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IN A SWINE HERD.

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Evaluation of selection practices
used in a swine herd

by

Larry Francis Vint

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Signature was redacted for privacy.

In Charge of Major Work

Signature was redacted for privacy.

Head of Major Department

Signature was redacted for privacy.

Dean of Graduate College

Iowa State University
Of Science and Technology
Ames, Iowa

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INTRODUCTION

The end of World War II marked the beginning of an unparalleled period of American economic growth. Increasing industrial growth and mechanization, urbanization, growing income levels, a spreading communication system and an expanding transportation industry were all factors in the increasing affluence and growing demand for consumables by the American public.

Changing consumer attitudes and appetites for meat products are a natural effect of growing prosperity. Demand for more meat, more of the prestige cuts, better quality meat and more convenience services have closely followed increases in per capita personal income. United States Department of Agriculture (1969) figures are presented in Table 1.

Table 1. Per capita income and meat consumption

Year	Per capita personal income (dollars)	Beef	Veal	Lamb & mutton	Pork	Poultry	Total meat & poultry
1940	760	54.9	7.4	6.6	73.5	17.0	159.4
1950	1,737	63.4	8.0	4.0	69.2	25.0	169.6
1960	2,448	85.0	6.1	4.8	64.9	34.1	194.9
1969	3,511 ^a	109.6	3.2	3.4	64.6	47.0	227.8

^a1967 figure.

Beef roasts and steaks are prestige products in the eyes of the American public. Ground beef has become widely accepted as a versatile convenience food. Consumer partiality and growing affluence have doubled per capita beef consumption in the past thirty years.

A dramatic increase in per capita consumption of poultry meat has been largely due to a modernized and highly efficient broiler industry. A consistent supply of high quality, inexpensive chicken has created a market for poultry meat.

In contrast to trends in total meat consumption, per capita pork consumption has decreased during the past 30 years. Traditionally pork has not been a highly prestigious product, providing the basis for weekday meals rather than Sunday or "company" dinners. Pork has developed an image as the "fat" meat. Increasing consumer sensitivity toward obesity and concern over the role of saturated animal fats and cholesterol in human health problems forced a metamorphosis in the swine industry. Consumer demands for more shopping convenience gave rise to self-service packaging of retail meat. Shopper selectivity forced retailers into new standards of trimming retail cuts which lead to a demand for more closely trimmed wholesale cuts. A differential pricing system for market hogs based on carcass cutability was forced upon the swine industry by consumer demands for lean, convenient-to-use pork products.

The economic incentive for producing leaner hogs created a need for methods to identify animals with genetically superior carcass merit. Development of the backfat probe by Hazel and Kline (1952) gave swine producers a simple, yet accurate method of estimating the backfat thickness of live hogs. Central boar testing stations were set up throughout the major swine producing areas during the mid-1950's. Collection of detailed performance and family carcass data under the standardized environmental conditions of the test stations gave commercial producers a genetic basis for comparing sources of breeding stock.

Early indications of rapid improvement in carcass traits measured at the Iowa Swine Testing Stations were encouraging. However, there was little information available from planned research experiments on how rapidly carcass merit could actually be increased by selection. In response to this need Iowa State University personnel undertook a study to measure rate of genetic improvement in meatiness resulting from individual, family and progeny selection within purebred seedstocks.

In 1962 a program of selection aimed at maximizing the rate of genetic improvement in meatiness was initiated in the Iowa State University swine breeding experimental herd at Napier. The selection program called for primary selection on minimum backfat probe as boars reached 200 pounds.

Additional selection was to be based on carcass records of at least two full sibs. Progeny test information was to provide the basis for final selection of boars to be retained in the breeding herd.

Three or four young boars were to be selected for use within each breed every season. These boars were also used a second season while data were being collected and processed on their progeny born in the first season. The best of the progeny tested boars were to be retained for breeding until superior progeny tested boars were available or until physical disability forced removal from the breeding herd.

Data on all purebred Duroc, Hampshire, Poland China and Yorkshire litters farrowed in an 8-year period from 1962 through 1969 are included in this study. Litter size at weaning, 56-day weight, 154-day weight, backfat probe, carcass backfat, loin eye area, and ham and loin percentage are among the traits being studied.

The purpose of this study is to evaluate the effectiveness of the selection program. The criteria, intensity and effectiveness of selection actually practiced will be investigated. Estimates of actual genetic gain will be compared with theoretical expectations.

REVIEW OF LITERATURE

The genetic composition of animal populations is a dynamic system modulated by the forces of mutation, migration, chance and selection. Mutation and migration are initiating forces, supplying new genetic material upon which the potentiality for genetic change is based. Chance is a moderating force, acting as a buffer against impetuous genetic change that could prove disastrous to the evolutionary development of a population. Selection is the guiding force which directs the path that genetic change shall follow.

Lush (1954) notes that the rate at which selection can change the genetic constitution of a population is dependent upon four factors; the intensity of selection, i , the amount of additive genetic variability in the population, i.e., σ_A , the accuracy with which selection is made, r_{XA} , and the time interval between successive generations, \bar{T} . The expected annual rate of genetic change, ΔG , is a function of these four factors.

$$\Delta G = i \sigma_A r_{XA} / \bar{T}$$

The amount of selection applied is commonly expressed in terms of the selection differential or the difference between the mean of the selected group, \bar{X}_s , and the mean of the population from which they were selected, \bar{X} . The standardized selection differential, $(\bar{X}_s - \bar{X})/\sigma_x$, is referred to as selection intensity and symbolized by i . When, X , the trait

under selection is normally distributed and truncation selection is practical on X , i can be expressed in terms of the proportion saved, p , and z , the height of the ordinate of the normal curve at the point of truncation.

$$i = z/p = (\bar{X}_s - \bar{X})/\sigma_x$$

Intensity of selection tables are presented in most animal breeding texts or they can be found in Fisher and Yates (1943). Smith (1969) states that i can be accurately estimated by the following formula: $i \approx 0.8 + 0.94 \log [(1/p) - 1]$.

Economic return from animals is almost always affected by several traits. Hazel and Lush (1942) have shown that selection based on an index of net merit is the most efficient method of changing the aggregate genotypic value of a population. They reported that the progress made in any one trait when selection is based on an index of n independent traits is only $1/\sqrt{n}$ times as much as if selection had been based on that trait alone. Therefore, the number of traits under selection will restrict the intensity of selection that could have been applied to each trait individually.

Factors influencing selection intensity in pig breeding operations have been discussed by Fredeen and Martin (1967). Since the relative superiority of selected individuals is limited by the proportion of the population required as parents, factors which either increase the size of the population upon which selection is based or reduce the pro-

portion of the population needed as replacements will intensify selection pressure. These authors suggested increasing the number of sows bred per boar, implementing management practices which would enhance litter production and removing closed herd restrictions as methods for augmenting selection opportunity. They cautioned that early castration of boars, failure to evaluate all pigs and slaughtering of litter samples for carcass information would restrict the size of the population upon which selection could be based.

Since relatively few boars are needed as replacements each generation and market discrimination against intact boars makes their commercial production uneconomical, it is a common practice to castrate the poorest male pigs at or before weaning. Dickerson and Hazel (1944b) concluded that little effectiveness in selection for growth rate is lost when up to $2/3$ of the boars were culled at 56 days, as long as 8 to 10 times the number finally needed were kept to 180 days. They found that at least $2/3$ of the gilts or 3 times the number needed should be retained until 180-day weights could be obtained.

Retention of the best sows in the breeding herd will allow for increased selection pressure on gilts and should increase population size because of the larger litters older sows have. Dickerson and Hazel (1944b) estimated that under

optimal conditions more than 50 percent of the pigs would be produced from sows which had produced at least two litters.

An evaluation of selection in the development of inbred lines of swine at 7 midwestern agricultural experiment stations was prepared by Dickerson et al. (1954). Data on 4,521 litters were included in their study. The percent of potential maximum selection intensity actually applied for number born, number weaned, 56-day weight and 154-day weight was 14%, 33%, 53% and 44% for males and 23%, 49%, 36% and 46% for females, respectively. The authors attributed the poor utilization of opportunity for selection to early culling on weaning weight, excessive culling of boars by castration, sexual abnormalities, hernias, postweaning mortality, discrimination against pigs from younger litters and reproductive failures.

Failure to fully utilize performance and carcass information may be a rather universal shortcoming among swine breeders. French breeders have made relatively little use of progeny test results according to a study by Czajewska and Ollivier (1969). Only the poorest 8%, 4% and 3% of boars on the basis of ham and loin percentage, feed efficiency and average daily gain were culled following progeny testing. The results of Fredeen's (1953) study would indicate that at least through 1950, Canadian swine breeders had not been utilizing testing station results. Cox and

Smith (1968) concluded that factors other than individual, sire and sib test information were providing the principal bases for selecting boars to be used in Iowa purebred herds.

While it does not appear to be a common problem, overly intense selection in a closed population can have detrimental effects. Smith (1969) cautions that selection for maximum immediate response will not always optimize genetic gain over a long period of time. Loss of genetic variation due to inbreeding, inbreeding depression in reproductive and growth traits, and loss of genetic variation from selection are what Smith regards as likely consequences of overly intense selection.

Genetic variability is a property of the population over which the breeder has but limited control. In a closed breeding herd, inbreeding is likely to have some effect on reduction of the genetic variability within the herd. Smith (1969) estimated that genetic variability would be reduced by $[(g-1)/2] (1/8Np)$ in g generations where p percent of N tested animals are used for replacements each generation.

Intense selection pressure can also cause a loss in additive genetic variation. Dickerson and Hazel (1944a) have shown that additive genetic variation in a selected group is reduced by $r_{XA}^2 [i(i-h)]$; where r_{XA}^2 is the squared correlation between the trait under selection, X , and transmitting ability, A , i is intensity of selection and h is the deviate

on the abscissa of the normal curve at the point of truncation. Most of the genetic variability lost in the selected population is restored in the population of their offspring by chance at Mendelian segregation. The net loss in genetic variation due to selection will depend upon the accuracy and intensity of selection.

Accuracy is defined by Lush (1954) as the correlation between the criterion of selection, X , and the breeding or genic value, A . Accuracy is also commonly expressed in terms of the regression of breeding value on the criterion of selection.

$$r_{XA} = b_{AX} (\sigma_X / \sigma_A)$$

Falconer (1960) defines heritability as the regression of breeding value on phenotypic value. Vast numbers of studies have been conducted to estimate the heritabilities of economically important traits. A list of heritability estimates for economically important traits in swine has been compiled by Christian (1970). These estimates as presented in Table 2 are close approximations of average values reported in a large body of literature from around the world.

Table 2. Heritability estimates for economically important swine traits

Trait	Heritability (percent)
Number of pigs farrowed	15
Number of pigs weaned	10
Weaning weight of litter	15
56-day weight	10
154-day weight	30
Average daily gain	30
Feed efficiency	30
Length of carcass	60
Backfat thickness	50
Loin eye area	50
Ham-loin percent	45

Since the economic production of swine depends on more than one factor, genetic correlations between traits are of more than academic concern. Strong genetic antagonisms between economically important traits could severely restrict change in net merit. Conversely desirable correlations between economically important traits can enhance opportunity to increase the net genetic merit of a population. Two genetically correlated traits provide information about each other supplemental to that available from direct measurement

of either trait.

The relationship between postweaning daily gain and feed efficiency has some automatic negativity built into it. This automaticity is a result of the denominator of feed efficiency being gain; also fast growing pigs require fewer days of body weight maintenance. A favorable genetic correlation of $-.70$ between gain and feed efficiency would closely approximate the average of estimates reported by Jonsson (1957), Smith (1965), Smith and Ross (1965) and Biswas et al. (1966).

The literature indicates that there are no genetic antagonisms among carcass measures of cutability in swine. Genetic correlations between backfat thickness and loin eye area, backfat thickness and percent lean cuts, and loin eye area and percent lean cuts average approximately $-.30$, $-.60$ and 0.60 , respectively, according to reports by Fredeen (1953), Brinks (1960), Smith and Ross (1965), Biswas et al. (1966), Jensen, Craig and Robison (1967), Hoffman, Miller and Goodman (1968), Arganosa, Omtvedt and Walters (1969), Isler and Swiger (1969), Siers and Christian (1970) and Moen, Vold and Standal (1970).

Studies dealing with relationships between performance and carcass cutability traits do not give a consistent view of what the genetic correlations among these traits actually are. For example, estimates of the relationship between

average daily gain and lean cut percentage range from 0.97 to -.61. The reader is referred to papers by Dickerson (1947), Fredeen (1953), Jonsson (1957), Brinks (1960), Smith and Ross (1965), Biswas et al. (1966), Stanislaw et al. (1967), Hoffman, Miller and Goodman (1968), Isler and Swiger (1969) and Edwards and Omtvedt (1970) for further information. In a summary of swine test station data from 15 states, Bruner (1965) observed that, "Improvement in rate of gain and feed efficiency has accompanied increase in carcass meatiness." This observation would lend support to the argument that genetic antagonisms between performance and carcass cutability traits are probably of little consequence to swine improvement programs.

Considerable evidence is accumulating both in research reports and in field observation that genetic antagonisms may exist between certain carcass cutability and meat quality traits in swine. Jensen, Craig and Robison (1967), Arganosa, Omtvedt and Walters (1969) and Moen, Vold and Standal (1970) report antagonistic genetic correlations between cutability traits indicating heavy muscling, i.e. loin eye area and ham and loin or lean cut percentage, and carcass quality traits such as muscle color, moisture retention and flavor.

Heritability and genetic correlation estimates provide some insight into the accuracy of selection based on individual records. In the special case of direct selection on

an individual record, accuracy is the square root of heritability. When indirect selection is based on a trait such as backfat probe with the desired goal being improvement in percent lean cuts, the accuracy with which the breeding value for lean cuts is measured by backfat probe is the square root of heritability of backfat probe times the genetic correlation between the two traits.

Selection is frequently based on information supplemental to or other than individual records on a single trait. In these cases the accuracy with which breeding values are estimated from phenotypic records requires more complex formulation. Basic formulation for computing accuracy can be found in Hazel (1943), Lush (1947), Skjervold and Odegard (1959), Falconer (1960) and Freeman (1970). Table 3 presents formulas for computing accuracy of breeding value estimates under different methods of selection.

The amount and source of pedigree information will determine its worth in breeding value estimation at a given heritability. Lush (1947) found that the value of family selection was dependent upon the genetic relationship, r , between family members being large, the phenotypic relationship, t , between family members being small and family size being large.

