an increase in ovulation rate but no change in embryo survival rate. These results indicate that increased litter size can result from increases in either ovulation rate or embryo survival rate.

However, it is difficult and impractical for a commercial producer to determine ovulation rates and embryo survival rates on all females. If some traits measured before breeding can be found which are highly correlated, both genetically and phenotypically, with ovulation rate or

embryo survival rate, then selection for increased litter size may be more efficient.

This study was initiated to evaluate the phenotypic and genetic relationships existing between a gilt's pre-breeding performance and her reproductive performance measured 30 days after breeding.

Materials and Methods

This study includes the data of 339 purebred Duroc, Hampshire and Yorkshire gilts and 192 two-breed cross gilts resulting from matings among the three breeds. The gilts came from phase I and II of the Oklahoma swine crossbreeding project and represent the eight breeding seasons from the fall of 1970 to the spring of 1974. The distribution of the gilts by breed group and season is presented in Table I.

The gilts were born at either the Stillwater or Fort Reno station and different management systems were employed at the two stations. The gilts at Stillwater were born in crates. Three to five days after birth, approximately one third of the litters and their dams were placed in individual pens with solid concrete floors open to the south. The remain litters and their dams were kept in pasture lots until weaning with two litters per lot. All litters were weaned at 42 days and a sample of the pigs were placed on the test floor at eight weeks of age and growth was measured from nine weeks of age to 100 kilogram. When gilts reached 100 kg, they were taken off the test floor and transferred to Fort Reno.

The gilts born at Fort Reno were also born in crates. At about three days of age they were moved with their dam to a concrete nursery pen with one litter per pen. The pigs were given access to creep feed at 21 days and the sow was removed at 42 days. The pigs were moved to

TABLE I

DISTRIBUTION OF GILTS BY BREED AND BREEDING SEASON

	BREED GROUP									
Season	DD	DH	DY	HD	HH	HY	YD	YH	YY	
70 Fall	14				16				15	45
71 Spring	29				24				8	61
71 Fall	14	8	8	5	10	3	10	9	11	78
72 Spring	16	13	10	7	21	8	12	14	13	114
72 Fall	21				18				10	49
73 Spring	11				20				11	42
73 Fall	7	8	9	8	12	7	7	8	7	73
74 Spring	14	7	6	5	9	6	7	7	8	69
Total	126	36	33	25	130	24	36	38	83	531

[a]First letter indicates breed of sire of gilt, second letter indicates breed of dam of gilt.

confinement feeding facility at eight weeks of age and growth was measured from nine weeks of age to 100 kilogram.

In the fall of 1970 and 1972 all purebred gilts were born at Stillwater. In the remaining seasons, the majority of the purebred gilts were born at Stillwater. All crossbred gilts were born at Fort Reno. In the seasons in which purebred and two-breed cross gilts were mated at Fort Reno, some of the purebred gilts had been born at Stillwater. These gilts had been transferred to Fort Reno at weaning and were placed on the growth test at Fort Reno with the Fort Reno born gilts. Thus, preweaning data on these gilts was obtained at Stillwater and postweaning data was obtained at Fort Reno. No attempt was made to correct for these various methods of handling. These different management systems probably created the most bias in weaning weights and litter size at weaning. Within a season-breed subclass all postweaning data was collected in contemporary surroundings.

After reaching 100 kg, all gilts were maintained at Fort Reno in drylot. The gilts were limited fed and were hand mated so as to produce a litter at approximately one year of age. However, the gilts used in this study were slaughtered approximately 30 days after breeding to provide information on ovulation rate, number of embryos and embryo survival rate.

The traits evaluated before breeding were: the size of litter a gilt was born in (NB) and weaned in (NW); her birth weight (BW), weaning weight (WW), average daily gain (ADG), age at 100 kg (AGE) and backfat thickness at 100 kg (BFT); the average of the litter she was born in for birth weight (LBW), weaning weight (LWW), average daily gain (LADG), age at 100 kg (LAGE) and backfat thickness (LBFT); the deviation of the

gilt's record from the litter average for birth weight (BWD), weaning weight (WWD), average daily gain (ADGD), age at 100 kg (AGED) and backfat thickness (BFTD); as well as breeding age (BRAGE), breeding weight (BRWT) and days from 100 kg to breeding (DAYS). The reproduction traits evaluated were: number of corpora lutea (CL), number of live embryos (EMB), the ratio of number of embryos to number of corpora lutea (E/CL) and its reciprocal (CL/E). All traits were considered to be traits of the gilt. A previous analysis of a portion of this data (Young et al., 1974) indicated that the gilt's individual record was not highly correlated with her reproductive ability. In view of these results and the rather large maternal effect on several of the traits measured, the litter averages and the gilt's deviation from the litter average were added to see if they were more reliable indicators of reproductive ability than was the gilt's individual performance.

These data were analyzed assuming a nested or hierarchial design in order to estimate components of variance for genetic correlations and heritabilities. However, in four seasons, purebred sires could have produced purebred gilts or two types of crossbred gilts. For example, a Duroc sire could have produced purebred Duroc, Duroc x Hampshire or Duroc x Yorkshire gilts. Sires within a breed were not represented by equal numbers of the various types of gilts. In an attempt to remove this bias, the following model was fit for all traits using the four seasons of data where sires produced both purebred and crossbred gilts:

$$Y_{ijkm} = u + A_i + S_j + D_{k(j)} + (AS)_{ij} + (AD)_{ik(j)} + e_{ijkm}$$

where

Y_{ijkm} = observed value of the trait for the $ijkm^{th}$ observation

u = overall mean

A_i = effect of the i^{th} season

S_j = effect of the j^{th} sire breed

$D_{k(j)}$ = effect of k^{th} breed of dam within j^{th} sire breed

$(AS)_{ij}$ and $(AD)_{ik(j)}$ are interaction terms

e_{ijkm} = random element

All effects were considered fixed except e_{ijkm}. The record of each crossbred gilt was adjusted to the mean of the purebred sire breed of gilt basis. For example, Duroc x Hampshire and Duroc x Yorkshire gilts were adjusted to purebred Duroc. Adjustments were made by using differences among appropriate least squares means for the trait when either $D_{k(j)}$ or $(AD)_{ik(j)}$ was a significant source of variation at the .10 level. There were three different $(AD)_{ik(j)}$ for each trait and there were 19 traits. Twenty-seven of the possible 57 interactions of year with breed of dam within breed of sire were significant at the .10 level. This adjustment attempts to make the expected value of the crossbred equal to its purebred half-sib as well as attempting to remove breed of dam of gilt and heterosis effects. Using the adjusted data set, estimates of heritability (h^2) and genetic (r_g) and phenotypic (r_p) correlations among the traits were obtained from a paternal half-sib analyses. The expected mean squares from the hierarchial analysis are presented in Table II.

A stepwise regression analysis was run on each reproductive trait with all traits measured before breeding being included as potential independent variables. The effects of season and breed of gilt were included as dummy variables in all models. A maximum R^2 improvement technique was used (Barr and Goodnight, 1972). This technique looks for the "best" one variable model, the "best" two variable model and so forth. It first finds the one variable model producing the highest R^2 statistic. It then adds the next variable which would yield the greatest increase in

R^2. Each of the variables in the model is compared to each variable not in the model. The procedure determines if removing the variable in the model and replacing it with the presently excluded variable would result in an increase in R^2. After all possible comparisons are made, the switch which produces the greatest increase in R^2 is made. Comparisons are made again, and the procedure continues until it finds that no switch will increase R^2. This is considered the "best" two-variable model. A third variable is added and the process continues. Only those models where the partial F statistic was significant for all effects at the .10 level are reported.