Sib testing is commonly practiced for traits that cannot be directly measured on the individual. Carcass data

Table 3. Formulas for computing accuracy

Method of selection	Accuracy ^a
Mass selection, single record	$\sqrt{h^2}$
Mass selection, m records	$\sqrt{mh^2/(1+(m-1)\rho)}$
Mass selection, correlated response in X from selection on Y	$r_{A_{X,Y}} \sqrt{h^2_Y}$
Mass selection, 1 record on n sibs or progeny	$r \sqrt{nh^2/(1+(n-1)t)}$
Mass selection, m records on n sibs or progeny	$r \sqrt{mnh^2/(1+(m-1)\rho + m(n-1)t^2)}$
Mass selection, index of information from several pedigree sources	$r_{IA} = \sqrt{\sum_j b_j \sigma_{X_j A} / \sigma_A}$
Mass selection, multiple trait index	$r_{IH} = \sigma_I / \sigma_H$
Family selection, n family members	$(1+(n-1)r) \sqrt{h^2/(n(1+(n-1)t)}$
Within family selection, n family members	$(1-r) \sqrt{(n-1)h^2/n(1-t)}$

^a h^2 refers to heritability
 r refers to Wright's coefficient of relationship
 t refers to the phenotypic correlation between members of families
 ρ refers to the phenotypic correlation between repeated records on the same individual
 $r_{A_{X,Y}}$ refers to the additive genetic correlation between traits X and Y
 b_j refers to the partial regression of breeding value on the jth source of information
 $\sigma_{X_j A}$ refers to the covariance between the jth source of information and A, the animal's breeding value
 σ_A refers to the standard deviation of breeding value, A
 σ_I refers to the standard deviation of the selection index, I
 σ_H refers to the standard deviation of the aggregate breeding value, H.

are often collected from littermates to provide information on an individual's carcass merit. Martin and Fredeen (1967) stated, "...that slaughtering of litter samples is, in terms of the information now being obtained therefrom, an unnecessary restriction of genetic improvement." They concluded that genetic improvement in lean cut percentage could be achieved more effectively by indirect selection on backfat probe. Martin and Fredeen contended that sib carcass testing unnecessarily reduced selection intensity.

Progeny test information probably provides the most accurate means of measuring an animal's genetic worth. However, Dickerson and Hazel (1944a) note that, "...the usefulness of the progeny test is greatly influenced by factors other than its relative accuracy. The most important of these are the age at which progeny tests can be obtained and the rate of reproduction." Progeny testing results in an increased generation interval which frequently means a net decline in the annual rate of genetic progress. Ronningen (1970) has concluded that progeny testing is apt to be most valuable when the heritability of the trait is low, when the environmental correlation between family members is low and when only a small number of animals are to be selected for rather intensive use.

Accuracy is a function of both genotypic and environmental effects. Breeders can increase the accuracy of

breeding value estimation by taking steps to eliminate extraneous environmental variation. Careful measurement of animals raised under standardized environmental conditions will enhance selection efforts. Statistical adjustment of records for known environmental effects such as sex, age at weaning, season of birth, age of dam, etc. is a commonly used means of removing environmental differences from data. Langholz (1965) proposed the practice of deviating records from a contemporary group mean as a means of removing environmental variation from swine data. This is a commonly used technique in handling dairy records that has not yet been widely used by meat animal breeders.

Willham (1965) notes that generation interval may be most conveniently measured as the average age of parents when their offspring are born. Since the annual rate of genetic progress is inversely proportional to generation interval, minimizing the interval between generations becomes extremely important to efforts aimed at maximizing the rate of genetic improvement.

Christian (1970) outlined a conventional plan of swine herd replacement that resulted in an average age of 1.75 years for females and 1.25 years for boars. The net generation interval under this system would be 1.5 years. Dickerson et al. (1954) reported a 1.33 year generation interval in a 7-state North Central Regional Swine Breeding Laboratory

study.

Genetic gain may be estimated from average phenotypic time trends according to Dickerson (1951). He cautions that phenotypic time trends may be misleading as measures of genetic change if they are influenced by environmental time trends and other factors.

After adjustment for effects of inbreeding, Dickerson et al. (1954) found the mean annual changes in litter size at birth, litter size at 56 days, 56-day weight and 154-day weight were $-.03$, $-.00$, $-.40$ lb. and -2.78 lb., respectively, from an 8-year North Central Regional Swine Breeding Laboratory study on the effectiveness of selection. Poor utilization of opportunity for selection was cited as a contributing factor to the apparent ineffectiveness of selection in these lines.

Selection experiments designed to change the backfat thickness of swine have been generally more successful than those aimed at increasing growth rate and reproductive performance. Gray et al. (1968) reported a 20 percent decrease in backfat thickness in 5 generations of mass selection for low backfat probe. Hetzer and Miller (1970) found regressions for breeding value of backfat on time of 0.19 cm., 0.13 cm., $-.10$ cm., $-.06$ cm., per year, in U.S.D.A. high fat Duroc and Yorkshire, and low fat Duroc and Yorkshire lines, respectively. Selection had separated the high

and low fatness U.S.D.A. Duroc lines by 3.5 cm. in 13 generations.

While Fredeen (1953) found no improvement in hogs entered in Canadian testing stations over a 20-year period most testing programs throughout the world have reported increases in carcass cutability traits and efficiency of gain.

Thomsen (1957) reported an increase of 1 pig in litter size at birth and weaning in 50 years of recorded test data on the Danish Landrace. Growth rate increased 125 gm. per day, feed per kg. of gain decreased 0.73 kg., carcass length increased 4 cm. and carcass backfat was decreased by 0.75 cm. in the Danish pigs over approximately the same time period.

A summary by Bruner (1965) showed boar testing stations in 15 states reporting improvement in rate of gain and feed efficiency. Midwestern testing stations that had been in operation for 6 years or more reported substantial improvement in backfat thickness, loin eye area and either ham and loin or lean cut percentages.

Quijandria, Woodward and Robison (1970) found significant regressions of breeding value on time of -1.31 kg., 1.17% and $-.071$ cm., per year, for feed required per 100 kg. gain, lean cut percentage and backfat, respectively, in North Carolina Swine Evaluation Station data. No significant changes in average daily gain or loin eye area were found in

the 7-year period involved in the North Carolina study.

Regressions of unweighted annual means on years from the Iowa Boar Testing Station were computed from data reported in the Iowa Tested Swine Directory (1970) and are listed in Table 4.

Table 4. Regressions of annual means on years from Iowa Boar Testing Station

Trait	Regression coefficient
Average daily gain	0.027 lb.
Feed required per cwt. gain	-3.622 lb.
Backfat probe	.034 in.
Carcass backfat	-.030 in.
Ham and loin percentage	0.811 %
Loin eye area	0.113 sq. in.
Index	7.248

The use of test station averages to estimate genetic improvement in swine populations can be criticized. The cumulative effects of changing breeder participation and progressive competency of breeders in selecting individual animals that will do well on test are confounded, as are environmental trends, with genetic trends. Cox and Smith (1968) were very pessimistic about the amount of genetic

change that has occurred in Iowa swine. Estimates derived from the mean performance of progeny of boars sampled from Iowa Duroc and Hampshire herds were found to disagree in sign with those obtained from testing station data. Cox and Smith's conclusions were based in part on the results of a survey on breeder boar selection criteria which indicated a lack of use of objective measurements by Iowa breeders. In contrast to Cox and Smith's findings, Langholz (1965) estimated that approximately 50 percent of the observed improvement in carcass measurements in the Norwegian Pig Progeny Test was actually genetic.

SOURCE OF DATA

Data used in this study were collected on 460 Duroc, 414 Hampshire, 661 Poland and 394 Yorkshire litters farrowed at the Iowa State University Napier Farm. Records on the 1,929 purebred litters included in this study were collected over an 8-year period from the spring of 1962 through the fall of 1969.

In 1961 an effort was made to make the herd specific-pathogen free (SPF). Litters were taken by Caesarean section and raised in isolation or transferred to SPF sows obtained from the Veterinary Medical Research Institute. Although a limited number of SPF boars and Caesarean litters have been introduced periodically to control the rate of inbreeding, the herd has essentially been kept isolated since 1962. Until the spring of 1969 no major disease outbreak had occurred in the herd. Vibrionic dysentery was diagnosed as the cause of increased mortality and poor performance of pigs born in the spring and fall of 1969.

In the spring of 1962 a study was initiated to measure the rate of genetic improvement in meatiness that could be obtained through utilization of individual, family and progeny records. Genetic improvement in ham and loin percentage was of particular interest. No specific index was used. The selection program consisted of primary selection for minimum probe as boars reached 200 pounds. Additional

selection was based on littermate carcass records. Progeny performance provided the basis for selection of boars to remain in the breeding herd for more than two seasons. A three-stage sequential culling system was followed in boar selection. Castration and culling on physical defects at weaning eliminated 3,806 of 5,004 males from further consideration as candidates for the breeding herd. Of the remaining 1,198 boars only 188 actually entered the breeding herd. Since progeny records from a boar's first season of use were not available at least until midway into the second season gestation, boars were not culled on progeny performance until after two seasons of use. Individuals which were not born in the herd or were born prior to 1962 were given zero selection differentials for all preprogeny test traits and made non-zero contributions to selection differentials only through this final stage of culling, the progeny test.

Two-stage sequential culling was practiced in gilt selection. Of 4,956 gilts weaned, 940 actually entered the purebred breeding herd. Progeny test selection following two seasons of use was the second stage of selection practiced on females. Although a crossbreeding study was being conducted concurrently with this study, no crossbred pigs were included in progeny test averages of this investigation.

While the selection criterion was meatiness, the

economic importance of reproductive and performance traits were probably not completely ignored in selection of breeding animals. Inbreeding of dams, inbreeding of pigs, litter size at birth, litter size at weaning, adjusted 56-day weight, adjusted 154-day weight and adjusted backfat probe are studied in this analysis. Backfat probes on boars only are included in this presentation as gilts were rarely probed. Littermate carcass averages for backfat probe, ham and loin percentage and loin eye area were not weighted for differences in number of full sibs included in the average at the time of selection and are handled in an identical fashion in this presentation. An average of 2.38, 2.02, 1.97 and 2.23 sibs were included in the littermate carcass averages of the selected Duroc, Hampshire, Poland and Yorkshire boars, respectively. An average of 2.00, 2.09, 2.08 and 2.25 sibs were included in the littermate carcass averages of selected gilts from the aforementioned breeds. An average of 1.96 pigs were slaughtered per litter farrowed in the 8-year period included in this study. Progeny test traits include the cumulative unweighted averages of progeny 154-day weight, carcass backfat, ham and loin percent, and loin eye area. Sow progeny test records include the cumulative average total litter weight at 56 days as a measure of reproductive and maternal performance.

Data in this study have been preadjusted for several

known sources of environmental variation. Weaning weights were adjusted to a 56-day basis using a formula developed by Whatley and Quaife (1937).

$$56\text{-day weight} = (\text{actual weight}) [41/(\text{actual age}-15)]$$

Five month weights were adjusted to a 154-day basis using a method reported by Taylor and Hazel (1955).

$$154\text{-day weight} = (\text{actual weight}+154) [199/(\text{actual age}+45)] - 154$$

An unpublished table developed from Iowa Agricultural Experiment Station data was used to adjust backfat probes to a 200-pound live weight basis.

Preliminary least squares analysis of the data showed that sex and carcass weight differences were important sources of variation in all carcass traits. Actual selection was practiced using unweighted means of carcass traits that were not corrected for either sex or carcass weight differences. For the purposes of computing selection differentials under actual selection conditions carcass data were not corrected for differences in sex or carcass weight.

Age of dam effects were found to be a significant source of variation for all performance traits. However, age of dam effects are confounded with selection. Therefore, no attempt has been made to remove variation associated with age of dam from the data.

An effort was made to grow prospective replacement boars and littermates to be sampled for carcass data in one

of 48 concrete record of performance (ROP) test pens. Replacement gilts and an occasional outstanding boar were grown out under a pasture management system. Preliminary least squares analysis showed that type of management was an important source of variation in all performance and carcass traits. A significant type of management mean square for 56-day weight and significant type of management by sex interaction mean squares for 56-day and 154-day weights illustrate the confounding of selection and type of management. These data are not corrected for type of management differences.

ANALYSIS AND RESULTS

Means and Standard Deviations

Number of observations, cumulative means and pooled within year-season standard deviations are presented by breed for males in Table 5 and for females in Table 6. Data from 1969 spring and fall seasons have been excluded from material presented in Tables 5 and 6 because of an extreme range in performance resulting from vibronic dysentery which was present during those seasons. Inclusion of 1969 data would appear to violate the supposition of homogeneity of variance, a prerequisite for pooling data over year-seasons. These analyses have been conducted under the assumption that there was normal variability, at least on a within-breed-sex basis, over year-seasons from the spring of 1962 through the fall of 1968.

Documentation of number of observations and means by breed and year-season for the various traits is presented in Tables 57 through 66 of the appendix.

Differences among breed means were found to be highly significant for all traits. The Duroc and Yorkshire lines of breeding were generally superior in performance but relatively inferior to the Hampshire and Poland lines in carcass cutability characteristics.

As Willham (1965) notes, breed means are a function of gene frequency and the effects of gene action. These

Table 5. Number of observations, cumulative means and within-year-season standard deviations by breed for all male pigs

Trait	Duroc	Hampshire	Poland	Yorkshire	Pooled
<u>Number weaned</u>					
n	1,115	1,004	1,634	1,251	5,004
\bar{X}	6.91	6.69	6.98	8.63	7.32
s	2.42	2.07	2.02	2.26	2.18
<u>56-day weight (lb.)</u>					
n	1,115	1,004	1,634	1,251	5,004
\bar{X}	44.39	39.98	42.10	42.56	42.30
s	8.90	8.58	8.42	8.78	8.65
<u>154-day weight (lb.)</u>					
n	1,045	974	1,565	1,215	4,799
\bar{X}	206.98	190.17	196.77	205.37	199.83
s	32.28	28.99	26.85	29.76	29.27
<u>Littermate carcass backfat average (in.)</u>					
n	1,038	938	1,536	1,202	4,714
\bar{X}	1.46	1.28	1.44	1.49	1.42
s	0.15	0.11	0.12	0.15	0.13
<u>Littermate ham and loin percent average (%)</u>					
n	1,038	938	1,536	1,202	4,714
\bar{X}	38.29	40.47	39.71	39.11	39.40
s	1.49	1.20	1.32	1.28	1.33
<u>Littermate loin eye area average (sq.in.)</u>					
n	1,038	938	1,536	1,202	4,714
\bar{X}	3.94	4.90	4.68	4.30	4.47
s	0.54	0.51	0.53	0.43	0.51
<u>Backfat probe (in.)</u>					
n	212	213	285	223	933
\bar{X}	0.95	0.81	0.95	0.91	0.91
s	0.14	0.10	0.13	0.14	0.13

Table 6. Number of observations, cumulative means and within-year-season standard deviations by breed for all female pigs

Trait	Duroc	Hampshire	Poland	Yorkshire	Pooled
<u>Number weaned</u>					
n	1,178	980	1,621	1,177	4,956
\bar{X}	6.94	6.85	7.01	8.58	7.33
s	2.28	2.13	2.10	2.25	2.18
<u>56-day weight (lb.)</u>					
n	1,178	980	1,621	1,177	4,956
\bar{X}	43.92	39.35	42.05	42.09	41.97
s	9.04	8.37	8.32	8.10	8.46
<u>154-day weight (lb.)</u>					
n	1,151	947	1,575	1,141	4,814
\bar{X}	190.44	172.82	181.00	184.10	182.38
s	27.07	26.44	23.91	23.84	25.19
<u>Littermate carcass backfat average (in.)</u>					
n	1,101	903	1,491	1,096	4,591
\bar{X}	1.45	1.27	1.44	1.46	1.41
s	0.15	0.11	0.12	0.14	0.13
<u>Littermate ham and loin percent average (%)</u>					
n	1,101	903	1,491	1,096	4,591
\bar{X}	38.68	40.55	39.88	39.29	39.58
s	1.48	1.19	1.35	1.34	1.35
<u>Littermate loin eye area average (sq.in)</u>					
n	1,101	903	1,491	1,096	4,591
\bar{X}	4.10	4.94	4.78	4.34	4.55
s	0.56	0.53	0.56	0.44	0.53

same gene frequencies contribute to the variation observed within breeds. Since breed means are frequently found to differ significantly, it would seem logical to expect that within-breed variances might also differ. Pooled estimates of within-breed variability are commonly used in animal breeding studies to make inferences about general properties of a species. However, Eisenhart, Hastay and Wallis (1947) state, "... , a pooled estimate of within-class variability, obtained by combining measures of the respective within-class dispersions, may be useless for practical purposes, unless there is homogeneity of within-class variability or the method of combining the within-class dispersions takes proper account of the relative importance.....of the respective classes under realistic conditions." It is not readily apparent that this latter alternative is frequently exercised. If there is lack of uniform intrinsic variability within breeds a problem exists that is analogous to the statistical situation where an interaction is found between two main effects. Generalizations about a species may not be appropriate; it may be necessary to confine inferences to specific breeds.

Bartlett's test for homogeneity of variance, to be found in Eisenhart, Hastay and Wallis (1947) or Snedecor (1956), was used to test the homogeneity of within-breed variances presented for each sex class in Tables 5 and 6. With the

exception of 56-day weight in males the results in Table 7 indicate highly significant differences among breed variances in all traits for each sex group. Comparisons of variances from data adjusted for differences in inbreeding of dam, inbreeding of pig, age of dam and, where appropriate, differences in cold carcass weight gave similar results.

Table 7. Bartlett's test for homogeneity of variance among breeds^a

Trait	Males ^b	Females ^b
Number weaned	50.02**	13.24**
56-day weight	4.87	16.20**
154-day weight	43.80**	31.69**
Littermate backfat ave.	112.83**	126.13**
Littermate ham and loin percent ave.	51.02**	45.62**
Littermate loin eye area ave.	71.48**	88.20**
Backfat probe	25.29**	

^a χ^2 values with 3 degrees of freedom.

^b ** $p < .01$.
* $p < .05$.

Subsequent analyses are conducted independently by breed. A pooled analysis has been continued as a matter of curiosity, realizing that it does not adequately describe

these data.

Inbreeding

Dickerson (1951), Dickerson et al. (1954) and Brinks, Clark and Kieffer (1965) have noted the effects of accumulating levels of inbreeding on time trends in performance. Increasing levels of inbreeding generally result in decreasing productivity. Therefore, the effects of inbreeding need to be considered in evaluating the effectiveness of selection programs.

Using 1961 pedigrees as a base population, Wright's (1922) coefficient of inbreeding was calculated for pigs (by litter) and their dam. A large capacity Fortran program with pedigree file updating capabilities was developed to accomplish this task on the IBM 360-65 computer. A covariance table method of computing inbreeding coefficients was used.

Breed mean levels of inbreeding of dam, inbreeding of pig and their respective within-breed standard deviations pooled across sexes and year-seasons are presented in Table 8. Within-breed variances are heterogeneous for both inbreeding of dam and inbreeding of pig. Year-season means for inbreeding of pig and inbreeding of dam are presented by breed in Tables 57 and 58 of the appendix.

Table 8. Mean levels of inbreeding and standard deviations for dams and pigs by breed

Breed	<u>Inbreeding of dam</u>		<u>Inbreeding of pig</u>	
	\bar{X}	s	\bar{X}	s
	<u>percent</u>	<u>percent</u>	<u>percent</u>	<u>percent</u>
Duroc	8.08	9.76	12.98	10.02
Hampshire	5.27	8.00	9.31	8.86
Poland	6.61	9.13	12.52	9.44
Yorkshire	3.20	6.19	6.00	6.66
Pooled	5.83	8.43	10.38	8.97

Inbreeding of pig coefficients ranged from 0 to 62.5%, 0 to 43.75%, 0 to 44.53% and 0 to 34.38% for Durocs, Hampshire, Polands and Yorkshires, respectively. Inbreeding of dam coefficients were as high as 37.5%, 43.75%, 37.5% and 34.38% for Durocs, Hampshires, Polands and Yorkshires, in that order.

Partial regression coefficients of litter, performance and carcass traits on inbreeding of dams and pigs are presented by breed in Table 9. These coefficients were obtained as part of the least squares analysis to be outlined in the following section on parameter estimation. Dickerson et al. (1954) reported regressions on inbreeding of litter (pig) ranging from -.024 to -.069, -.042 to 0.102, -.282 to -.449 for number weaned, 56-day weight and 154-day weight,

Table 9. Partial regression of litter, performance and carcass traits on inbreeding of dams and pigs by breed

Trait	Partial regression on inbreeding			
	Duroc	Hampshire	Poland	Yorkshire
	<u>Inbreeding of Dam</u>			
Number weaned	-.018	-.014	-.047	-.058
Total litter weight at 56 days	-.76	-.86	-1.97	-2.50
56-day weight	0.011	-.060	-.005	-.018
154-day weight	0.143	-.174	0.012	-.039
Backfat probe	-.001	-.000	-.002	-.000
Carcass backfat	-.001	-.001	-.000	0.001
Ham and loin percent	0.006	0.001	0.011	0.002
Loin eye area	0.004	0.003	0.001	0.003
	<u>Inbreeding of Pig</u>			
Number weaned	-.036	-.017	-.035	-.052
Total litter weight at 56 days	-2.49	-.61	-2.22	-2.54
56-day weight	-.156	0.023	-.128	-.066
154-day weight	-.854	-.295	-.699	-.669
Backfat probe	-.000	0.002	0.000	-.005
Carcass backfat	-.001	-.001	-.000	-.001
Ham and loin percent	0.026	0.009	-.010	0.018
Loin eye area	0.009	0.004	0.000	-.000

respectively. They found regressions of $-.025$, 0.006 and $-.013$ for number weaned, 56-day weight and 154-day weight, in order, on inbreeding of dam.

Annual realized selection differentials for inbreeding of dam averaged 0.3 , $-.6$, 0.4 , 0.3 and 0.1 , percent, for Durocs, Hampshires, Polands, Yorkshires and pooled data, respectively. Average annual realized selection differentials for inbreeding of pigs were -1.3 , -1.4 , -1.2 , $-.1$ and $-.9$, percent, in order of above. There was a consistent tendency in all breeds to retain sows that were less highly inbred than average. Selected gilt replacements tended to be less highly inbred than average. Discrimination against more highly inbred boars was consistent only in the initial selection of Hampshire replacement boars. Dickerson et al. (1954) reported selection differentials ranging from 0.32% to -1.51% for inbreeding of dam and $-.05\%$ to -2.20% for inbreeding of litters (pig).

Linear regression coefficients of inbreeding of pig on year-seasons were not significantly different than zero for any breed. These coefficients were 0.28 , $-.38$, $-.56$, 0.42 and $-.20$, percent per year-season, for Durocs, Hampshires, Polands, Yorkshires and pooled data, respectively. Since no marked accumulation of the level of inbreeding with time appears in these data, subsequent estimates of genetic time trends should not be greatly influenced by the

effects of inbreeding.

Parameter Estimation

Estimates of phenotypic and genetic parameters will be needed in subsequent steps involving selection index construction and estimation of genetic gain.

Phenotypic correlations are pooled within-year-season estimates computed separately by breed and sex. Littermate and progeny averages were treated as observations on an individual and were not weighted by the number of observations contributing to the average nor were they adjusted for differences in age of dam, sex, inbreeding or carcass weight. Phenotypic correlations among number weaned, 56-day weight, 154-day weight, littermate backfat average, littermate ham and loin percentage average, littermate loin eye area average, backfat probe of boars or average total weight of progeny litters at 56 days of sows, progeny 154-day weight average, progeny carcass backfat average, progeny ham and loin percentage average and progeny loin eye area average are presented by breed in Tables 11 through 15. A numerical coding system was used to identify traits in Tables 11 through 15. This coding system is presented in Table 10.

Notable differences between the correlations of the two sexes are not apparent. However, there does appear to be some subtle differences among the breeds. Phenotypic

Table 10. Reference number and list of traits included in phenotypic correlation tables

Trait number	Description of trait
1	Number weaned
2	56-day weight
3	154-day weight
4	Littermate carcass backfat average
5	Littermate ham and loin percentage average
6	Littermate loin eye area average
7	Backfat probe (for males) or Average total weight of progeny litters at 56 days (for females)
8	Progeny 154-day weight average
9	Progeny carcass backfat average
10	Progeny ham and loin percentage average
11	Progeny loin eye area average

Table 11. Phenotypic correlations for Duroc breed by sex^a

Trait	1	2	3	4	5	6	7 ^b	8	9	10	11
1	1.00	0.13	0.08	-.02	-.03	0.02	-.04	-.10	-.07	0.09	-.00
2	0.02	1.00	0.56	-.04	-.10	-.06	0.04	0.08	-.23	0.00	-.08
3	0.02	0.60	1.00	0.07	-.08	0.01	0.25	0.13	-.20	-.03	-.11
4	-.09	-.10	0.02	1.00	-.69	-.27	0.17	0.18	0.17	-.25	-.13
5	0.01	0.02	-.05	-.57	1.00	0.64	-.24	-.11	-.02	0.32	0.32
6	-.01	-.02	0.02	-.20	0.65	1.00	-.20	0.06	0.33	0.55	0.11
7 ^b	0.01	0.16	0.08	-.05	-.08	-.22	1.00	0.08	0.00	-.05	-.10
8	-.11	0.21	0.18	0.02	-.14	-.19	0.31	1.00	0.11	0.08	0.13
9	-.11	-.08	-.07	0.05	-.00	0.01	-.20	-.05	1.00	-.56	-.13
10	0.02	-.03	0.00	-.02	0.08	0.22	0.06	-.04	-.59	1.00	0.62
11	-.01	-.01	0.09	0.05	0.14	0.35	0.02	-.02	-.23	0.64	1.00

^aMale correlations listed above diagonal; female correlations listed below diagonal.

^bBackfat probe in males, average total litter weight of progeny litters at 56 days.

Table 12. Phenotypic correlations for Hampshire breed by sex^a

Trait	1	2	3	4	5	6	7 ^b	8	9	10	11
1	1.00	-.09	-.04	-.04	-.18	-.13	0.01	-.26	-.03	0.11	0.04
2	-.01	1.00	0.54	-.10	0.06	0.16	0.02	-.16	-.33	0.35	0.12
3	-.01	0.65	1.00	0.03	-.12	0.14	0.15	0.21	-.13	0.08	-.04
4	-.10	-.02	0.05	1.00	-.53	-.24	0.08	0.33	-.16	0.00	-.08
5	-.09	-.02	-.06	-.53	1.00	0.48	-.16	-.22	0.26	0.07	0.17
6	-.08	-.01	0.05	-.20	0.50	1.00	-.19	-.22	-.14	0.18	0.23
7 ^b	-.07	0.14	0.00	-.08	-.00	0.03	1.00	0.22	0.16	-.18	-.12
8	-.08	0.09	0.15	0.12	-.14	-.04	0.23	1.00	0.26	-.37	-.09
9	-.03	0.06	0.06	-.04	0.08	-.01	-.00	0.03	1.00	-.67	-.42
10	-.01	-.03	-.05	0.01	0.04	0.10	-.08	-.07	-.57	1.00	0.54
11	0.08	-.07	-.02	-.08	0.10	0.16	0.00	0.05	-.26	0.47	1.00

^aMale correlations listed above diagonal; female correlations listed below diagonal.

^bBackfat probe in males, average total litter weight of progeny litters at 56 days.

Table 13. Phenotypic correlations for Poland breed by sex^a

Trait	1	2	3	4	5	6	7 ^b	8	9	10	11
1	1.00	-.05	0.01	0.19	-.16	-.07	-.00	0.01	0.03	0.04	0.04
2	0.02	1.00	0.62	-.03	-.07	-.18	0.00	0.06	-.10	-.17	-.10
3	0.07	0.67	1.00	-.02	-.11	-.11	0.17	0.21	-.09	-.19	-.27
4	0.15	0.05	0.17	1.00	-.50	-.17	0.05	0.20	0.06	-.08	0.08
5	-.09	-.06	-.18	-.58	1.00	0.54	-.15	-.34	0.08	0.19	0.07
6	-.06	-.00	-.09	-.25	0.62	1.00	-.12	-.12	0.01	0.03	0.00
7 ^b	0.12	0.02	0.05	-.03	0.01	-.09	1.00	0.03	0.25	-.28	-.20
8	-.04	0.10	0.17	0.04	-.09	-.10	0.32	1.00	0.03	-.22	-.10
9	0.02	0.06	0.12	0.17	-.10	0.00	0.04	0.13	1.00	-.56	-.29
10	-.05	-.19	-.17	-.16	0.21	0.13	-.07	-.17	-.56	1.00	0.74
11	0.03	-.12	-.11	-.08	0.21	0.22	-.06	-.15	-.23	0.65	1.00

^aMale correlations listed above diagonal; female correlations listed below diagonal.

^bBackfat probe in males, average total litter weight of progeny litters at 56 days.

Table 14. Phenotypic correlations for Yorkshire breed by sex^a

Trait	1	2	3	4	5	6	7 ^b	8	9	10	11
1	1.00	-.11	-.11	0.05	-.13	-.14	-.02	-.09	-.13	0.05	-.20
2	-.10	1.00	0.62	0.20	-.23	-.11	0.04	-.35	0.08	-.05	0.25
3	-.03	0.60	1.00	0.20	-.26	-.09	0.38	-.10	0.08	-.12	0.04
4	0.07	0.07	0.14	1.00	-.64	-.27	0.23	-.05	-.00	-.11	-.11
5	-.15	-.05	-.16	-.66	1.00	0.47	-.27	0.05	-.02	0.05	0.07
6	-.12	-.04	-.06	-.34	0.49	1.00	-.27	-.14	-.15	0.12	0.21
7 ^b	0.04	-.02	-.03	0.02	0.06	0.01	1.00	0.29	0.23	-.17	-.12
8	-.18	0.01	0.13	0.04	-.06	-.05	0.16	1.00	0.29	-.29	-.28
9	-.06	0.14	0.25	0.17	-.22	-.16	0.03	0.29	1.00	-.69	-.31
10	-.05	0.07	-.19	-.11	0.19	0.12	-.01	-.27	-.63	1.00	0.60
11	-.11	-.10	-.08	-.14	0.12	0.13	-.11	-.12	-.28	0.51	1.00

^aMale correlations listed above diagonal; female correlations listed below diagonal.