TABLE II

EXPECTED MEAN SQUARES

Source	df	EMS
Season Breed Comb.	23	
Sire/w S-B.C.	144	$\sigma^2 + 1.45\sigma^2 + 2.96\sigma^2$
Dams/w Sires	211	$\sigma^2 + 1.33\sigma^2$
Progeny/w Dam	152	σ^2

Results and Discussion

Johnson et al. (1973) and Johnson and Omtvedt (1975) have previously reported the mean performance of the population which was sampled to

provide the gilts used in this study. Young et al. (1974) have also reported the mean performance of the gilts represented in five of these eight seasons. Backfat probes were not taken on the gilts in one season. Analysis of the seven seasons when backfat data was available, indicated that backfat thickness was not correlated phenotypically with any reproductive traits ($r < .10$) over the range of BFT in this study ($x = 1.15$, S.D. = .13). So that all seasons of data could be used, BFT, LBFT, and BFTD were deleted from the rest of the analyses.

Heritabilities

The heritability estimates and their standard errors are presented in Table III. The standard errors of the heritability estimates were estimated according to procedures presented by Swieger et al. (1964).

Many of the heritability estimates, especially for NW, are higher than those generally reported in the literature. This may possibly result from the fact that preweaning data was obtained on gilts from two different stations as previously described and postweaning performance may be affected by preweaning management. Therefore, variation between sires was confounded with variation between stations since no attempt was made to adjust for station differences. This may have resulted in an overestimation of the sire component of variance. However, these estimates follow the general pattern normally found in that the h^2 for traits measured after weaning are larger than those measured while the pigs were under the influence of the maternal ability of the dam. All traits were considered traits of the gilt so that genetic correlations could be calculated using the paternal half-sib method. This makes the interpretation of the heritabilities of NB, NW, LBW, LWW, LADG, and LAGE

TABLE III

HERITABILITY ESTIMATES AND THEIR STANDARD ERRORS

Trait	h^2	S.E.
NB	-.05	.18
BW	.07	.19
LBW	.18	.19
BWD	.21	.20
NW	1.18	.21
WW	.12	.19
LWW	.27	.20
WWD	.72	.21
ADG	1.03	.21
LADG	-.71	.14
ADGD	.62	.21
AGE	.70	.21
LAGE	.39	.20
AGED	.51	.20
BRAGE	.66	.21
BRWT	.74	.21
DAYS	.93	.21
CL	.21	.20
EMB	-.39	.17
E/CL	-.22	.18
CL/E	.28	.20

difficult since they are characteristics of the litter she was a member of rather than her own characteristic.

These gilts were part of the Oklahoma crossbreeding study in which replacement females were randomly selected. If all gilts are chosen entirely at random, the expected value of BWD, WWD, ADGD and AGED is zero for each sire resulting in a zero heritability. However, the heritability estimates for these traits were all positive and those for ADGD and AGED were significant. This suggests that some sires were represented by an above average sample of daughters while other sires were represented by either a below average or at least less superior sample of daughters. However, this does not imply selection for these traits. The mean values for BWD, WWD, ADGD and AGED were .07 lb, .18 lb, -.04 lb and -.02 days, respectively. This indicates that there was very little selection for these traits.

The sire component of variance was negative for NB, LADG, EMB and E/CL and resulted in negative heritability estimates. The heritability of .21 for CL was not significant and was half as large as the realized heritability of .40 reported by Zimmerman and Cunningham (1975) when they selected for ovulation rate. CL and EMB were direct measures of reproduction. The ratios of these numbers, E/CL and CL/E, are both measures of embryo survival rate. High E/CL and low CL/E indicate high embryo survival rates. When E/CL is used as the measure of embryo survival, the sire component is negative. However, when CL/E is used, the sire component was positive. Simple inversion of the ratio changes the sign of the sire component of variance in this case. The sire components of variance for these ratios have the same sign as the sire component of variance for the trait in the numerator. Robison and Berruecos (1973), when evaluating

feed efficiency, noted differences in the sign of the sire component of variance for the ratios, feed/gain and gain/feed. The only negative components found were for gain/feed even though the corresponding estimates for feed/gain, feed and gain were positive.

Genetic Correlations

The genetic correlations among traits are reported above the diagonal in Table IV. The main interest of this paper is to investigate the relationship of pre-breeding traits with reproductive traits. Therefore, the correlations among pre-breeding traits and among reproductive traits are presented but will not be discussed in this paper.

The sire component of variance was negative for EMB, E/CL, NB and LADG and prevented the estimation of genetic correlations when these traits were involved. BW, BWD, WW, LWW, WWD, ADG, ADGD, BRWT and DAYS were positively and moderately to highly correlated with CL (r_g = .42 to .82), while AGE, LAGE and AGED were negatively and highly correlated with CL (r_g = -.73 to -1.21). In general, as the age at which the measurement was taken increased so did the correlation with CL. These results indicate that some genes with above average effects for growth also have above average effects for ovulation rate. It also appears that later measures of growth are superior to early measures of growth in predicting genetic ability for ovulation rate.

A low value for CL/E is desirable and reflects a high embryo survival rate. The correlations of BWD, LAGE, BRAGE and DAYS with CL/E were very small and had absolute values less than .10. The correlations of NW, LWW, ADG, ADGD, AGE, AGED and BRWT with CL/E were also low and had absolute values between .17 and .28. The traits which were highly correlated

TABLE [redacted]

PHENOTYPIC[a,b] AND GENETIC[c] CORRELATIONS AMONG TRAITS (X100)[d]

	NB	BW	LBW	BWD	NW	WW	LWW	WWD	ADG	LADG	ADGD	AGE	LAGE	AGED	BRAGE	BRWT	DAYS	CL	EMB	E/CL	CL/E
NB		+	+	+	+	+	+	-	+	+	+	-	-	-	-	+	-	-	-	-	+
BW	-.24		.64	-.48	.35	-1.94	-1.33	-.31	.25	-	1.14	-.39	-.93	.45	.38	.64	.47	.42	+	-	-.90
LBW	-.31	.76		-1.06	.41	-1.63	-.29	-.93	.37	-	1.15	-.40	-.72	.26	.70	.55	.78	-.23	-	-	-.44
BWD	.02	.56	-.10		-.24	.31	-.86	1.00	-.42	+	-.80	.32	.29	.18	-.70	-.39	-.72	.39	+	+	-.09
NW	.60	-.07	.01	-.12		-.28	-.15	-.04	.04	-	.09	.02	-.04	.10	.20	.01	.09	.46	-	-	.22
WW	-.14	.38	.27	.23	-.08		.37	.50	.82	+	1.34	-1.02	-.66	-1.08	-1.02	-.16	-.18	1.96	-	-	.91
LWW	-.23	.27	.39	-.08	-.12	.66		-.71	.47	-	.63	-.58	-.75	.05	-.31	-.11	.30	.41	+	-	-.20
WWD	.04	.24	-.03	.42	.02	.62	-.13		.06	+	.17	-.15	.28	-.71	-.44	-.04	-.36	.58	-	-	.72
ADG	.05	.20	.15	.11	.08	.30	.19	.19		+	.55	-.96	-1.16	-.49	.58	.80	.79	.79	+	-	.27
LADG	-.14	.08	.11	-.02	-.07	.06	.10	-.01	.24		-	-	-	-	+	+	+	+	+	+	-
ADGD	.04	.07	-.01	.09	.03	.10	-.07	.18	.55	-.10		-.94	-1.22	-.48	.70	.50	.81	.82	-	-	.20
AGE	.01	-.30	-.23	-.17	.00	-.54	-.36	-.34	-.89	-.19	-.50		.88	.87	-.47	-.67	-.75	-1.21	-	+	-.28
LAGE	.04	-.27	-.32	.00	-.04	-.42	.52	-.04	-.63	-.27	-.00	.72		.54	-.79	-.92	-1.04	-.73	-	+	.10
AGED	-.02	-.14	.01	-.24	.04	-.28	.08	-.47	-.55	.03	-.75	.60	-.08		-.14	-.32	-.31	-.97	-	+	-.28
BRAGE	.03	.10	.12	-.01	.06	-.06	.01	-.09	.09	.06	-.06	-.05	-.12	.06		.54	.92	.28	+	+	-.07
BRWT	-.03	.26	.19	.14	-.04	.29	.20	.19	.53	.20	.15	-.53	-.42	-.26	.42		.76	.49	+	+	.17
DAYS	-.00	.25	.25	.05	.05	.20	.23	.04	.49	.16	.13	-.51	-.53	-.15	.84	.60		.69	+	+	-.08
CL	.03	.09	.07	.05	.09	.14	.08	.10	.21	.08	.01	-.16	-.15	-.05	.12	.27	.18		-	-	1.83
EMB	-.03	.01	.05	-.05	.05	.10	.10	.03	.08	.05	-.08	-.04	-.07	.02	.17	.20	.16	.41		-	+
E/CL	-.05	-.04	.02	-.09	.01	.00	.06	-.06	-.02	-.01	-.07	.06	.01	.05	.08	.01	.05	-.26	.75		+
CL/E	.03	.03	-.03	.08	-.02	-.01	-.09	.07	-.00	-.01	.05	-.05	-.00	-.05	-.05	.02	-.03	.21	-.68	-.85	