^bBackfat probe in males, average total litter weight of progeny litters at 56 days.

Table 15. Phenotypic correlations for pooled analysis by sex^a

Trait	1	2	3	4	5	6	7 ^b	8	9	10	11
1	1.00	-.03	-.02	0.05	-.12	-.07	-.02	-.09	-.05	0.06	-.02
2	-.01	1.00	0.59	0.03	-.10	-.07	0.02	-.05	-.13	0.00	0.01
3	0.02	0.63	1.00	0.08	-.15	-.03	0.25	0.13	-.09	-.08	-.12
4	0.02	0.00	0.10	1.00	-.60	-.23	0.14	0.17	0.05	-.12	-.05
5	-.08	-.03	-.12	-.59	1.00	0.53	-.21	-.17	0.05	0.17	0.17
6	-.06	-.02	-.03	-.24	0.58	1.00	-.18	-.16	-.02	0.15	0.26
7 ^b	0.04	0.08	0.03	-.03	-.01	-.08	1.00	0.13	0.13	-.17	-.14
8	-.10	0.12	0.16	0.05	-.11	-.11	0.26	1.00	0.14	-.17	-.04
9	-.05	0.03	0.07	0.10	-.06	-.03	-.04	0.08	1.00	-.58	-.24
10	-.02	-.09	-.10	-.08	0.13	0.15	-.02	-.13	-.59	1.00	0.64
11	0.00	-.07	-.03	-.06	0.15	0.23	-.03	-.06	-.24	0.59	1.00

^aMale correlations listed above diagonal; female correlations listed below diagonal.

^bBackfat probe in males, average total litter weight of progeny litters at 56 days.

correlations between performance traits and measures of carcass meatiness are more consistently negative in the Yorkshire line of breeding than any of the other lines. This antagonism between performance and cutability traits is not as pronounced in the Duroc line of breeding. Littermate carcass data on Duroc boars was more highly related to corresponding data on their progeny than in the other breeds. In contrast backfat probes on Duroc boars showed little relationship to progeny carcass cutout characteristics.

Sampling errors were not computed for these phenotypic correlations, but will range from approximately 0.01 for moderately high (0.50) correlations between performance traits to slightly more than 0.10 for very low correlations between progeny test averages on boars.

A Henderson (1953) Method 3 approach was used in the estimation of genetic parameters from paternal half-sib correlations. To make the Method 3 analysis computationally feasible some restriction had to be placed on the number of sires used in the analysis. A total of 28 sires from each breed were selected for use in this analysis. These were boars that had been used over a period of several year-seasons and had relatively large numbers of progeny. Approximately 67%, 77%, 61% and 71% of all data available from Duroc, Hampshire, Poland and Yorkshire breeds, respectively,

were included in the genetic analysis. With the exception of the Poland breed, most of the data eliminated were from sires that had been used in only one season or which had had only limited use over a period of two seasons.

The least squares analysis followed procedures outlined by Harvey (1966). A separate analysis was conducted for each breed. With exceptions to be noted later, the following linear model was used:

$$\begin{aligned}
 X_{ijklmn} = & \mu + y_i + d_j + (yd)_{ij} + c_k + a_l + s_m + \beta_1 \\
 & (F_{DAM_{ijklmn}} - \bar{F}_{DAM}) + \beta_2 (F_{PIG_{ijklmn}} - \bar{F}_{PIG}) \\
 & + \beta_3 (W_{ijklmn} - \bar{W}) + e_{ijklmn} \\
 & i = 1 \text{ to } 7, j = 1 \text{ to } 2, k = 1 \text{ to } 2, l = 1 \text{ to } 4, \\
 & m = 1 \text{ to } 28, n = 1 \text{ to } N_m
 \end{aligned}$$

where

X_{ijklmn} = the observed value of a particular trait in a given breed for the nth pig of the kth sex sired by the mth boar and from a dam of the lth age class, born in the jth season of the ith year.

μ = mean of a particular trait for a given breed

y_i = effect of the ith year

d_j = effect of the jth season

$(yd)_{ij}$ = interaction effects for year and season

c_k = effect of the kth sex

a_1 = effect of the lth age of dam

s_m = effect of the mth sire

β_1 = partial regression of a particular trait on in-breeding of dam

$F_{DAM,ijklmn}$ = computed inbreeding coefficient of the dam of a given pig

\bar{F}_{DAM} = average inbreeding of dams in a particular breed-trait analysis

β_2 = partial regression of a particular trait on in-breeding of pig

$F_{PIG,ijklmn}$ = computed inbreeding coefficient of a given pig

\bar{F}_{PIG} = average inbreeding of pigs in a particular breed-trait analysis

β_3 = partial regression of a particular trait on cold carcass weight

W_{ijklmn} = cold carcass weight of a given pig

\bar{W} = average cold carcass weight for a particular breed

e_{ijklmn} = random effect associated with a given pig

All effects except the e's were assumed to be fixed. Each fixed effect is expressed as a deviation from its mean; i.e. the sum across the several effects of a given set of fixed effects equals zero. The random components, e's, were assumed to be normally distributed about a mean of zero with variance σ_e^2 within each breed.

The full linear model described above was used in the analysis of variance and covariance for carcass traits. A reduced model, deleting the partial regression on cold carcass weight, was used in the analysis of 56-day weight and 154-day weight and their covariance. Carcass data were adjusted for differences in cold carcass weight prior to analysis of the covariances between carcass traits and other traits.

Sex effects as well as the regression on cold carcass were deleted from the model used to describe progeny litter weight, number weaned and backfat probe.

Least squares means, year-season constants, age of dam constants and partial regression coefficients by breed are presented for each trait in Tables 67 through 74 of the appendix. Mean squares, degrees of freedom, mean values of inbreeding of pig and k values (coefficients of sire quadratic effects) are presented by trait for each breed in Tables 75 through 78 of the appendix.

Since the breeding groups represented in this study were partially inbred, K_s^2 , the sire quadratic effect estimates $[(1 + \bar{F}_{\text{PIG}})/4]\sigma_A^2$ rather than $(1/4)\sigma_A^2$. Willham (1965) notes that the heritability of a partially inbred population increases from σ_A^2/σ_P^2 to $\sigma_A^2(1 + \bar{F})/\sigma_P^2$, providing the phenotypic variance remains constant. Heritability estimates were computed as:

$$h^2 = [4/(1 + \bar{F}_{\text{PIG}})] [K_S^2 / (K_S^2 + \hat{\sigma}_e^2)]$$

Standard errors of heritability estimates were calculated using the following formula adapted from Falconer (1960):

$$\sigma_h^2 = [4/(1 + \bar{F}_{\text{PIG}})] \sqrt{2[1 + (k-1)t]^2 (1-t)^2 / [k(k-1)(S-1)]}$$

where $t = K_S^2 / (K_S^2 + \hat{\sigma}_e^2)$, $k = [1/(S-1)] [\sum_i^S n_i - (\sum_i^S n_i^2 / \sum_i^S n_i)]$,

n_i = number of progeny of the i th boar and S = number of boars.

Heritability estimates and their standard errors are reported in Table 16. Sums of squares were pooled across breeds to obtain pooled heritability estimates. Estimates of heritability from the pooled analysis agree fairly well with those reported by Christian (1970) and are very similar to those computed by Siers and Christian (1970) from portions of these same data but by a Henderson Method 2 technique.

These heritability estimates indicate there was less genetic variability in carcass characteristics of the Hampshire line of breeding than in the other breed groups. The heritability estimate of ham and loin percentage in the Duroc breed group is notably lower than similar estimates in other breed groups.

Estimates of genetic correlations are presented by breed in Tables 17 through 21. The following formula was used to estimate the genetic correlation between traits i and j :

Table 16. Heritability estimates and their standard errors by breed

Trait	Duroc	Hampshire	Poland	Yorkshire	Pooled
Total litter wt. at 56 day	0.19 \pm 0.13	-.02 \pm 0.09	0.09 \pm 0.09	0.08 \pm 0.13	0.09 \pm 0.06
Number weaned	0.09 \pm 0.11	-.02 \pm 0.09	0.10 \pm 0.09	0.06 \pm 0.12	0.07 \pm 0.06
56-day wt.	0.16 \pm 0.06	0.19 \pm 0.06	0.08 \pm 0.03	0.22 \pm 0.07	0.16 \pm 0.03
154-day wt.	0.35 \pm 0.10	0.33 \pm 0.09	0.18 \pm 0.06	0.16 \pm 0.05	0.25 \pm 0.04
Carcass backfat	0.28 \pm 0.11	0.20 \pm 0.09	0.47 \pm 0.14	0.41 \pm 0.14	0.36 \pm 0.06
Ham and loin percentage	0.15 \pm 0.08	0.35 \pm 0.12	0.61 \pm 0.16	0.56 \pm 0.16	0.42 \pm 0.07
Loin eye area	0.71 \pm 0.19	0.49 \pm 0.15	0.62 \pm 0.16	0.65 \pm 0.18	0.62 \pm 0.08
Backfat probe	0.06 \pm 0.16	0.65 \pm 0.26	0.53 \pm 0.23	0.25 \pm 0.20	0.27 \pm 0.10

Table 17. Genetic correlations for Duroc breed

Trait	1	2	3	4	5	6	7	8
1. Total litter wt. at 56 days	1.00	1.04	0.75	0.48	-.02	-.21	0.14	-.04
2. Number weaned		1.00	0.44	0.41	0.13	-.21	0.16	0.03
3. 56-day wt.			1.00	0.35	-.34	-.45	-.44	-.29
4. 154-day wt.				1.00	-.18	-.25	0.05	0.55
5. Carcass backfat					1.00	-.31	-.26	— ^a
6. Ham and loin percentage						1.00	0.99	— ^a
7. Loin eye area							1.00	— ^a
8. Backfat probe								1.00

^aNot estimable from these data.

Table 18. Genetic correlations for Hampshire breed

Trait	1	2	3	4	5	6	7	8
1. Total litter wt. at 56 days	1.00	— ^a	0.42	0.25	-1.02	-.95	-.09	0.35
2. Number weaned		1.00	-.14	-.08	-.02	-.57	0.41	0.26
3. 56-day wt.			1.00	0.70	0.52	-.60	-.28	— ^a
4. 154-day wt.				1.00	0.11	-.66	-.29	0.48
5. Carcass backfat					1.00	-.78	-.64	— ^a
6. Ham and loin percentage						1.00	0.52	— ^a
7. Loin eye area							1.00	— ^a
8. Backfat probe								1.00

^aNot estimable from these data.

Table 19. Genetic correlations for Poland breed

Trait	1	2	3	4	5	6	7	8
1. Total litter wt. at 56 days	1.00	1.00	0.33	0.34	0.17	-.11	-.01	0.80
2. Number weaned		1.00	-.14	0.05	0.17	-.05	0.03	0.48
3. 56-day wt.			1.00	0.60	0.28	-.47	-.47	— ^a
4. 154-day wt.				1.00	0.25	-.37	-.39	0.13
5. Carcass backfat					1.00	-.64	-.38	— ^a
6. Ham and loin percentage						1.00	0.80	— ^a
7. Loin eye area							1.00	— ^a
8. Backfat probe								1.00

^aNot estimable from these data.

Table 20. Genetic correlations for Yorkshire breed

Trait	1	2	3	4	5	6	7	8
1. Total litter wt. at 56 days	1.00	0.88	0.47	0.29	0.08	-.32	-.22	89.32
2. Number weaned		1.00	-.09	-.07	0.04	-.22	0.05	1.34
3. 56-day wt.			1.00	0.64	-10.89	-1.02	-2.81	-.32
4. 154-day wt.				1.00	0.44	-.75	-1.16	-61.48
5. Carcass backfat					1.00	-.63	-.55	— ^a
6. Ham and loin percentage						1.00	0.58	— ^a
7. Loin eye area							1.00	— ^a
8. Backfat probe								1.00

^aNot estimable from these data.

Table 21. Genetic correlations for pooled analysis

Trait	1	2	3	4	5	6	7	8
1. Total litter wt. at 56 days	1.00	0.93	0.51	0.36	0.09	-.26	0.01	35.90
2. Number weaned		1.00	0.04	0.11	0.11	-.17	0.14	0.73
3. 56-day wt.			1.00	0.66	0.12	-.37	-.43	-.11
4. 154-day wt.				1.00	0.21	-.41	-.29	-44.87
5. Carcass backfat					1.00	-.60	-.34	— ^a
6. Ham and loin percentage						1.00	0.72	— ^a
7. Loin eye area							1.00	— ^a
8. Backfat probe								1.00

^aNot estimable from these data.

$$r_{A_i A_j} = K_{s_i s_j} / \sqrt{K_{s_i}^2 K_{s_j}^2}, \text{ where the } K_s^2 \text{ represent}$$

sire quadratic effects obtained from the previously described least squares analysis. There were insufficient numbers of probed pigs with carcass data to allow estimation of genetic correlations between probe and carcass traits.

Pooled estimates of the genetic relationships among carcass traits from these data are in good agreement with those found in the literature. While sampling errors of genetic correlations estimated within a given breed are likely to be large, there appear to be some differences among breeds. A fairly strong genetic antagonism between performance and carcass cutability characteristics is evident in all but the Duroc breed. This antagonism is most pronounced in the Yorkshire line of breeding. Both of these observations are supported by similar relationships noted in the phenotypic correlations which were estimated by another procedure.

Since heritabilities involving littermate and progeny traits are based on family averages, estimates were needed of \bar{n} , the average number of family members contributing information to the family mean, and t , the phenotypic correlation among family members. An estimate of ρ , the repeatability of total litter weight at 56 days, was also needed.

The average size of families contributing to the variance of family averages was computed directly from the

data. Phenotypic correlations among family members and repeatability were estimated from comparison of the variances of individual measures and family averages. Falconer (1960) gives the relationship between these variances as:

$$\sigma_{\bar{X}}^2 = [1 + (n-1)t]\sigma_X^2/n$$

When n (in this case \bar{n} was used) is known, t (or ρ) can be estimated as: t (or ρ) = $[(\bar{n}\sigma_{\bar{X}}^2/\sigma_X^2) - 1]/(\bar{n} - 1)$. The

average family size, \bar{n} , and phenotypic correlations (or repeatability), t (or ρ), among family members are presented by breed in Tables 22 and 23 for each sex. It should be noted that estimates of the repeatability of total litter weight appear to be much too large. As a consequence, the heritability of average total weight of progeny litters at 56 days will probably be underestimated.