[a]Phenotypic correlations below diagonal
[b]If $|r_p| < .16$ then $p < .05$
[c]Genetic correlations above diagonal
[d]Sign of the covariance

with CL/E were BW (r_g = -.90), WW (r_g = .91) and WWD (r_g = .72). This indicates that gilts which are genetically superior for birth weight are also genetically superior for embryo survival rate. In general, gilts which are genetically superior for weaning weight and postweaning growth are genetically inferior for embryo survival rate.

Squiers et al. (1952) estimated the correlations of age at breeding and weight at breeding with embryo mortality to be -.11 and -.05, respectively. Rathnasabapthy et al.(1956) reported correlations of .32 and .35 for embryo mortality with age at breeding and gain from 200 lb to the 55th day of gestation, respectively. Reddy et al. (1958) reported correlations of .16, .11, -.21 and .41 for embryo mortality with weight at 154 days, weight at breeding, rate of gain from 154 days to breeding and age at breeding, respectively. The above authors measured embryo mortality as the number of corpora lutea not represented by live embryos at slaughter.

In all but one case, the correlation of the gilt's individual value for a trait with CL or CL/E was larger than the correlation of her deviation for the trait with CL or CL/E. The correlations of litter averages with CL and CL/E were even less. Indicating the gilts own record is probably more valuable than her litter average or her deviation from litter average.

Phenotypic Correlations

The phenotypic correlations among all traits are presented below the diagonal in Table IV. Only the correlations of pre-breeding traits with reproductive traits will be discussed.

All of the phenotypic correlations of the pre-breeding traits with the reproductive traits were small and only eight out of 68 correlations,

about 12%, were significant at the .05 level. No traits measured before breeding were significantly correlated with either E/CL or CL/E. ADG, AGE, LAGE, BRWT and DAYS were significantly correlated with CL (r = .21, -.16, -.15, .27 and .18, respectively) while BRAGE, BRWT and DAYS were significantly correlated with EMB (r = .17, .20 and .16, respectively). This indicates that gilts which grow faster, are younger at 100 kg, heavier at breeding and had more days from 100 kg to breeding also tend to ovulate more eggs. Gilts which had more days from 100 kg to breeding and were older and heavier at breeding tended to have more embryos.

Rathnasabapathy et al. (1956) found that weaning weight, 154-day weight and age at breeding were positively and significantly correlated with ovulation rate (r = .33, .34 and .32, respectively) but showed no significant relationship to litter size. Squiers et al. (1952) found a correlation of .10 between growth rate and ovulation rate. Similar results have been found by Young and Omtvedt (1973). Reddy et al. (1958) reported that the correlation of ovulation rate with weight and age at breeding was .35 and .56, respectively, and the correlation of litter size with age at breeding was .41. Several workers (Stewart, 1945; Olbrycht, 1943; Korkman, 1947; and Omtvedt et al. 1965) have found a positive correlation between age at breeding and litter size.

Regression Models

The regression models for CL, EMB, E/CL and CL/E are presented in Table V. The models reported are those for which the partial F statistic was significant at the .10 level for every effect in the model.

None of the models were very successful in predicting the four measures of reproductive performance. The "best" single variable model

TABLE V

MAXIMUM R^2 REGRESSION RESULTS WITH DEPENDENT VARIABLE CL, EMB, E/CL AND CL/E

Dependent Variable	Model	R^2
CL	βo[a]	.068
CL	βo + .0246 BRWT	.140
CL	βo + .0248 BRWT + .0870 NW	.146
EMB	βo[a]	.127
EMB	βo + .0210 BRWT	.162
EMB	βo + .0224 BRWT - 2.6926 ADGD	.172
EMB	βo + .0232 BRWT - 2.4672 ADGD - .5613 BWD	.177
E/CL	βo[a]	.075
E/CL	βo - .0542 BWD	.085
E/CL	βo - .0533 BWD + .0008 BRAGE	.091
CL/E	βo[a]	.049
CL/E	βo + .1460 BWD	.057
CL/E	βo + .1384 BWD - .0136 LWW	.063

[a]Mean after fitting season and breed of gilt.

was very similar for CL and EMB. The variable included in this model was BRWT and the regression coefficients were very similar for both traits. The next and last variable picked to predict CL was NW. When it was included, the "best" two variable model accounted for approximately 15% of the variation in ovulation rate. This indicates that gilts which are heavy at breeding and are selected from litters which are large at weaning should, on the average, have higher than average ovulation rates. The "best" model to predict EMB included BRWT, ADGD and BWD and accounted for about 18% of the variation in number of embryos. Because of the negative coefficients for ADGD and BWD, these results may indicate that gilts that are below litter average for birth weight and average daily gain but are taken to heavy weights before breeding should have more embryos than the average.

BWD was chosen to be in the "best" one variable model to predict both E/CL and CL/E. The "best" two variable model for E/CL include BWD and BRAGE and accounted for approximately 9% of the variation in E/CL. While the "best" two variable model for CL/E accounted for only 6% of the variation and included BWD and LWW. Prediction of embryo survival rate (E/CL and CL/E) was not as successful as the prediction of the components of embryo survival rate (CL and EMB). It is interesting to note that the first variable chosen to predict CL and EMB was a measure of growth taken late in life (BRWT) while the first variable chosen to predict embryo survival (E/CL or CL/E) was a measure of growth taken early in life (BWD). By fitting season and breed of gilt (βo), one could account for 6.8, 12.7, 7.5 and 4.9% of the variation in CL, EMB, E/CL and CL/E, respectively.

In general, these data indicate that gilts which are genetically superior for growth are genetically superior for ovulation rate but

possibly genetically inferior for embryo survival rate. Gilts which grew faster, were heavier and older at breeding and had more days from 100 kg to breeding tended to have higher ovulation rates and more embryos. Very little of the variation in CL, EMB, E/CL or CL/E could be accounted for by regression on the traits measured before breeding.

CHAPTER IV

PRINCIPAL COMPONENTS AS MEASURES OF GROWTH AND REPRODUCTION IN GILTS

Summary

Seventeen variables measured before breeding and three measures of reproduction were taken on 339 purebred Duroc, Hampshire and Yorkshire gilts and 192 two-breed cross gilts resulting from matings among these breeds. Eight principal components accounted for 90% of the dependency structure existing among the 17 traits measured before breeding. Two principal components accounted for 97% of the dependency structure existing among the three reproductive traits.

The first principal component (PC11) from the prebreeding traits was a general measure of growth ability and accounted for 28% of the variation in the 17 measurements. The second principal component (PC12) from these measurements contrasted slow growing gilts from fast growing litters with fast growing gilts from slow growing litters and accounted for 14.5% of the total variation. The heritability for PC11 was .71 and indicates that selection for gilts with high values for PC11 (good growth characteristics) would be very successful.

The first principal component (PC21) from the reproductive traits contrasted gilts having large numbers of embryos and good embryo survival rates with gilts having few embryos and poor embryo survival. The second

principal component (PC22) contrasted gilts having high ovulation rates and poor embryo survival with gilts having low ovulation rates and good embryo survivals. PC21 and PC22 accounted for 57.2% and 39.5%, respectively, of the dependency structure existing between ovulation rate, embryo numbers and embryo survival rate.

Based on the correlations of principal components from growth traits with principal components from reproductive traits, the following conclusions can be made. If litter averages are indications of the genetic potential of a gilt selected from that litter, then gilts with a high genetic potential (good litter averages) that exhibit that potential (good individual performance) have high PC11 values and are genetically superior for ovulation rate but are genetically inferior for embryo survival rates (high PC22 values). Gilts with a good genetic potential (good litter average) that fail to meet that potential (poor individual performance) have high PC12 values and are genetically inferior for ovulation rate but genetically superior for embryo survival rate (low PC22 values).

Introduction

Multivariate techniques, other than path coefficients and multiple regression, have been used only to a very limited extent in the field of animal science. In many experiments, a large number of measurements are taken on each animal. The experimenter then calculates all possible simple correlations in an attempt to evaluate the interrelationships among the measurements.

If the researcher took ten measurements he would have 45 simple correlations. To think about all 45 correlations simultaneously is very

difficult if the aim is to generalize about the interrelationships of the ten measurements. Principal component analysis is a multivariate technique for reducing p correlated measurement variables to a smaller set of statistically independent linear combinations of the original measurements. This technique attempts to find linear compounds of the original variables which can account for the dependency structure existing among the original measurements. This technique was used by Wright (1932) and more recently by Carpenter et al. (1971) and Brown et al. (1973).

The objective of this study was to investigate the potential of principal components as a means of evaluating the interrelationship of various measures of growth and the interrelationships of three measures of reproductive ability.

Materials and Methods

This study included the records of 339 purebred Duroc, Hampshire and Yorkshire gilts and 192 two-breed cross gilts resulting from matings among the three breeds. The maintenance of these gilts was described in detail in the previous chapter. The pre-breeding traits evaluated were: the size of litter the gilt was born in (NB) and weaned in (NW); her birth weight (BW), weaning weight (WW), average daily gain (ADG) and age at 100 kg (AGE); the average of the litter from which the gilt came for birth weight (LBW), weaning weight (LWW), average daily gain (LADG) and age at 100 kg (LAGE); the deviation of the gilt's record from the litter average for birth weight (BWD), weaning weight (WWD), average daily gain (ADGD), age at 100 kg (AGED) and backfat thickness (BFTD); as well as breeding age (BRAGE), breeding weight (BRWT) and days from 100 kg to breeding (DAYS). The reproductive traits measured were: number of corpora lutea

(CL), number of embryos (EMB) and number of corpora lutea per embryo (CL/E). The phenotypic and genetic correlations among all traits were reported in the previous chapter. The phenotypic correlation matrix previously reported will serve as the input data for the principal component analysis.

For a more detailed and technical discussion of principal component analyses see Anderson (1958), Morrison (1967) and Overall and Klett (1972). Brown et al. (1973) provides a good example of the interpretation of principal components as well as a good discussion on the theory of principal components. The correlation matrix and standardized variates are normally used in the calculation of principal components when the traits measured are in different units or are largely different in magnitude. Principal component analysis is a method for reducing p correlated measurement variables to a smaller set of statistically independent linear combinations of the original measurements which have unique properties. The first principal component is that weighted combination of the several original variables which accounts for a maximum amount of the total variation represented in the complete set of original variables. The second principal component is that weighted combination of the original variables which, of all possible weighted combinations uncorrelated with the first principal component, accounts for the maximum amount of the remaining variation. The r^{th} principal component is that weighted combination uncorrelated with the first r - 1 principal components, accounts for a maximum amount of the remaining variation among the original variables (Overall and Klett, 1972).

Assume a sample is taken from a population and measurements X_1, X_2, . . ., X_p are taken on each element in the sample. The j^{th} principal

component of the complex of sample values of X_1, X_2, . . ., X_p is the linear compound

$$Y_j = a_{1j}X_1 + a_{2j}X_2 + \ldots + a_{pj}X_p$$

whose coefficients a_{ij} are the elements of the characteristic vector associated with the j^{th} largest characteristic root, λ_j, of the sample correlation matrix R. The a_{ij} are unique up to a multiple by a scalar. If they are scaled such that $a'_j a_j = 1$, the characteristic root, λ_j, is interpreted as the sample variance of Y_j. The total variance of all possible principal components derived from the matrix R is $\sum_i \lambda_i = p$ where p is the dimension of R. The relative value of the i^{th} principal component can be measured by $\frac{\lambda_i}{p}$.

The magnitude and sign of the a_{ij} for a given component determines the importance and grouping, respectively, of the i^{th} measurement (Brown et al., 1973). Within a component, measurements that are weighted by large a_{ij} are more important than those weighted with small a_{ij}. Within a component, measurements whose a_{ij}'s have the same sign are grouped together and contrasted against the group of opposite sign.

Principal components were obtained separately for the traits measured before breeding and for the reproductive traits. In this study, it was decided to calculate enough principal components to account for at least 90% of the total variation in the dependency structure of the original response variates. A value for each principal component was calculated for every gilt and was considered as a new variable. Using the paternal half-sib method, genetic and phenotypic correlations between principal components and of principal components with the original variates of the opposite group were calculated. Heritability estimates were also calculated for the principal components.

The traits measured before breeding were denoted as group 1 and the reproductive traits were denoted as group 2. The j^{th} principal component from group i will be denoted as PCij.

Results and Discussion

Principal Components for Pre-Breeding Traits

The principal components obtained for traits measured before breeding are presented in Table VI. Ignoring the near zero coefficients for NB and NW, the coefficients for all measurements in the first principal component (PC11) are fairly similar in magnitude. However, for every character, the coefficient for the gilt's individual value is slightly greater than the coefficient for the litter average which in turn is slightly greater than the coefficient for the gilt's deviation from litter average. This indicates that in this component the gilt's individual record is the most important. The first principal component was interpreted as a general measure of growth ability. Gilts with large values for PC11 were from litters which exhibited good growth at all ages while the gilt's own record was also good and even above litter average. Basically, this component contrasts slow growing gilts from slow growing litters with fast growing gilts from fast growing litters. It is somewhat surprising that this basic contrast did not account for more than 28% of the variation among the original variates. Similar values for this component do not necessarily mean similar growth patterns. For example, assume two gilts have exactly the same measurements for all traits except that the first gilt was one standard deviation above average for BW but average for ADG and the second gilt was average for BW but was .68 of a standard

TABLE VI

COEFFICIENTS OF PRINCIPAL COMPONENTS OBTAINED FROM TRAITS MEASURED BEFORE BREEDING (GROUP 1)

	PC11	PC12	PC13	PC14	PC15	PC16	PC17	PC18
NB	-.06	-.24	.36	.02	.52	-.01	.05	-.13
BW	.25	.14	-.32	.36	.14	.34	.23	-.11
LBW	.20	.32	-.18	.07	.09	.56	.11	.27
BWD	.13	-.18	-.26	.47	.12	-.19	.22	-.51
NW	-.02	-.11	.33	-.02	.58	.26	.13	.22
WW	.30	.01	-.30	-.10	.28	-.25	-.33	.23
LWW	.21	.32	-.17	-.32	.16	-.02	-.32	-.11
WWD	.18	-.31	-.24	.21	.21	-.32	-.09	.42
ADG	.37	-.16	.18	-.21	-.09	.05	.18	-.16
LADG	.11	.15	.05	-.11	-.14	-.31	.70	.40
ADGD	.19	-.41	.05	-.12	-.25	.36	-.07	-.02
AGE	-.41	.13	-.05	.22	.01	.02	-.04	.12
LAGE	-.32	-.23	-.11	.27	-.16	.14	-.12	.29
AGED	-.23	.45	.05	.00	.21	-.16	.08	-.19
BRAGE	.12	.22	.40	.45	-.14	-.04	-.25	.14
BRWT	.31	.06	.20	.17	-.10	-.17	-.02	.04
DAYS	.30	.18	.36	.25	-.10	-.04	-.17	.01
% Total Variation	28.3	14.5	12.3	9.0	8.4	6.9	6.0	4.6

deviation above average for ADG. Since all measurements are standardized, these gilts will have the same value for PC11 but will have different growth patterns.