The heritability of a full sib or progeny family average, h_f^2 , may be computed as:

$$\begin{aligned} h_f^2 &= 0.5 \sigma_A^2 / \sigma_{\bar{X}}^2 \\ &= 0.5 h^2 \sigma_X^2 / \sigma_{\bar{X}}^2 \\ &= 0.5 nh^2 / [1 + (n-1)t] \end{aligned}$$

Table 22. Average size of family (\bar{n}) and phenotypic correlations (t) among family members by breed for boars

Trait	<u>Duroc</u>		<u>Hampshire</u>		<u>Poland</u>		<u>Yorkshire</u>		<u>Pooled</u>	
	\bar{n}	t	\bar{n}	t	\bar{n}	t	\bar{n}	t	\bar{n}	t
<u>Littermate ave.</u>										
Carcass backfat	2.38	0.37	2.02	0.32	1.97	0.12	2.23	0.41	2.14	0.32
Ham and loin %	2.38	0.49	2.02	0.37	1.97	0.14	2.23	0.46	2.14	0.37
Loin eye area	2.38	0.90	2.02	0.51	1.97	0.55	2.23	0.16	2.14	0.53
<u>Progeny ave.</u>										
154-day wt.	40.12	0.25	44.00	0.18	45.05	0.22	45.91	0.14	43.77	0.20
Carcass backfat	14.70	0.31	15.77	0.09	16.08	0.16	15.22	0.16	15.47	0.20
Ham and loin %	14.70	0.15	15.77	0.22	16.08	0.33	15.22	0.26	15.47	0.24
Loin eye area	14.70	0.45	15.77	0.21	16.08	0.30	15.22	0.22	15.47	0.30

Table 23. Average size of family (\bar{n}) and phenotypic correlations (t) among family members by breed for females

Trait	<u>Duroc</u>		<u>Hampshire</u>		<u>Poland</u>		<u>Yorkshire</u>		<u>Pooled</u>	
	\bar{n}	t	\bar{n}	t	\bar{n}	t	\bar{n}	t	\bar{n}	t
<u>Littermate ave.</u>										
Carcass backfat	2.00	0.31	2.09	0.15	2.08	0.32	2.25	0.38	2.10	0.32
Ham and loin %	2.00	0.40	2.09	0.25	2.08	0.57	2.25	0.50	2.10	0.46
Loin eye area	2.00	0.78	2.09	0.48	2.08	0.64	2.25	0.27	2.10	0.55
<u>Progeny ave.</u>										
Total litter wt.	1.69	0.84 ^a	1.83	0.53 ^a	1.78	0.80 ^a	1.74	0.63 ^a	1.76	0.76 ^a
154-day wt.	9.22	0.35	10.18	0.41	10.46	0.39	12.97	0.27	10.60	0.36
Carcass backfat	3.43	0.41	3.61	0.23	3.78	0.27	4.32	0.41	3.76	0.34
Ham and loin %	3.43	0.42	3.61	0.29	3.78	0.48	4.32	0.47	3.76	0.43
Loin eye area	3.43	0.61	3.61	0.38	3.78	0.45	4.32	0.33	3.76	0.45

^aRepeatability.

Selection Intensity

Dickerson and Hazel (1944a) note that annual improvement from selection is a function of selection intensity and generation interval. Selection intensity is dependent upon population size and the proportion of the population required as replacement breeding animals. A theoretically maximum population size could be based on the number of animals born, but this would require the assumption of 100 percent survival to selection age. Dickerson et al. (1954) suggest using the number of pigs surviving until weaning, when the first stage of culling occurs, as the base population for estimating potential maximum selection intensity.

The percentage of pigs born that survived until weaning, number weaned, number used in the breeding herd, percent used and potential maximum selection intensity, i_{\max} , for boar and gilt pigs are presented by breed in Table 24. Full-term stillborn pigs which had not been partially reabsorbed or mummified were included with pigs born alive in the total number of pigs born. Number of boars used includes 2 Duroc, 6 Hampshire, 1 Poland and 11 Yorkshire boars that were brought into the herd from outside sources. Neither foundation animals nor pigs born in 1969 were included in data presented in Table 24. The proportion of pigs weaned that entered the breeding herd in this study were about half as large as those reported by Dickerson et al. (1954) in their

Table 24. Percent weaned, number weaned, number used, percent used and potential maximum selection intensity for boars and gilts by breed

	Duroc	Hampshire	Poland	Yorkshire	Pooled
	<u>Population</u>				
Percent weaned	61.97	65.70	71.76	70.11	67.66
	<u>Boars</u>				
Number weaned	1,115	1,004	1,634	1,251	5,004
Number used	49	46	63	50	208
Percent used	4.39	4.58	3.86	4.00	4.16
i_{\max}	2.10	2.08	2.15	2.14	2.12
	<u>Gilts</u>				
Number weaned	1,178	980	1,621	1,177	4,956
Number used	221	194	329	196	940
Percent used	18.76	19.80	20.30	16.65	18.97
i_{\max}	1.44	1.41	1.40	1.50	1.43

evaluation of a 7-state cooperative Regional Swine Breeding Laboratory selection project. An average of 8.3 percent of boar pigs weaned and 33 percent of gilt pigs weaned were used as herd replacements in that Regional Swine Breeding Laboratory study.

Kinney and Shoffner (1967) use unweighted or expected selection differentials to represent selection that was intended to be applied to the population. They used comparisons of expected and realized or weighted selection differentials to provide information about the importance of natural selection in their broiler populations. Factors

other than natural selection would likely be included in the difference between expected and realized selection differentials in a swine population. Generation interval, differences in the numbers of litters sired by certain boars, and management differences which might favor the survival of progeny from certain individuals would also appear in the realized selection differentials of a swine population. Expected differentials computed from these data will be used to represent the level of intentional selection on preprogeny test records.

Kinney and Shoffner (1967) computed expected selection differentials using a formula similar to that which follows:

$$ES = \frac{\sum_i^n (X_{Si} - \bar{X})}{n}$$
 where ES represents the expected selection differential for a particular trait in a given sex, X_{Si} is the phenotype of the i th selected individual, \bar{X} is the population mean and n is the number of selected individuals in a given sex. Both expected and realized selection differentials are computed separately for each sex. ES and ED will be used to designate expected selection differentials for boars and gilts, respectively.

Preprogeny test boar selection involves two steps. Boars are initially culled by castration at weaning and then subjected to a second stage of culling prior to entering the breeding herd. The difference between the phenotypic averages of pigs which remain boars after weaning and all

male pigs comprises the expected differential resulting from the first stage of boar culling. The mean difference between boars which are selected for use in the breeding herd and all pigs which remained as boars after weaning is the expected selection differential from the second stage of boar culling. Expected selection differentials for two stages of preprogeny test selection in boars and for preprogeny test selection of gilts; the total expected selection differentials for boars, ES, and gilts, ED; and the net expected selection differential, EP, for a breed are presented in Table 25.

Dickerson and Hazel (1944a) have developed formulas for computing realized selection differentials and estimating genetic gain under systems of multistage or sequential selection. Examples of the application of these formulas in evaluation of response to selection for various species may be found in Dickerson et al. (1954), swine; Brinks, Clark and Kieffer (1965), beef cattle; and Kinney and Shoffner (1967), broilers.

Weighted or realized selection differentials represent the selection that was actually attained in the population. In addition to weighting individual parent selection differentials by the number of pigs weaned from those parents, realized selection differentials are commonly adjusted to a constant time interval base. Dickerson et al. (1954) note

Table 25. Expected selection differentials for boars and gilts by breed

Breed	Boars			Gilts	Net
	Stage 1	Stage 2	ES	ED	EP
<u>Number weaned</u>					
Duroc	0.083	0.397	0.480	0.261	0.300
Hampshire	0.134	-.462	-.328	0.088	0.120
Poland	0.292	-.386	-.094	0.224	0.065
Yorkshire	0.122	-.237	-.115	-.299	-.207
Pooled	0.171	-.176	-.004	0.096	0.046
<u>56-day weight, lb.</u>					
Duroc	5.19	1.61	6.80	2.44	4.62
Hampshire	5.22	0.94	6.16	3.71	4.94
Poland	4.84	-.34	4.50	3.37	3.94
Yorkshire	5.20	1.10	6.30	3.16	4.73
Pooled	5.09	0.72	5.81	3.18	4.49
<u>154-day weight, lb.</u>					
Duroc	24.43	7.50	31.94	12.51	22.12
Hampshire	20.24	10.00	30.24	13.83	22.04
Poland	14.39	6.16	20.55	10.13	15.34
Yorkshire	19.33	9.18	28.51	11.75	20.13
Pooled	19.17	7.94	27.11	11.79	19.45
<u>Littermate carcass backfat average, in.</u>					
Duroc	-.013	-.047	-.060	-.012	-.036
Hampshire	-.007	-.014	-.021	-.003	-.012
Poland	-.031	-.038	-.069	-.020	-.044
Yorkshire	0.013	0.006	0.019	-.016	.002
Pooled	-.013	-.026	-.038	-.014	-.026
<u>Littermate ham and loin percent average, %</u>					
Duroc	0.327	0.854	1.181	0.377	0.778
Hampshire	0.196	0.580	0.776	0.107	0.442
Poland	0.281	0.687	0.968	0.399	0.684
Yorkshire	0.124	0.295	0.419	0.285	0.352
Pooled	0.242	0.624	0.866	0.310	0.588

Table 25 (Continued)

Breed	Boars			Gilts	Net
	Stage 1	Stage 2	ES	ED	EP
<u>Littermate loin eye area average, sq. in.</u>					
Duroc	0.108	0.418	0.526	0.254	0.390
Hampshire	0.052	0.250	0.302	0.136	0.219
Poland	0.068	0.284	0.352	0.175	0.264
Yorkshire	0.108	0.317	0.425	0.147	0.286
Pooled	0.083	0.317	0.400	0.180	0.290
<u>Backfat probe, in.</u>					
Duroc	0.0	-.037	-.037	0.0	-.018
Hampshire	0.0	-.016	-.016	0.0	-.008
Poland	0.0	-.021	-.021	0.0	-.010
Yorkshire	0.0	-.066	-.066	0.0	-.033
Pooled	0.0	-.033	-.033	0.0	-.016

that average annual realized selection differentials provide a convenient basis for comparison of selection across different age groups of parents and among different breeding groups.

Proportions of progeny weaned from preprogeny test parent groups (under 2 years of age) and progeny tested parents and the weighted mean ages of each parental group are presented in Table 26. S1, S2, D1, D2, S, D and P are used to represent young sires (under 2 years of age), progeny tested sires, young dams (under 2 years of age), progeny tested dams, and sire, dam and breed population averages, respectively.

The weighted mean age of the i th parent group, T_i , was computed as follows:

$$T_i = \frac{\sum_{jk} n_{ijk} T_{ijk}}{\sum_{jk} n_{ijk}},$$

where n_{ijk} is the number of progeny weaned from the j th parent of the i th parent group in the k th year-season and T_{ijk} is the age of that parent in the k th year-season. The weighted mean age of the parent population (generation interval), \bar{T} was computed as:

$$\bar{T} = \frac{\sum_{ijk} n_{ijk} T_{ijk}}{\sum_{ijk} n_{ijk}}.$$

Table 26. Proportions of progeny weaned from young and progeny tested sires and dams and weighted mean ages of parental groups by breed

Parent group	Duroc	Hampshire	Poland	Yorkshire	Pooled
<u>Proportion of progeny weaned from parent groups</u>					
S1	0.69	0.70	0.72	0.61	0.68
S2	0.31	0.30	0.28	0.39	0.32
D1	0.69	0.68	0.74	0.67	0.70
D2	0.31	0.32	0.26	0.33	0.30
<u>Weighted mean age of parents, years</u>					
S1	1.23	1.21	1.21	1.23	1.22
S2	2.26	2.19	2.12	2.35	2.23
D1	1.23	1.17	1.16	1.23	1.19
D2	2.22	2.32	2.38	2.28	2.30
S	1.55	1.50	1.46	1.67	1.54
D	1.54	1.54	1.48	1.58	1.52
P	1.54	1.52	1.47	1.62	1.53

Yorkshire boars were used for a longer period of time than boars in the other breeds. Since older Yorkshire boars also sired a proportionally higher percentage of litters, the generation interval for the Yorkshire line of breeding was longer than for the other breeds. The Poland breeding group had the shortest generation interval as a result of proportionally more litters being from young parents. Also Poland boars were not used for as long a period of time as boars from the other breeds.

Formulas used to compute average annual realized selection differentials are basically those presented by

Dickerson et al. (1954) as adapted from Dickerson and Hazel (1944a). The increment of the j th boar's selection differential resulting from culling and castration at weaning shall be defined as:

$$S_{0j} = \bar{X}_{Bj} - \bar{X}_{Mj} ,$$

where \bar{X}_{Bj} is the average level of performance of all boar pigs not castrated or culled at weaning and \bar{X}_{Mj} is the average level of performance of all male pigs in the year-season of the j th boar's birth. Subsequent selection of boars to be retained for breeding results in an additional increment;

$$S_{1j} = X_{SBj} - \bar{X}_{Bj} ,$$

where X_{SBj} is the observed phenotype of the j th selected boar. Further selection of boars after progeny test records became available adds still another increment to the boars' selection differential, S_{2j} .

For performance and sib traits;

$$S_{2j} = (X_{SBj} - \bar{X}_{Bj}) - \frac{\sum_i^m (X_{SBi} - \bar{X}_{Bi})}{m} ,$$

where S_{2j} represents the deviation of the j th boar from the group of m contemporarily progeny tested boars from which he was selected. Records of each boar, X_{SBi} , in this contemporary group were deviated from appropriate year-season averages, \bar{X}_{Bi} , to adjust for year-season environmental

differences as recommended by Langholz (1965). The j th boar's deviate was included in the contemporary group average.

In the case of progeny test traits;

$$S_{2j} = \left[\sum_{k=1}^q n_{jk} (\bar{X}_{jk} - \bar{X}_k) / \sum_{k=1}^q n_{jk} \right] - \sum_{i=1}^m \left[\sum_{k=1}^q n_{ik} (\bar{X}_{ik} - \bar{X}_k) / \sum_{k=1}^q n_{ik} \right] / m ,$$

where S_{2j} represents the deviation of the j th boar's cumulative, deviated progeny average from the average of m contemporary boar progeny deviations, n_{jk} represents the number of progeny of the j th boar weaned in year-season k , \bar{X}_{jk} is the average level of performance of progeny of the j th boar in that year-season and \bar{X}_k is the population average in the k th year-season. Boar progeny averages were deviated from their appropriate year-season means and were accumulated over q year-seasons of boar usage. Progeny test selection differentials for year-season k were based on data that were available through year-season $k-2$. Data on progeny born in year-season $k-1$ were not available at the time matings were made for the k th year-season. An exception applies to selection differentials for average total weight of progeny litters at 56 days. Information on $k-1$ year-season litter performance was available before the k th year-season matings were made and was included in the k th year-season sow selection differentials.

Since gilts had no initial stage of culling, D_1 and D_2 ,

sequential increments of female selection differentials were calculated in the same manner as S_1 and S_2 , using the female population as a base for comparison.