The second principal component (PC12) contrasts the gilt's individual performance with the average performance of the litter she came from. For every character, the coefficient for the deviation of the gilt's performance from litter average has the opposite sign as the coefficient for the litter average. This component contrasts slow growing gilts from small, fast growing litters with fast growing gilts from large, slow growing litters. If one considers the litter average to be some indicator of genetic potential, then this component may contrast gilts which had good genetic background (high litter average) but had poor individual performance (possibly due to poor individual environment) with gilts from poor genetic background (low litter average) but had good individual performance (possibly due to good individual environment). This component accounted for 14.5% of the variation among the original variates.

Gilts with large values for the third principal component (PC13) came from large litters where the pigs had low birth weights and low weaning weights with the gilt's own record being below litter average for these traits; however, the litter grew well in the feedlot and the gilt was above litter average for growth and age at 100 kg and was heavier and older at breeding. This component contrasts gilts which came from large litters and got off to a poor start due to competition in the large litter but grew well in the feedlot with gilts which came from small litters and got off to a good start but their performance fell off in the feedlot.

The fourth principal component (PC14) gave very little weight to NB or NW and accounted for only 9.0% of the variation among the original

variates. Gilts with large values for this component came from litters with high average birth weights with the gilt's birth weight being above litter average, but as time passes the litter's performance deteriorates to below average and the gilt's performance deteriorates even faster so that she is below litter average for average daily gain, has more days from 100 kg to breeding and is older and heavier at breeding.

The fifth principal component (PC15) gives considerable weight to NB and NW and accounts for 8.4% of the total variation. Gilts with high values for PC15 came from large litters at birth and weaning where the pigs had large birth weights and weaning weights but poor average daily gains with the gilt being above litter average for birth and weaning weights and below litter average for average daily gain and also young and light in weight at breeding. This component contrasts gilts which are from large litters and get off to a good start but slow down in the feedlot with gilts from small litters that get off to a poor start but do well in the feed lot.

Similar interpretations can be developed for PC16, PC17 and PC18. Because they account for so little of the total variation and in order to conserve space, this will be left to the reader.

Principal Components for Reproductive Traits

The principal components derived for the three reproductive traits are presented in Table VII. Two of the three possible principal components accounted for almost 97% of the dependency structure existing among these three variables.

The first principal component for this group (PC21) explained 57% of the total variation. This component gives relatively little weight to

TABLE VII

COEFFICIENTS OF PRINCIPAL COMPONENTS OBTAINED FROM REPRODUCTIVE TRAITS (GROUP 2)

	PC21	PC22
CL	.23	.87
EMB	.74	.14
CL/E	-.64	.48
% Total Variation	57.2	39.5

ovulation rate and, in general, it contrasts gilts having large numbers of embryos and good embryo survival rates with gilts having few embryos and poor embryo survival rates. The second principal component (PC22) gives relatively little weight to embryo numbers and contrasts gilts having high ovulation rates and poor embryo survival rates with gilts having low ovulation rates but good embryo survival rates. Embryo survival was measured as number of corpora lutea per embryo and low values for this trait indicate good embryo survival. These two basic contrasts explain most of the dependency structure existing between ovulation rate, number of embryos and embryo survival rate.

Heritability Estimates

The heritability estimates and standard errors for all principal components are presented in Table VIII. The sire component of variance was negative for PC17 and PC21 resulting in negative estimates of

heritability for these components. The heritability estimates for PC12, PC14 and PC18 were not large or significant when compared to their standard errors. PC11, PC13 and PC16 had heritabilities that were greater than .70 and significant. The component which would seem to describe the most desirable gilt from a growth standpoint would be PC11. Thus, the high heritability found for this component, indicates that selection for gilts with good performance at all stages would be very successful. The heritabilities of PC15 and PC22 were around .50 and significant.

TABLE VIII

HERITABILITY ESTIMATES AND STANDARD ERRORS FOR ALL PRINCIPAL COMPONENTS

Trait	h^2	S.E.
PC11	.71	.21
PC12	.28	.20
PC13	.73	.21
PC14	.31	.20
PC15	.55	.20
PC16	.74	.21
PC17	-.24	.17
PC18	.03	.19
PC21	-.28	.17
PC22	.50	.20

Genetic and Phenotypic Correlations

The phenotypic (r_p) and genetic (r_g) correlations of variables in group 1 with principal components from group 2 are reported in Table IX. The sire component of variance was negative for PC21 thus preventing the estimation of the genetic correlations for this trait. Genetic correlations of WW, AGE and AGED with PC22 were large ($|r_g| > .60$). Genetically, PC22 was moderately correlated with WWD, ADG, ADGD ($r_g \approx .50$) and lowly correlated with LBW, BWD, NW, LWW, BRAGE, BRWT and DAYS. This suggests that selection of gilts with genetic ability for good growth, especially for good growth rate in the feedlot, will result in gilts with genetic ability for high ovulation rate but poor embryo survival rate. The phenotypic correlations of variables in group 1 with principal components from group 2 were very small. Only one of the 34 phenotypic correlations, about 3%, was significant. This indicates that none of the variables measured before breeding would be very helpful in selecting replacement gilts with reproductive patterns described by PC21 or PC22. The absence of any large phenotypic correlations even though several of the genetic correlations are large implies a rather large negative environmental correlation for many of the individual growth traits with PC21 and PC22 especially when the heritabilities of both traits are large. This may indicate that replacement gilts should be genetically superior for growth but should be developed slower than are slaughter pigs.

The phenotypic and genetic correlations of variables in group 2 with principal components from group 1 are presented in Table X. Genetic correlations for EMB could not be calculated because of the negative sire component of variance found for this trait. Genetic correlations for

TABLE IX

PHENOTYPIC (r_p) AND GENETIC (r_g) CORRELATIONS OF VARIABLES IN GROUP 1 WITH PRINCIPAL COMPONENTS OF GROUP 2[a]

	PC21		PC22	
	r_g	r_p	r_g	r_p
NB	-[b]	-.03	+	.04
BW	+	.00	-.06	.09
LBW	-	.05	.32	.05
BWD	+	-.06	.22	.07
NW	-	.05	.30	.07
WW	-	.08	1.29	.11
LWW	+	.11	.15	.03
WWD	-	-.01	.51	.11
ADG	+	.07	.51	.12
LADG	+	.04	+	.06
ADGD	+	-.07	.49	.02
AGE	-	-.03	-.73	-.15
LAGE	-	-.06	-.35	-.13
AGED	-	.03	-.61	-.06
BRAGE	+	.14	.16	.09
BRWT	+	.14	.35	.25
DAYS	+	.14	.37	.14

[a] if $|r_p| > .16$ then $P < .05$
[b] sign of the covariance

TABLE X

PHENOTYPIC (r_p) AND GENETIC (r_g) CORRELATIONS OF VARIABLES IN GROUP 2 WITH PRINCIPAL COMPONENTS OF GROUP 1

	CL		EMB		CL/E	
	r_g	r_p	r_g	r_p	r_g	r_p
PC11	1.05	.21	+[a]	.11	.18	.02
PC12	-.86	.03	+	.12	-.81	-.09
PC13	.37	.09	+	.11	.07	-.04
PC14	-.28	.08	+	.07	-.27	.03
PC15	.06	.06	-	.01	.29	.01
PC16	-.18	-.07	-	-.09	-.32	-.01
PC17	-[a]	-.01	+	-.10	-	.07
PC18	1.50	.04	-	.10	2.02	-.05

[a]sign of the covariance

PC18 were considerably greater than one and reflect the very small sire component of variance found for that trait. PC11 was highly and favorably correlated, genetically, with CL (r_g = 1.05) but not CL/E (r_g = .18). The genetic correlations of PC12 with CL and CL/E were -.86 and -.81, respectively. Gilts with high values for PC11 exhibited good performance at all stages of growth while gilts with high values for PC12 were poor performing gilts from good performing litters. Litter averages should be some indication of genetic potential for a gilt selected from that litter. The results seem to suggest that gilts which have the genetic potential for good growth (high litter average) and exhibit this potential (good individual performance) are genetically superior for PC11 and are also genetically superior for ovulation rate. While gilts which have the genetic potential for good growth (high litter average) but fail to meet that potential (poor individual performance) are genetically superior for PC12 and embryo survival rate but are genetically inferior for ovulation rate. All phenotypic correlations of variables in group two with principal components from group one were very small and only the correlation of .21 between PC11 and CL was significant. Again, the abscence of any large phenotypic correlations even though the genetic correlations of CL with PC11 and PC12 and of CL/E with PC12 were large implies some corresponding large negative environmental correlations.

The phenotypic and genetic correlations of principal components from group one with principal components from group two are presented in Table XI. Again, genetic correlations for PC21 could not be calculated due to the negative sire component of variance found for this trait. The genetic correlations of PC11 and PC12 with PC22 were .62 and -.69, respectively. Large values of PC22 denoted gilts with high ovulation rates

TABLE XI

PHENOTYPIC (r_p) AND GENETIC (r_g) CORRELATIONS OF PRINCIPAL COMPONENTS OF GROUP 1 WITH PRINCIPAL COMPONENTS OF GROUP 2

	PC21		PC22	
	r_g	r_p	r_g	r_p
PC11	+[a]	.09	.62	.19
PC12	+	.11	-.69	.00
PC13	+	.10	.24	.07
PC14	+	.03	-.19	.09
PC15	-	.01	.08	.05
PC16	+	-.06	-.22	-.07
PC17	+	.09	-	.01
PC18	-	.08	1.32	.02

[a]sign of the covariance

and poor embryo survival rates. Assuming that a high litter average indicates a high genetic potential, these data indicate that a gilt with a high genetic potential which exhibits that potential (high PC11 values) will be genetically superior for ovulation rate and genetically inferior for embryo survival rate (high PC22). While gilts with a high genetic potential that fail to meet that potential (high PC12) are genetically inferior for ovulation rates and genetically superior for embryo survival rates (low PC22). All phenotypic correlations of principal components in group 1 with principal components in group 2 were very small and were not significant.

In general, these data indicate that there are some fairly large genetic correlations between growth measures and reproductive measures. However, the phenotypic correlations between growth and reproduction are small due to large negative environmental correlations. This suggests that replacement gilts should be genetically superior for growth but they should be grown out more slowly than slaughter pigs are grown out.

CHAPTER V

CANONICAL CORRELATION ANALYSIS AS A METHOD FOR EVALUATING THE DEPENDENCY EXISTING BETWEEN PRE-BREEDING TRAITS AND REPRODUCTIVE TRAITS

Summary

Seventeen variables measured before breeding and three measures of reproduction were taken on 339 purebred Duroc, Hampshire and Yorkshire gilts and 192 two-breed cross gilts resulting from matings among the three breeds. The purpose of this paper was to investigate the potential of canonical correlation analysis as a means of explaining the dependency structure existing between traits measured on gilts before breeding and their reproductive performance. In this analysis, possibly because of the low correlations of pre-breeding traits with reproductive traits, the results were hard to interpret because of biological contradictions. However, this paper does provide an example of the use and interpretation of a canonical correlation analysis.

The canonical correlation between the first pair of canonical variates was .38, between the second pair it was .32 and between the third pair it was .18. The major link between these two groups of variates was that gilts which are light at birth but grow fast after weaning also have high ovulation rates and good embryo survival rates. If certain assumptions are made the second pair of variates imply that the next most

important link was that gilts with good preweaning growth and poor postweaning growth have many embryos despite poor embryo survival rates. The last pair of variates indicate that gilts with good preweaning growth that are younger at 100 kg tend to have high ovulation rates, low numbers of embryos and poor embryo survival rates.

Introduction

Very frequently an experimenter will have several measurements on an experimental unit which fall into two distinct categories. For example, one group may be several measurements of growth ability and the other group may be several measurements of reproductive ability. When the experimenter wanted to investigate the relationship of variables in the first group with variables in the second group, two statistical procedures were normally used: 1) calculation of simple correlations of variables in group one with variables in group two or 2) one group of variables were considered as independent variables and the other group was considered as dependent variables and then multiple regression equations and multiple correlation coefficients were obtained. The first procedure calculates the correlation between two individual variables while the second calculates the correlation between a variable of one group and a linear combination of variables from another group.

The next step is the use of canonical correlation analysis which calculates the correlation of a linear combination of variables in group one with a linear combination of variables in group two subject to certain restrictions. This technique provides a method of explaining the dependency existing between two distinct groups of measurements by generating a smaller number of artificial variables. It attempts to find

the factors which generated the dependency structure existing between the two groups.

The purpose of this paper is to investigate the potential of the canonical correlation analysis as a means of explaining the dependency structure existing between traits measured on gilts before breeding and their reproductive performance measured 30 days after breeding.

Materials and Methods

The data utilized in these analyses consisted of various growth and reproductive measurements taken on 339 purebred Duroc, Hampshire and Yorkshire gilts. The description of the gilts used in this analysis has been described in detail in Chapter III. The pre-breeding traits measured were: the size of litter the gilt was born in (NB) and weaned in (NW); the gilt's own birth weight (BW), weaning weight (WW), average daily gain (ADG) and age at 100 kg (AGE); the average of the litter the gilt came from for birth weight (LBW), weaning weight (LWW), average daily gain (LADG) and age at 100 kg (LAGE); the deviation of the gilt's own record from the litter average for birth weight (BWD), weaning weight (WWD), average daily gain (ADGD) and age at 100 kg (AGED); as well as breeding age (BRAGE), breeding weight (BRWT) and days from 100 kg to breeding (DAYS). The phenotypic and genetic correlations among these traits have been reported in Chapter III and a principal component analysis on the phenotypic correlation matrix has been presented in Chapter IV. The phenotypic correlation matrix from Chapter III will serve as the input data for this analysis.

One method of evaluating the interrelationship existing between variables of two distinct groups is by the use of canonical correlation

analysis. This process develops two sets of linear combinations of the original variables. One set is derived for the p-variates in group one (call it $U_i = a'_i X_p$) and one set is derived for the q-variates of group two (call it $V_i = b'_i X_q$) subject to the following restrictions:

1. U_i and U_j are uncorrelated for $i \neq j$.
2. V_i and V_j are uncorrelated for $i \neq j$.
3. U_i and V_j are uncorrelated for $i \neq j$.
4. U_1 and V_1 are the pair of linear compounds of X_p and X_q, respectively, which have the highest possible correlation.
5. U_2 and V_2 are the pair of linear compounds of X_p and X_q, respectively, with the next highest possible correlation subject to restrictions 1, 2 and 3.
6. Etc.