Comparison of the relative contribution to realized selection differentials of young versus progeny tested parents can be accomplished by computing separate selection differentials for each sex and age group. The comparison of young and progeny tested parents should include some adjustment for the amount of time required to gather progeny test information. Use of annual realized selection differentials, averaged over q years;

$$s_1 = \frac{\sum_{i,j}^q \sum_{ij}^m n_{ij} (S_{0j} + S_{1j})}{\sum_{i,j}^q \sum_{ij}^m n_{ij} T_{ij}},$$

$$s_2 = \frac{\sum_{i,k}^q \sum_{ik}^p n_{ik} (S_{0k} + S_{1k} + S_{2k})}{\sum_{i,k}^q \sum_{ik}^p n_{ik} T_{ik}},$$

$$d_1 = \frac{\sum_{i,j}^q \sum_{ij}^m n_{ij} D_{1j}}{\sum_{i,j}^q \sum_{ij}^m n_{ij} T_{ij}},$$

$$d_2 = \frac{\sum_{i,k}^q \sum_{ik}^p n_{ik} (D_{1k} + D_{2k})}{\sum_{i,k}^q \sum_{ik}^p n_{ik} T_{ik}},$$

provide an equitable basis for comparison of the m young and p progeny tested parents of each sex.

The average annual realized selection differential for boars was computed as:

$$S = \frac{\sum_{i,j}^q [\sum_{ij}^m n_{ij} (S_{0j} + S_{1j}) + \sum_k^p n_{ik} (S_{0k} + S_{1k} + S_{2k})]}{[\bar{T} \sum_{i,j}^q (\sum_{ij}^m n_{ij} + \sum_k^p n_{ik})]}.$$

The average annual realized selection differential for dams was computed as:

$$D = \frac{\sum_{i,j}^q \sum_{ij}^m D_{1j} + \sum_{k}^p \sum_{ik} (D_{1k} + D_{2k})}{[\bar{T} \sum_{i,j}^q \sum_{ij}^m + \sum_{k}^p \sum_{ik}]}. \quad .$$

The net average annual realized selection differential for a breed is the unweighted mean of sire and dam selection differentials; i.e. $P = (S + D)/2$. Average annual realized selection differentials for young and progeny tested males and females are compared by breed and trait in Table 27.

With only a few exceptions the difference in age between young and progeny tested parents more than made up for any additional selection pressure on individual and sib information of progeny tested parents. Littermate ham and loin percentage averages on progeny tested Hampshire boars and sows and Yorkshire boars were enough higher than those on younger parents to overcome the time interval handicap. The same was true of littermate loin eye area averages on progeny tested Duroc, Hampshire and Yorkshire boars.

There was a tendency for older Yorkshire boars and sows to come from smaller litters than younger Yorkshire replacement animals. Progeny tested Poland boars and sows were substantially lighter at 154 days than younger Poland parents.

Dickerson et al. (1954) used s_2 and d_2 to represent the superiority of older boars and sows over those used at one year of age; i.e. $s_2 = \frac{\sum_{i,k}^q \sum_{ik}^p S_{2k}}{\sum_{i,k}^q \sum_{ik}^p (\bar{T}_{ik} - \bar{T}_{ij})}$, and similarly for d_2 , where \bar{T}_{ij} is the average age of the younger

Table 27. Realized selection differentials for sires and dams by breed

Breed	Sires			Dams			Net P
	s ₁	s ₂	S	d ₁	d ₂	D	
	<u>Number weaned</u>						
Duroc	0.299	-.131	0.106	0.134	0.249	0.185	0.146
Hampshire	-.347	0.056	-.171	0.071	0.030	0.052	-.059
Poland	-.151	0.001	-.090	0.308	0.094	0.218	0.064
Yorkshire	-.212	-.619	-.447	-.144	-.179	-.156	-.302
Pooled	-.107	-.222	-.160	0.109	0.039	0.077	-.042
	<u>56-day weight, lb.</u>						
Duroc	5.10	2.00	3.72	2.69	1.41	2.10	2.91
Hampshire	4.88	2.07	3.62	3.30	1.68	2.55	3.08
Poland	3.71	1.25	2.70	3.12	0.84	2.16	2.43
Yorkshire	3.59	2.32	2.98	2.38	1.85	2.07	2.52
Pooled	4.23	1.91	3.18	2.87	1.42	2.20	2.69
	<u>154-day weight, lb.</u>						
Duroc	24.97	9.14	17.92	11.17	5.83	8.73	13.32
Hampshire	23.18	14.26	19.05	11.27	4.72	8.21	13.63
Poland	15.85	4.43	11.20	8.98	0.55	5.44	8.32
Yorkshire	15.99	10.02	13.10	8.23	4.72	6.38	9.74
Pooled	19.39	9.10	14.73	9.71	3.73	6.96	10.84

Table 27 (Continued)

Breed	Sires			Dams			Net P
	s ₁	s ₂	S	d ₁	d ₂	D	
<u>Littermate carcass backfat average, in.</u>							
Duroc	-.035	0.003	-.018	-.019	0.006	-.007	-.013
Hampshire	-.016	-.022	-.018	-.004	-.011	-.007	-.013
Poland	-.053	-.016	-.038	-.024	-.033	-.028	-.033
Yorkshire	0.014	-.028	-.009	-.016	-.001	-.009	-.009
Pooled	-.026	-.017	-.022	-.017	-.011	-.014	-.018
<u>Littermate ham and loin percentage average, %</u>							
Duroc	0.915	0.572	0.763	0.310	0.045	0.190	0.476
Hampshire	0.494	0.468	0.476	0.125	0.164	0.146	0.311
Poland	0.823	0.442	0.666	0.386	0.362	0.378	0.522
Yorkshire	0.255	0.422	0.357	0.290	0.156	0.220	0.288
Pooled	0.644	0.468	0.565	0.295	0.195	0.248	0.407
<u>Littermate loin eye area average, sq. in.</u>							
Duroc	0.445	0.574	0.504	0.180	0.106	0.146	0.325
Hampshire	0.281	0.230	0.255	0.143	0.092	0.120	0.188
Poland	0.311	0.098	0.224	0.161	0.053	0.116	0.170
Yorkshire	0.236	0.262	0.258	0.130	0.096	0.110	0.184
Pooled	0.317	0.278	0.300	0.154	0.084	0.122	0.211

Table 27 (Continued)

Breed	Sires			Dams			Net P
	s ₁	s ₂	S	d ₁	d ₂	D	
<u>Backfat probe, in.</u>							
Duroc	-.036	-.016	-.027	0.0	0.0	0.0	-.014
Hampshire	-.014	0.002	-.007	0.0	0.0	0.0	-.003
Poland	-.017	-.023	-.019	0.0	0.0	0.0	-.010
Yorkshire	-.043	-.030	-.037	0.0	0.0	0.0	-.018
Pooled	-.026	-.019	-.023	0.0	0.0	0.0	-.012
<u>Average total weight of progeny litters at 56 days, lb.</u>							
Duroc	0.0	0.0	0.0	0.0	16.25	7.33	3.66
Hampshire	0.0	0.0	0.0	0.0	13.85	6.82	3.41
Poland	0.0	0.0	0.0	0.0	19.27	8.24	4.12
Yorkshire	0.0	0.0	0.0	0.0	18.37	8.42	4.21
Pooled	0.0	0.0	0.0	0.0	17.20	7.81	3.90
<u>Progeny 154-day weight average, lb.</u>							
Duroc	0.0	-.34	-.15	0.0	0.62	0.28	0.06
Hampshire	0.0	0.88	0.37	0.0	-.30	-.15	0.11
Poland	0.0	-2.45	-.98	0.0	0.62	0.27	-.35
Yorkshire	0.0	0.19	0.11	0.0	0.63	0.29	0.20
Pooled	0.0	-.51	-.24	0.0	0.42	0.19	-.02

Table 27 (Continued)

Breed	Sires			Dams			Net P
	s ₁	s ₂	S	d ₁	d ₂	D	
<u>Progeny carcass backfat average, in.</u>							
Duroc	0.0	0.007	0.003	0.0	-.008	-.004	-.000
Hampshire	0.0	-.003	-.001	0.0	0.004	0.002	0.000
Poland	0.0	-.008	-.003	0.0	-.010	-.004	-.004
Yorkshire	0.0	0.004	0.002	0.0	-.000	-.000	0.001
Pooled	0.0	0.000	0.000	0.0	-.004	-.002	-.001
<u>Progeny ham and loin percentage average, %</u>							
Duroc	0.0	0.078	0.035	0.0	0.073	0.033	0.034
Hampshire	0.0	0.029	0.012	0.0	-.041	-.020	-.004
Poland	0.0	0.230	0.091	0.0	0.114	0.049	0.070
Yorkshire	0.0	0.001	0.000	0.0	0.024	0.011	0.006
Pooled	0.0	0.085	0.039	0.0	0.047	0.021	0.030
<u>Progeny loin eye area average, sq. in.</u>							
Duroc	0.0	0.135	0.061	0.0	0.015	0.007	0.034
Hampshire	0.0	0.035	0.015	0.0	0.011	0.005	0.010
Poland	0.0	0.111	0.044	0.0	0.012	0.005	0.025
Yorkshire	0.0	0.027	0.015	0.0	-.005	-.002	0.006
Pooled	0.0	0.074	0.034	0.0	0.008	0.003	0.019

age group of a particular sex. As used in this presentation s_2 and d_2 represent the entire selection differential attributable to older boars and sows. Dickerson's usage of s_2 and d_2 requires assumptions that preprogeny test selection is consistent over time and that preprogeny test selection differentials are the same for young and older parents.

Standardized selection differentials provide a basis for comparing differences in selection intensity across breeds, among traits or between sexes. Potentially maximum selection intensities can be compared with the realized selection intensity of each trait when realized selection differentials are standardized. Potentially maximum selection intensities were previously presented in Table 24. Expected and realized selection intensities are contrasted in Table 28.

The selection intensity for each sex is the sum of selection intensities computed independently for each stage of selection. Expected, i_{ES} and i_{ED} , and realized, i_S and i_D , selection intensities were computed as follows:

$$i_{ES} = [(\bar{X}_B - \bar{X}_M)/\sigma_M] + [(\bar{X}_{SB} - \bar{X}_B)/\sigma_B]$$

$$i_{ED} = [(\bar{X}_{SG} - \bar{X}_G)/\sigma_G]$$

$$i_S = \left[\left(\frac{\sum_j n_j S_{0j}}{\sum_j n_j} \right) / \sigma_M \right] + \left[\left(\frac{\sum_j n_j S_{1j}}{\sum_j n_j} \right) / \sigma_B \right] + \left[\left(\frac{\sum_j n_j S_{2j}}{\sum_j n_j} \right) / \sigma_{SB} \right] / \sum_j n_j \bar{T}$$

$$i_D = \left[\left(\frac{\sum_j n_j D_{1j}}{\sum_j n_j} \right) / \sigma_G \right] + \left[\left(\frac{\sum_j n_j D_{2j}}{\sum_j n_j} \right) / \sigma_{SG} \right] / \sum_j n_j \bar{T}$$

where n_j represents the number of progeny weaned by the i th

Table 28. Expected and realized selection intensities for sires and dams by breed

Breed	Expected			Realized		
	i_{ES}	i_{ED}	i_{EP}	i_S	i_D	i_P
<u>Number weaned</u>						
Duroc	0.214	0.118	0.166	0.038	0.082	0.060
Hampshire	-.196	0.041	-.077	-.099	0.024	-.037
Poland	-.064	0.111	0.024	-.055	0.104	0.025
Yorkshire	-.065	-.132	-.099	-.215	-.069	-.142
Pooled	-.011	0.044	0.017	-.086	0.035	-.025
<u>56-day weight</u>						
Duroc	0.829	0.273	0.551	0.451	0.235	0.343
Hampshire	0.761	0.446	0.604	0.457	0.309	0.383
Poland	0.534	0.414	0.474	0.308	0.258	0.283
Yorkshire	0.764	0.388	0.576	0.369	0.259	0.314
Pooled	0.704	0.380	0.542	0.384	0.262	0.323
<u>154-day weight</u>						
Duroc	1.127	0.477	0.802	0.608	0.327	0.467
Hampshire	1.145	0.530	0.838	0.738	0.316	0.527
Poland	0.842	0.446	0.644	0.432	0.218	0.325
Yorkshire	1.014	0.499	0.756	0.480	0.271	0.375
Pooled	1.017	0.482	0.749	0.546	0.276	0.411
<u>Littermate carcass backfat average</u>						
Duroc	-.437	-.088	-.262	-.110	-.049	-.079
Hampshire	-.196	-.027	-.111	-.151	-.068	-.110
Poland	-.617	-.178	-.398	-.318	-.229	-.273
Yorkshire	0.143	-.121	0.011	-.065	-.061	-.063
Pooled	-.315	-.114	-.214	-.163	-.108	-.136
<u>Littermate ham and loin percentage average</u>						
Duroc	0.843	0.268	0.555	0.503	0.127	0.315
Hampshire	0.640	0.095	0.367	0.371	0.121	0.246
Poland	0.810	0.307	0.558	0.549	0.284	0.417
Yorkshire	0.345	0.231	0.288	0.283	0.165	0.224
Pooled	0.691	0.242	0.466	0.427	0.184	0.306

Table 28 (Continued)

Breed	Expected ^a			Realized		
	i _{ES}	i _{ED}	i _{EP}	i _S	i _D	i _P
<u>Littermate loin eye area average</u>						
Duroc	0.992	0.497	0.744	0.836	0.258	0.547
Hampshire	0.491	0.272	0.381	0.480	0.228	0.354
Poland	0.694	0.341	0.518	0.404	0.205	0.304
Yorkshire	1.057	0.354	0.706	0.629	0.252	0.440
Pooled	0.819	0.368	0.593	0.563	0.230	0.396
<u>Backfat probe</u>						
Duroc	-.265	0.0	-.132	-.194	0.0	-.097
Hampshire	-.128	0.0	-.064	-.066	0.0	-.033
Poland	-.158	0.0	-.079	-.149	0.0	-.075
Yorkshire	-.476	0.0	-.238	-.269	0.0	-.134
Pooled	-.256	0.0	-.128	-.180	0.0	-.090
<u>Average total weight of progeny litters at 56 days</u>						
Duroc				0.0	0.069	0.035
Hampshire				0.0	0.076	0.038
Poland				0.0	0.084	0.042
Yorkshire				0.0	0.076	0.038
Pooled				0.0	0.077	0.039
<u>Progeny 154-day weight average</u>						
Duroc				-.010	0.015	0.002
Hampshire				0.030	-.008	0.011
Poland				-.079	0.016	-.032
Yorkshire				0.010	0.019	0.014
Pooled				-.018	0.011	-.004
<u>Progeny carcass backfat average</u>						
Duroc				0.027	-.026	0.001
Hampshire				-.026	0.021	-.003
Poland				-.044	-.041	-.042
Yorkshire				0.028	-.000	0.014
Pooled				0.000	-.015	-.007

^aExpected selection intensities are not applicable to progeny test traits.