In order to derive the canonical variates (U_i and V_i), one must use either the correlation matrix or the covariance matrix for all variates. The correlation matrix and standardized variates are normally used when the units of measurement are quite different for different traits.

To derive the canonical variates, one must first construct the symmetric correlation matrix, R, of order p + q and subdivide it as follows:

$$R = \left[\begin{array}{c|c} R_{11} & R_{12} \\ \hline R_{21} & R_{22} \end{array}\right]$$

where R_{11} contains the correlations among the elements of the p-variates and R_{22} contains the correlations among the q-variates. The correlations of the p-variates with the q-variates are contained in R_{12} and $R_{12} = R'_{21}$. The characteristic roots, λ_i, of the matrix

$$\left[R^{-1}_{11} R_{12} R^{-1}_{22} R_{21}\right]$$

are the squares of the canonical correlations. The coefficient vectors, a_i and b_i, corresponding to each λ_i are obtained as solutions to the following:

$$\left[R_{12}\, R^{-1}_{22}\, R_{21} - \lambda_i\, R_{11}\right]\, a_i = 0$$
$$\left[R_{21}\, R^{-1}_{11}\, R_{22} - \lambda_i\, R_{22}\right]\, b_i = 0$$

For a more detailed discussion of canonical correlation analysis see Morrison (1967) and Anderson (1958).

The interpretation of canonical variates is similar to the interpretation of principal components. The magnitude and sign of the coefficients, a_{ij}, within a canonical variate U_i determines the importance and grouping, respectively, of the j^{th} measurement. Measurements with large coefficients are more important than those with small coefficients. Measurements with negative coefficients are contrasted against those with positive coefficients. Similar interpretations apply to the coefficients, b_{ij}, within a canonical variate, V_i. In this analysis, the coefficients within a canonical variate were scaled such that the largest coefficient was unity.

A value for each canonical variate was obtained for each animal and was considered a new trait. The canonical variates were analyzed using the paternal half-sib method to provide heritability estimates (h^2), and genetic (r_g) and phenotypic (r_p) correlations with the original variables and the canonical variates from the opposite group. Standard errors of heritability estimates were estimated according to procedures outlined by Swieger et al. (1964).

The following notation will be used: U_i and V_i will denote the i^{th} canonical variate derived from group one (pre-breeding traits) and group two (reproductive traits), respectively. The canonical variate pairs are

ordered, according to the size of the corresponding canonical correlation, from highest to lowest.

Results and Discussion

Canonical Variates

The canonical variates derived from the correlation matrix are presented in Table XII. The first canonical variate derived from the pre-breeding traits gave relatively little weight to NB, NW, LWW, WWD, LADG, LAGE, AGED, BRAGE, or DAYS. Considerable positive weight was given to ADG and AGE and moderate positive weight was given to LBW, BWD and WW and moderate negative weight was given to BW. Gilts with high values for U_1 had low birth weights, above average weaning weights and high average daily gains but were still older at 100 kg. It seems that gilts with high values for U_1 are slow starters but do exceptionally well in the feedlot but due to the rather slow start they are also older at 100 kilogram. The first canonical variate (V_1) derived from the reproductive traits gave relatively little weight to EMB but high positive weight to CL and moderate negative weight to CL/E. If one ignores the relatively small weight given to EMB, then a gilt with a high value for V_1 has a high ovulation rate and good embryo survival rate. Low values of CL/E indicate good embryo survival rates. Thus, the major link between the pre-breeding traits and the reproductive traits seems to be that gilts which are slow starters but exhibit good postweaning growth but are still older at 100 kg also have high ovulation rates and good embryo survival rates. The canonical correlation between U_1 and V_1 was .38.

TABLE XII

COEFFICIENTS FOR CANONICAL VARIATES

Trait	U_1	U_2	U_3
NB	-.03	-.14	.16
BW	-.33	.52	-1.00
LBW	.29	-.54	.94
BWD	.21	-.43	.86
NW	.13	.10	-.05
WW	.40	.04	.42
LWW	-.01	-.21	-.58
WWD	-.09	.03	-.31
ADG	.99	-.76	-.14
LADG	-.03	.00	.04
ADGD	-.22	-.07	.22
AGE	1.00	-1.00	-.53
LAGE	-.07	.21	.08
AGED	-.16	.23	.34
BRAGE	.04	.28	-.10
BRWT	.20	.41	.13
DAYS	.03	-.23	-.13
	V_1	V_2	V_3
CL	1.00	-.47	.96
EMB	-.27	1.00	-1.00
CL/E	-.66	.91	.51
Correlation Coefficient	.38	.32	.18

The second pair of canonical variates illustrate some of the problems of canonical correlation analysis in that some of the variates may be very difficult to interpret. The coefficients of BW, LBW and BWD in U_2 describe a gilt with a high individual birth weight from a litter with a low average birth weight and the gilt's record was below litter average. This appears to be a biological impossibility. Similar problems arise in the second canonical correlation (V_2) derived from the reproductive traits. If all coefficients are considered, gilts with high values for V_2 have low ovulation rates, high embryo numbers but low embryo survival rates. Again, this appears to be biologically impossible. However, if one arbitrarily ignores the somewhat smaller coefficient for CL and the coefficients for LBW and BWD, a plausible interpretation can be developed for U_2 and V_2 in order to illustrate the use of canonical variates. If this is done, then U_2 gives moderate positive weight to birth weight and breeding weight and large negative emphasis to average daily gain and age at 100 kilograms. Thus, U_2 describes a gilt which starts off growing well before weaning but tapers off in the feedlot with low average daily gains but manages to be young at 100 kg and heavy at breeding. If the coefficient for CL is ignored, gilts with high values for V_2 have high embryo numbers despite poor embryo survival rates. If this were true, the gilts would have had to have high ovulation rates which contradicts the negative coefficient for CL. Thus, the second major link between these two groups seems to be that gilts with good preweaning growth but poor postweaning growth also have more embryos despite poor embryo survival rates. The correlation between U_2 and V_2 was .32.

The correlation between the third pair of canonical variates was .18. Again some contradictions seem to be present. The coefficients for

BW, LBW and BWD describe a gilt with a poor individual birth weight from a litter with high average birth weights and the gilt's own record was above litter average. The coefficients for WW, LWW and WWD describe a gilt with a high individual weaning weight from a litter with low average weaning weights and the gilt's own record is below litter average. Both of the situations seem impossible. In order to further illustrate the use of canonical variates, the coefficients for LBW, BWD, LWW and WWD will be ignored. If this is done, gilts with high values for U_3 have very low birth weights and above average weaning weights (indicating good preweaning growth) and somewhat younger ages at 100 kilograms. Gilts with high values for V_3 have high ovulation rates, low embryo numbers and poor embryo survival rates. Thus, the third link between these two groups seems to be that gilts with good preweaning growth and are younger at 100 kg tend to have high ovulation rates, low embryo numbers and poor embryo survival.

These results indicate some of the problems and limitations of the canonical correlation analysis. This is an investigative procedure and may produce results which are difficult to interpret. The difficulties found in this analysis probably result from the very low correlations ($r < .20$ in most cases) found between pre-breeding traits and the reproductive traits.

Heritabilities and Genetic Correlations Among Canonical Variates

The genetic correlations among canonical variates are presented in Table XIII. By derivation all phenotypic correlations among canonical variates with different subscripts are zero. However, this does not necessarily apply to genetic correlations. The sire component of variance

was negative for V_1 thus preventing the estimate of genetic correlations for that trait. The covariance of U_1 with V_1 was negative. The sire component of variance for U_3 was very small, resulting in genetic correlations greater than one when this trait was involved. The phenotypic correlation between U_2 and V_2 was .32 and the genetic correlation was .42. Several of the genetic correlations among principal components with different subscripts were moderate in size.

TABLE XIII

GENETIC CORRELATIONS BETWEEN CANONICAL VARIATES

	U_2	U_3	V_1	V_2	V_3
U_1	-.26	1.52	-[a]	.41	.21
U_2		-1.64	+	.42	.48
U_3			+	-.76	3.28
V_1				-	+
V_2					1.18

[a]sign of the covariance

The heritabilities of the canonical variates are presented in Table XIV. The only heritability esitmates that were large or significant were for U_1 (h^2 = .94) and V_2 (h^2 = .72) indicating that selection for gilts described by these two canonical variates should be very effective. The

heritability estimate for V_1 was negative due to the negative sire component of variance for that trait.

TABLE XIV

HERITABILITIES ESTIMATES AND ESTIMATED STANDARD ERRORS FOR ALL CANONICAL VARIATES

	h^2	S.E.
U_1	.94	.21
U_2	.13	.19
U_3	.04	.19
V_1	-.13	.18
V_2	.72	.21
V_3	.20	.19

Phenotypic (r_p) and Genetic (r_g) Correlations of Variables in Group One With Canonical Variates of Group Two

The phenotypic and genetic correlations of variables in group one with canonical variates from group two are presented in Table XV. Because of a negative sire component of variance, genetic correlations for NB, LADG and V_1 could not be calculated. The genetic correlation of BW and LBW with V_2 were -.76 and -.94. This indicates that selection for low birth weights would produce a high positive correlated response for V_2. WW and WWD were very highly and positively correlated with V_3 (r_g = 1.88 and

TABLE XV

PHENOTYPIC (r_p) AND GENETIC (r_g) CORRELATIONS OF VARIABLES IN GROUP 1 WITH CANONICAL VARIATES OF GROUP 2

	V_1		V_2		V_3	
	r_g	r_p	r_g	r_p	r_g	r_p
NB	-[a]	.02	-	-.03	-	.05
BW	+	.07	-.76	.01	-.44	.06
LBW	+	.08	-.95	-.01	.02	.00
BWD	+	.01	.44	.02	-.27	.09
NW	+	.10	-.03	-.02	.43	.01
WW	+	.13	-.26	.05	1.88	.02
LWW	+	.13	-.26	-.04	.06	-.05
WWD	+	.04	.05	.10	1.01	.07
ADG	+	.14	.08	.01	.53	.04
LADG	+	.08	+	.01	-	.02
ADGD	+	-.01	-.17	-.06	.62	.07
AGE	-	-.13	.02	-.03	-.74	-.09
LAGE	-	-.14	.25	-.02	-.27	-.04
AGED	-	-.03	-.09	.00	-.59	-.06
BRAGE	+	.13	.32	.11	-.19	-.05
BRWT	+	.23	.43	.18	.09	.05
DAYS	+	.17	.10	.09	.06	-.01

[a]sign of the covariance

1.01, respectively). The correlations of V_3 with ADG, ADGD, AGE and AGED were .53, .62, -.74 and -.59. These results indicate that selection based on late measurements of growth (average daily gain or age at 100 kg) should result in a correlated change in V_3. None of the phenotypic correlations of variables in group one with canonical variates in group two were large. Only the correlations of BRWT with V_1 and V_2 (r_p = .23 and .18, respectively) and DAYS with V_1 (r_p = .17) were significant.

Phenotypic and Genetic Correlations of Variates in Group Two With Canonical Variates of Group One

The phenotypic and genetic correlations of variates in group two with canonical variates of group one are presented in Table XVI. Because of a negative sire component of variance, genetic correlations could not be calculated for EMB. The genetic correlations of CL with U_2 and U_3 and CL/E with U_3 were considerably greater than unity and are therefore highly subject to doubt. The genetic correlation of U_1 with CL/E was .37. All other genetic correlations were small.

U_1 was significantly and positively correlated with CL (r_p = .41) and EMB (r_p = .25) but not CL/E (r_p = -.13). This indicates that if a producer selects replacement gilts with high U_1, they should also have a high ovulation rate and, to a smaller extent, more embryos. The only other phenotypic correlation which was significant was .23 between CL and U_2.

TABLE XVI

PHENOTYPIC (r_p) AND GENETIC (r_g) CORRELATIONS OF VARIABLES IN GROUP 2 WITH CANONICAL VARIATES OF GROUP 1

	CL		EMB		CL/E	
	r_g	r_p	r_g	r_p	r_g	r_p
U_1	.08	.41	+	.25	.37	-.13
U_2	1.75	.23	+	.12	.15	.08
U_3	2.84	.05	-	-.07	2.40	.09

CHAPTER VI

SUMMARY

The purpose of this paper was to evaluate the dependency structure existing between a gilt's pre-breeding traits and her reproductive traits. Four procedures were used: simple correlation analysis, multiple regression analysis, principal component analysis and canonical correlation analysis.

The simple correlation analysis was useful in determining relationships between a single pre-breeding trait and a single reproductive trait. None of the phenotypic relationships were strong but there was considerable evidence for some rather strong genetic relationships. Because of the low phenotypic relationships, no single pre-breeding trait was very useful in selecting replacement gilts with superior reproduction. Although some of the genetic relationships were rather large, it was difficult to look at such a large number of correlations and develop any general relationships between pre-breeding traits and reproductive traits. This was especially difficult because of the correlations among traits within a group.

The multiple regression technique was not very successful in using the pre-breeding traits to predict the individual reproductive traits when measured by R^2 values. However, when the multiple correlation coefficients were calculated, they were somewhat larger than the simple correlations. The multiple regression technique was somewhat superior to

the simple correlations but still failed to discover the basic factors generating the dependency structure.

The principal component analysis was very useful in determining basic relationships within pre-breeding traits and within reproductive traits. However, none of the phenotypic correlations between principal components of different groups were large. Only genetic correlations of the first (PC11) and second PC12) principal component from pre-breeding traits with the second principal component (PC22) from the reproductive traits were large. None of the phenotypic correlations of principal components from pre-breeding traits with individual reproductive traits were large. PC11 and PC12 were highly correlated genetically with CL and the genetic correlation of PC12 with CL/E was high. These results imply that the principal component analysis was not effective in elucidating the general phenotypic relationships between pre-breeding traits and reproductive traits but was of some limited value in finding general genetic relationships.

The canonical correlation analysis was fairly effective in finding some general phenotypic relationships which existed between pre-breeding traits and reproductive traits. However, the genetic correlations between the canonical variates with the same subscript were less than .50 and not as large as would have been desired. In this analysis, the major criticism of the canonical correlation procedure was that it produced results which were difficult to interpret because they suggested situations which were biologically impossible. This may have resulted from the very small phenotypic correlations found between pre-breeding traits and reproductive traits.

This author feels that the principal component analysis and canonical correlation analysis are very valuable multivariate techniques that should see more extensive use in the field of animal science. These techniques are very useful in elucidating the unmeasurable factors which generate the dependency structure existing among many variates.

In general, these data indicate that gilts that grow fast and are heavy at all ages tend to have higher than average ovulation rates. However, gilts with high postweaning average daily gains tend to have poor embryo survival. This may suggest new management practices for replacement gilts. It may be advantageous for a commercial producer to select replacement gilts which are heavy at birth and weaning and are from large litters. Rather than full feeding, it may be better to reduce growth rate by limiting feed intake from weaning to breeding but take them to normal breeding weights. Other evidence for this system has been presented by Aherne (1975). Gilts fed ad lib from 45 kg to breeding farrowed 1.2 pigs less and weaned 1.0 pigs less than gilts which were fed at a level of 85 percent of the ad lib intake over the same period.

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