Table 28 (Continued)

Breed	Expected ^a			Realized		
	i _{ES}	i _{ED}	i _{EP}	i _S	i _D	i _P
<u>Progeny ham and loin percentage average</u>						
Duroc				0.045	0.025	0.035
Hampshire				0.015	-.019	-.002
Poland				0.098	0.041	0.070
Yorkshire				0.000	0.009	0.005
Pooled				0.045	0.018	0.032
<u>Progeny loin eye area average</u>						
Duroc				0.146	0.013	0.079
Hampshire				0.048	0.012	0.030
Poland				0.120	0.011	0.065
Yorkshire				0.051	-.006	0.022
Pooled				0.095	0.007	0.051

parent, σ_M , σ_B , σ_{SB} , σ_G and σ_{SG} represent the standard deviations of all males, boars surviving culling at weaning, selected boars, all gilts and selected gilts, respectively. Net selection intensities were computed as the unweighted average of male and female selection intensities as follows:

$$i_{EP} = (i_{ES} + i_{ES})/2$$

$$i_P = (i_S + i_D)/2 \quad .$$

Realized selection intensities will generally be smaller than expected selection intensities because of the inclusion of generation interval in the equation for computing realized selection intensity. Several boars from outside sources were included in these data. The fact that these boars were given zero selection differentials for preprogeny test traits would probably result in underestimation of the actual realized selection intensities. Boars from outside sources were not included in computation of expected selection intensities.

The selection intensities in Table 28 point out the fact that very little attention was given to number weaned in the litters of selected replacements. Carcass backfat measurements on littermates received very little attention in the selection program. It was surprising that backfat probes were given little emphasis in all but the Yorkshire breed.

The differences among breeds in the attention given to different traits suggests that some effort was made to im-

prove certain deficiencies in particular lines of breeding. The Hampshire line averaged about 10 pounds less at 154 days than the other breed groups. Realized selection intensity for 154-day weight was greatest in the Hampshire line. Littermate loin eye area averages received the most attention in the Duroc and Yorkshire breeding groups where loin eye areas were relatively deficient.

Selection intensities for females were generally much lower than for males. Based on the potential maximum selection intensities, the realized differences between males and females indicate that more careful attention could have been given to the selection of female replacements.

Selection Indexes

While no index was used to select breeding animals in this study, an index can be constructed in retrospect to characterize the selection that was practiced. Dickerson et al. (1954) have demonstrated the method involved in computing an index in retrospect from realized selection intensities and phenotypic correlations. Harvey and Bearden (1962) have used essentially the same formulation in developing tables of expected genetic progress in each of two traits with varying genetic parameters and intensities of selection. Brinks, Clark and Kieffer (1965) present an example of the practical application of these formulas in

their study of response to selection in a closed line of Hereford cattle.

A posteriori knowledge of the phenotypic and genetic parameters of these data allow construction of an "idealized" selection index that might have been used as a criteria for selecting animals on the basis of net genetic worth. Hazel (1943) presented the principles for constructing and using a selection index which would permit the attainment of maximum genetic progress in net genetic merit of an animal population. Comparison of estimated genetic gain resulting from realized selection, as described by the index in retrospect, and that which might have occurred from selection on some "idealized" selection index may provide some insight into the effectiveness of selection for meatiness as a means of increasing the efficiency with which high quality pork is produced.

Hazel (1943) noted that when indexes are computed in standard measure, the resulting index weights will be standard partial regression coefficients. Snedecor (1956) indicated that standard partial regression coefficients provide a sound basis for comparing the relative weights given traits which differ in variability. To facilitate the comparison of selection emphasis given to different traits and give validity to comparisons across breeds where unequal variation has previously been noted, all

indexes were computed in standard measure.

The phenotypic correlations, realized average annual selection differentials and genetic parameters used to construct the index in retrospect and "idealized" index were those presented in previous sections, with the following exceptions.

Negative heritability estimates were replaced with a value of 0.0001. Theoretically the heritability of a trait cannot be less than zero. The value 0.0001 was chosen as a matter of computational convenience to be a more realistic estimate of the population parameter than a negative estimate.

Estimates of genetic correlations that were greater than 1.0 or less than -1.0 were replaced with 1.0 or -1.0, depending upon the sign of the estimate.

Genetic parameter estimates involving backfat probe were replaced with corresponding estimates involving carcass backfat. Genetic parameter estimates involving backfat probes appear to fluctuate greatly and were subject to larger sampling variances than genetic parameter estimates involving other traits. Additionally, genetic correlations between backfat probe and carcass traits were not estimable from these data. Hazel and Kline (1952) developed the backfat probe as a means of measuring backfat thickness on live pigs. They noted that the phenotypic correlations of lean loin area and percent primal cuts with carcass backfat and

probed backfat, respectively, were not significantly different. Arganosa, Omtvedt and Walters (1969) found the genetic correlations involving probe and carcass backfat with loin eye area and percent lean cuts to be nearly identical. The genetic relationship between backfat probe and carcass backfat was set equal to 1.0 on the assumption that genetic differences in backfat probes were exactly proportional to genetic differences in carcass backfat.

Hazel (1943) noted that estimates of the economic importance of traits included in a multiple trait index were needed to construct the index. It is beyond the scope of this study to go into the detailed procedures needed to obtain accurate estimates of economic weights. Robison, Chapman and Self (1960) have reported a set of economic weights that would appear to realistically apply to these data. They found that each additional pig produced increased net profits by \$2.18. An additional increase of one percent in lean cut percentage was found to increase net returns by \$.29. An additional pound of weight per individual pig at 154 days meant an increase of \$.109 in net profit. It was assumed that their economic weights would be satisfactory estimates of the economic value of number weaned, ham and loin percentage and 154-day weight as measured in these data. It was assumed that the same set of economic values would be equally applicable to all the breeding groups included in

this study. Other traits of interest; 56-day weight, carcass backfat and loin eye area; were considered as indicator traits and assigned zero economic weights.

Since the "idealized" index was to be expressed in units of standard measure, it was necessary to convert the economic values to units of standard measure. The economic value of trait i , a_i , was converted to a standardized economic weight, e_i , as follows:

$$e_i = a_i \sigma_i$$

where σ_i is the phenotypic standard deviation, pooled across sexes, of the i th trait. Standardized economic weights computed separately for each breed are presented in Table 29.

Table 29. Standardized economic weights by trait and breed

Trait	Duroc	Hampshire	Poland	Yorkshire	Pooled
Number weaned	\$5.12	\$4.58	\$4.49	\$4.91	\$4.76
56-day wt.	0.00	0.00	0.00	0.00	0.00
154-day wt.	3.23	3.03	2.77	2.95	2.98
Carcass backfat	0.00	0.00	0.00	0.00	0.00
Ham and loin %	0.50	0.44	0.44	0.45	0.46
Loin eye area	0.00	0.00	0.00	0.00	0.00

Weights for the indexes in retrospect were obtained as solutions to equations 1.

$$\begin{aligned}
 & B_1 + r_{x_1 x_2} B_2 + \dots + r_{x_1 x_N} B_N = i_{p_1} \\
 (1) \quad & r_{x_2 x_1} B_1 + B_2 + \dots + r_{x_2 x_N} B_N = i_{p_2} \\
 & \quad \cdot \quad \quad \cdot \quad \quad \quad \cdot \quad \quad \cdot \\
 & \quad \cdot \quad \quad \cdot \quad \quad \quad \cdot \quad \quad \cdot \\
 & \quad \cdot \quad \quad \cdot \quad \quad \quad \cdot \quad \quad \cdot \\
 & r_{x_N x_1} B_1 + r_{x_N x_2} B_2 + \dots + B_N = i_{p_N}
 \end{aligned}$$

"Idealized" selection index weights were obtained from a procedure described by Henderson (1963). Separate indexes were constructed for each of the constituent traits; i.e. number weaned, 56-day weight, 154-day weight, carcass back-fat, ham and loin percentage and loin eye area. "Idealized" selection index weights were then obtained by weighting the constituent index standard partial regression coefficients by the standardized economic value of the appropriate constituent trait.

Constituent selection index weights for the j th trait were obtained as solutions to equations 2.

$$\begin{aligned}
 & b_{1j} + r_{x_1 x_2} b_{2j} + \dots + r_{x_1 x_N} b_{Nj} = r_{x_1 A_j} h_j \\
 (2) \quad & r_{x_2 x_1} b_{1j} + b_{2j} + \dots + r_{x_2 x_N} b_{Nj} = r_{x_2 A_j} h_j \\
 & \quad \cdot \quad \quad \cdot \quad \quad \quad \cdot \quad \quad \cdot \\
 & \quad \cdot \quad \quad \cdot \quad \quad \quad \cdot \quad \quad \cdot \\
 & \quad \cdot \quad \quad \cdot \quad \quad \quad \cdot \quad \quad \cdot \\
 & r_{x_N x_1} b_{1j} + r_{x_N x_2} b_{2j} + \dots + b_{Nj} = r_{x_N A_j} h_j
 \end{aligned}$$

In equations 2, $r_{x_k A_j}$ refers to the accuracy with which the breeding value, A , of trait j is estimated by phenotypic observations on trait k , x_k , and h_j refers to the square root of the heritability of trait j . A general formula for $r_{x_k A_j}$ is:

$$r_{x_k A_j} = r_{A_j A_k} h_{f_k} = r_{A_j A_k} \alpha_k h_k \sqrt{\bar{n}_k / [1 + (\bar{n}_k - 1) t_k]}$$

where $r_{A_j A_k}$ is the genetic correlation between traits j and k , α_k is the numerator of Wright's (1922) coefficient of the relationship between the individual indexed and the pedigree source of the x_k phenotypic measurement, h_k is the square root of the heritability of trait k , \bar{n}_k is the average number of family members (or repeated records) in the k th phenotypic observation and t_k (or ρ_k) is the phenotypic correlation between family members (or repeated observations) in the k th phenotypic observation. It should be noted that number weaned is a trait measured on the dam of an individual pig, i.e. $\alpha = 0.5$. Traits measured directly on individuals being indexed include 56-day weight, 154-day weight, backfat probe and the average total weight of progeny litters at 56 days, i.e. $\alpha = 1.0$. The latter involves repeated observations on the same sow. For traits involving littermate and progeny averages α was set equal to 0.5.

"Idealized" selection index weights were obtained as

follows:

$$"I" = \sum_j e_j I_j \quad .$$

An individual "idealized" selection index weight, b_k , was computed as:

$$b_k = \sum_j e_j b_{kj} \quad .$$

The procedure used for constructing the "idealized" selection index as taken from Henderson (1963) is equivalent to methods given by Hazel (1943) but is more adaptable to conditions where change in economic values occurs or where it may be desirable to compare alternative sets of economic values. Also, the standard deviation of each constituent index, I_j , provides a measure of the potential annual genetic change in the j th trait; i.e.

$$\Delta G_j = i_{\max} r_{I_j H} \sigma_H / \bar{T} = i_{\max} \sigma_{I_j} / \bar{T} \quad .$$

where \bar{T} is the average generation interval.

"Idealized" selection index weights could have been obtained directly as solutions to equations 3, using the method presented by Hazel (1943). Where $"I" = \sum_k b_k (X_k - \bar{X}_k) / \sigma_{X_k}$ and $H = \sum_j a_j A_j$, a set of standardized normal equations (equations 3) can be obtained by minimizing $E(H - "I")^2$ with respect to the b_k 's. As Hazel (1943) notes the b_k 's are in fact standard partial regression coefficients, i.e.

$$b_k = \beta_k \sigma_{X_k} / \sigma_H \quad .$$

$$b_1 + r_{x_1 x_2} b_2 + \dots + r_{x_1 x_N} b_N = \sigma_{x_1 H}$$

$$r_{X_N X_1} b_1 + r_{X_N X_2} b_2 + \dots + b_N = \sigma_{X_N H}$$

where,

$$\sigma_{X_k H} = \sum_j a_j \sigma_{A_k A_j} / \sigma_{X_k}$$

or

$$\sigma_{X_k H} = \sum_j e_j r_{A_k A_j} h_k h_j$$

Solving equations 1 for each sex and breed group gives an index in retrospect,

$$I = B_1(X_1 - \bar{X}_1)/\sigma_{X_1} + B_2(X_2 - \bar{X}_2)/\sigma_{X_2} + \dots + B_N(X_N - \bar{X}_N)/\sigma_{X_N} \quad ,$$

which describes the average selection that was practiced in each breed and sex group. Solving equations 2 for each trait in each breed and sex group results in a constituent index,

$$I_j = b_{1j}(x_1 - \bar{x}_1)/\sigma_{x_1} + b_{2j}(x_2 - \bar{x}_2)/\sigma_{x_2} + \dots + b_{Nj}(x_N - \bar{x}_N)/\sigma_{x_N},$$

for each trait in every breed and sex group. Weighting constituent indexes by their corresponding standardized economic value yields the "idealized" index,

$$"I" = b_1 (X_1 - \bar{X}_1) / \sigma_{X_1} + b_2 (X_2 - \bar{X}_2) / \sigma_{X_2} + \dots + b_N (X_N - \bar{X}_N) / \sigma_{X_N} ,$$

for each breed and sex group.

Standard partial regression coefficients and standard deviations of the index in retrospect, "idealized" index and constituent indexes are presented for each breed and sex in Tables 30 through 39. The standard partial regression coefficients of the index in retrospect represent the average amount of attention given each item of information for a particular sex within each breed.

The differences between sexes in the average amount of selection actually practiced in all breeds were markedly greater than estimates of the potential selection opportunity indicate they should have been. It is evident that attention given to female selection was minimal.

Weight at 154 days received considerable emphasis in all breeds. In the Duroc and Yorkshire breeds littermate loin eye area averages were given at least twice as much emphasis as sib ham and loin percentages. Littermate ham and loin percentage averages were relatively more important in selection of Hampshire and Poland boars. Backfat probes received relatively little attention in the selection of boars from all but the Yorkshire breed.

Comparison of the index in retrospect with the "idealized" index shows that more attention might have been given to number weaned and to progeny averages. Comparison of the index in retrospect with the constituent index for ham

Table 30. Standard partial regression coefficients and standard deviations of the index in retrospect, "idealized" index and constituent indexes for Duroc boars

Trait ^a	Index in retrospect	"Idealized" index	Constituent indexes					
			Number weaned	56-day weight	154-day weight	Carcass backfat	Ham and loin %	Loin eye area
1	-.02	0.47	0.05	0.02	0.07	0.03	-.02	0.01
2	0.26	-.80	0.01	0.12	-.26	0.07	-.05	-.25
3	0.47	1.52	0.03	-.02	0.42	-.02	-.02	0.17
4	0.28	-1.26	-.05	-.12	-.30	0.39	-.04	-.11
5	0.36	-1.56	-.08	-.08	-.32	0.49	-.15	-.31
6	0.73	1.68	0.13	0.05	0.28	-.48	0.23	0.46
7	-.17	-.45	0.02	-.09	-.16	0.27	-.02	-.08
8	0.08	1.89	0.10	0.14	0.43	-.25	-.03	0.06
9	0.00	-.86	-.04	-.12	-.20	0.40	-.05	-.07
10	-.10	-1.52	-.11	-.14	-.30	0.27	0.03	0.05
11	-.23	0.39	0.04	-.07	0.04	0.02	0.12	0.28
σ_I	1.08	2.45	0.14	0.25	0.58	0.49	0.26	0.58

^aTraits as described by reference numbers in Table 10.

Table 31. Standard partial regression coefficients and standard deviations of the index in retrospect, "idealized" index and constituent indexes for Duroc sows

Trait ^a	Index in retrospect	"Idealized" index	Constituent indexes					
			Number weaned	56-day weight	154-day weight	Carcass backfat	Ham and loin %	Loin eye area
1	0.08	0.41	0.05	0.01	0.05	0.05	-.02	0.02
2	0.05	-.86	-.00	0.14	-.26	-.03	-.04	-.24
3	0.29	1.70	0.05	-.01	0.45	0.00	-.06	0.10
4	0.00	-.29	0.01	0.05	-.09	0.26	-.06	-.10
5	-.07	-.63	-.06	-.06	-.09	0.21	-.07	-.13
6	0.37	0.97	0.10	0.00	0.12	-.14	0.15	0.37
7	0.12	1.00	0.15	0.10	0.07	0.05	-.01	0.12
8	-.02	0.84	0.02	-.00	0.23	-.03	-.01	0.07
9	0.03	0.03	0.04	-.04	-.04	0.29	-.06	-.06
10	0.06	-.47	-.03	-.02	-.08	0.23	-.10	-.15
11	-.17	0.18	0.02	-.07	-.01	-.15	0.20	0.38
σ_I	0.46	2.17	0.18	0.22	0.47	0.32	0.25	0.55

^aTraits as described by reference numbers in Table 10.

Table 32. Standard partial regression coefficients and standard deviations of the index in retrospect, "idealized" index and constituent indexes for Hampshire boars

Trait ^a	Index in retrospect	"Idealized" index	Constituent indexes					
			Number weaned	56-day weight	154-day weight	Carcass backfat	Ham and loin %	Loin eye area
1	0.06	0.41	-.00	0.08	0.14	-.02	-.05	-.03
2	0.03	0.47	0.00	0.34	0.20	0.31	-.34	-.18
3	0.80	0.46	-.00	-.03	0.16	-.11	-.04	-.02
4	0.15	-.43	-.00	0.02	-.13	0.16	-.07	-.09
5	0.49	0.02	-.01	-.13	-.02	-.22	0.26	-.05
6	0.16	-.07	0.00	0.06	-.02	0.05	-.07	0.18
7	-.10	-.36	-.00	0.01	-.11	0.13	-.06	-.09
8	-.07	1.16	-.00	0.17	0.40	-.14	-.07	-.05
9	-.13	-.68	-.00	0.18	-.18	0.43	-.30	-.19
10	-.28	-.77	-.01	-.10	-.28	-.03	0.25	-.16
11	0.04	-.36	0.01	0.03	-.04	0.00	-.05	0.45
σ_I	0.92	1.48	0.01	0.37	0.54	0.45	0.54	0.57

^aTraits as described by reference numbers in Table 10.

Table 33. Standard partial regression coefficients and standard deviations of the index in retrospect, "idealized" index and constituent indexes for Hampshire sows

Trait ^a	Index in retrospect	"Idealized" index	Constituent indexes					
			Number weaned	56-day weight	154-day weight	Carcass backfat	Ham and loin %	Loin eye area
1	0.05	-.04	-.00	0.00	-.01	0.01	0.01	-.03
2	0.18	-.16	0.00	0.15	-.05	0.15	-.03	0.03
3	0.20	0.90	-.00	0.05	0.32	-.08	-.16	-.13
4	0.00	-.33	-.00	0.02	-.10	0.10	-.02	-.09
5	0.03	-.34	-.01	-.07	-.13	-.06	0.17	-.09
6	0.21	-.01	0.00	0.00	-.01	-.04	0.01	0.27
7	0.06	-.17	-.00	-.05	-.06	-.02	0.04	-.01
8	-.05	0.53	-.00	0.10	0.19	-.00	-.10	-.07
9	-.02	-.34	-.00	0.02	-.10	0.11	-.04	-.11
10	-.04	-.49	-.01	-.09	-.18	-.05	0.20	-.09
11	0.00	-.02	0.00	0.00	-.02	-.05	0.02	0.31
σ_I	0.42	1.17	0.01	0.26	0.43	0.27	0.40	0.45

^aTraits as described by reference numbers in Table 10.

Table 34. Standard partial regression coefficients and standard deviations of the index in retrospect, "idealized" index and constituent indexes for Poland boars

Traits ^a	Index in retrospect	"Idealized" index	Constituent indexes					
			Number weaned	56-day weight	154-day weight	Carcass backfat	Ham and loin %	Loin eye area
1	0.03	0.20	0.05	-.01	-.01	-.06	0.05	0.04
2	0.02	-.18	-.01	0.08	-.03	0.18	-.09	-.10
3	0.58	0.57	0.02	-.01	0.17	-.04	0.05	0.10
4	-.09	0.10	0.01	0.02	0.03	0.24	-.08	-.08
5	0.46	0.15	-.00	-.04	0.00	-.20	0.32	0.16
6	0.20	-.03	0.01	-.01	-.04	0.09	0.08	0.24
7	-.14	0.11	0.03	0.03	0.02	0.35	-.16	-.06
8	-.01	0.47	0.00	0.06	0.16	0.01	0.05	-.04
9	0.01	0.40	0.04	0.07	0.11	0.59	-.26	-.16
10	-.21	0.37	0.01	0.07	0.11	0.39	0.04	-.23
11	0.38	-.08	0.02	-.10	-.10	-.22	0.27	0.65
σ_I	0.82	0.80	0.08	0.15	0.27	0.71	0.67	0.66

^aTraits as described by reference numbers in Table 10.

Table 35. Standard partial regression coefficients and standard deviations of the index in retrospect, "idealized" index and constituent indexes for Poland sows

Trait ^a	Index in retrospect	"Idealized" index	Constituent indexes					
			Number weaned	56-day weight	154-day weight	Carcass backfat	Ham and loin %	Loin eye area
1	0.13	0.15	0.03	-.01	-.01	-.02	0.03	0.01
2	0.17	-.38	-.02	0.06	-.09	0.05	-.03	-.02
3	0.17	0.68	0.01	0.02	0.22	-.04	0.00	-.04
4	-.14	0.07	0.02	0.00	-.00	0.23	-.02	0.01
5	0.21	0.06	-.01	-.02	0.01	-.00	0.21	0.05
6	0.08	0.04	0.02	-.03	-.04	-.05	0.09	0.24
7	0.06	0.48	0.11	0.01	-.00	0.03	-.00	0.05
8	-.01	0.14	-.03	0.03	0.10	-.01	0.00	-.02
9	-.00	0.13	0.03	0.02	0.01	0.32	-.09	-.05
10	0.08	0.15	0.01	-.01	0.00	0.04	0.22	0.04
11	-.08	-.09	0.00	-.03	-.05	-.06	0.09	0.29
σ_I	0.45	0.82	0.12	0.12	0.23	0.42	0.49	0.49

^aTraits as described by reference numbers in Table 10.

Table 36. Standard partial regression coefficients and standard deviations of the index in retrospect, "idealized" index and constituent indexes for Yorkshire boars

Trait	Index in retrospect	"Idealized" index	Constituent indexes					
			Number weaned	56-day weight	154-day weight	Carcass backfat	Ham and loin %	Loin eye area
1	-.03	0.00	0.03	-.16	-.05	-.01	-.03	0.09
2	0.27	0.25	-.04	0.45	0.25	-.74	-.65	-.86
3	0.63	0.25	-.01	-.02	0.05	0.39	0.30	0.09
4	0.17	-.24	-.03	-.69	-.07	0.29	0.19	0.01
5	0.17	-.27	-.05	-.55	-.06	0.05	0.35	-.07
6	0.65	-.26	0.02	-.21	-.10	-.11	-.10	0.15
7	-.46	-.12	0.01	-.39	-.02	0.17	-.22	-.07
8	0.35	0.38	-.02	0.36	0.21	-.26	-.32	-.48
9	0.23	-.24	-.04	-1.14	-.04	0.59	0.17	-.16
10	0.38	-.20	-.12	-.92	0.07	0.15	0.40	-.60
11	-.30	-.60	0.08	-.23	-.37	-.02	0.19	1.00
σ_I	0.99	0.97	0.09	1.14	0.44	0.78	0.77	1.02

^aTraits as described by reference numbers in Table 10.

Table 37. Standard partial regression coefficient and standard deviations of the index in retrospect, "idealized" index and constituent indexes for Yorkshire sows

Trait ^a	Index in retrospect	"Idealized" index	Constituent indexes					
			Number weaned	56-day weight	154-day weight	Carcass backfat	Ham and loin %	Loin eye area
1	-.01	-.01	0.02	-.11	-.03	-.07	0.01	0.02
2	0.14	-.09	0.00	0.26	0.03	-.61	-.39	-.26
3	0.22	0.36	-.01	0.00	0.12	0.41	0.09	-.12
4	0.05	-.25	-.02	-.58	-.06	0.22	0.07	0.01
5	0.12	-.27	-.05	-.53	-.06	0.11	0.31	-.04
6	0.23	-.39	0.02	-.21	-.18	-.12	0.07	0.38
7	0.07	0.36	0.07	0.11	0.01	-.01	-.08	0.02
8	-.00	0.15	-.02	0.10	0.10	-.03	-.12	-.24
9	-.02	-.29	-.02	-.66	-.09	0.24	0.16	0.04
10	0.01	-.19	-.06	-.45	-.02	0.10	0.35	-.11
11	-.02	-.40	0.04	-.18	-.20	-.20	0.03	0.43
σ_I	0.42	0.89	0.09	0.79	0.35	0.61	0.59	0.72

^aTraits as described by reference numbers in Table 10.

Table 38. Standard partial regression coefficients and standard deviations of the index in retrospect, "idealized" index and constituent indexes for boars in the pooled analysis

Trait ^a	Index in retrospect	"Idealized" index	Constituent indexes					
			Number weaned	56-day weight	154-day weight	Carcass backfat	Ham and loin %	Loin eye area
1	-.03	0.28	0.04	0.02	0.04	0.01	-.02	0.03
2	-.47	-.01	-.01	0.16	0.02	0.09	-.09	-.17
3	0.96	0.71	0.01	0.01	0.22	-.05	0.01	0.07
4	0.09	-.14	-.01	-.02	-.03	0.18	0.02	-.00
5	0.33	-.10	-.03	-.00	-.01	-.00	0.16	0.03
6	0.32	0.11	0.03	-.02	-.01	0.02	0.04	0.19
7	-.29	-.11	0.01	-.01	-.04	0.31	-.13	-.05
8	-.05	0.73	0.01	0.14	0.24	-.02	-.05	-.07
9	0.05	0.03	-.01	0.02	0.03	0.36	-.07	-.08
10	-.05	-.35	-.08	0.01	-.03	0.11	0.24	-.07
11	0.09	0.29	0.07	-.11	-.03	-.07	0.09	0.50
σ_I	0.94	1.13	0.08	0.24	0.36	0.51	0.48	0.60

^aTraits as described by reference numbers in Table 10.

Table 39. Standard partial regression coefficients and standard deviations of the index in retrospect, "idealized" index and constituent indexes for sows in the pooled analysis

Trait ^a	Index in retrospect	"Idealized" index	Constituent indexes					
			Number weaned	56-day weight	154-day weight	Carcass backfat	Ham and loin %	Loin eye area
1	0.05	0.17	0.03	0.00	0.01	0.02	0.00	0.02
2	0.13	-.23	-.01	0.11	-.06	0.00	-.01	-.08
3	0.22	0.81	0.01	0.05	0.26	0.03	-.08	-.05
4	-.03	-.06	-.00	-.01	-.01	0.20	-.01	-.01
5	0.09	-.19	-.04	-.01	-.02	0.03	0.16	-.01
6	0.20	0.18	0.04	-.05	-.02	-.04	0.06	0.28
7	0.08	0.42	0.08	0.03	0.01	0.02	-.03	0.05
8	-.02	0.38	-.01	0.06	0.15	0.01	-.03	-.03
9	-.00	-.03	0.00	-.01	-.01	0.24	-.02	-.03
10	0.04	-.19	-.04	0.00	-.02	-.04	0.17	-.03
11	-.06	0.10	0.04	-.06	-.04	-.05	0.09	0.34
σ_I	0.41	1.03	0.10	0.20	0.31	0.33	0.38	0.50

^aTraits as described by reference numbers in Table 10.

and loin percentage indicates that considerably less attention should have been given to 154-day weight if the desired objective was improvement in ham and loin percentage.

Harvey and Bearden (1962) have noted an interesting property of the index in retrospect. The selection intensity of the index in retrospect is equal to the standard deviation of the index in retrospect. The selection intensity of the index in retrospect can be written as: $i_I = (I - u_I)/\sigma_I$. Since u_I is zero; $i_I = [\sum_k B_k (x_k - \mu_k)/\sigma_{x_k}] / \sigma_I$, or more simply, $i_I = \sum_k B_k i_k / \sigma_I$. Using the relationship from

equations 1 $i_k = \sum_j B_j r_{x_k x_j}$, it follows that

$$i_I = [\sum_k B_k \sum_j B_j r_{x_k x_j}] / \sigma_I = \sigma_I^2 / \sigma_I = \sigma_I.$$

The relationship $i_I = \sigma_I$ can be used to partition realized selection intensity into the average amount of attention given individual, sib and progeny records in the selection program. The amount of attention given individual records can be determined by solving equations 1 for traits measured on the individual and computing the standard deviation of this reduced index in retrospect. The second step involves solving equations 1 for traits measured on the individual and on littermate averages, deleting progeny test data. The amount of attention given sib data after having accounted for selection on individual records can

be determined as the difference between standard deviations of the indexes in retrospect on individual and littermate records and on individual records alone. Selection emphasis on progeny test data after having accounted for selection based on individual and sib records is the difference between the standard deviations of the full index in retrospect and of the index in retrospect from which progeny records have been deleted. The intensity of selection on the full index in retrospect, i_I , and relative attention given individual, sib and progeny records, expressed as a proportion of i_I , are presented in Table 40 by breed and sex.

Quite obviously, very little selection was applied to progeny test data that had not already been accounted for by selection on individual and sib records. Breed differences are also evident. More attention was given to the individual performance of Hampshire pigs than was evidenced in the other breeds. Relatively more attention to sib carcass data was applied in the selection of Poland breeding animals.

Table 40. Intensity of selection on index in retrospect (i_I) and relative attention given individual, sib and progeny records by breed and sex

	Duroc	Hampshire	Poland	Yorkshire	Pooled
BOARS					
Individual	0.661	0.834	0.604	0.715	0.813
Sib	0.336	0.146	0.347	0.204	0.182
Progeny	0.002	0.020	0.049	0.081	0.004
SOWS					
Individual	0.743	0.825	0.618	0.716	0.738
Sib	0.192	0.160	0.363	0.266	0.236
Progeny	0.065	0.016	0.019	0.017	0.026

The index in retrospect describes the average selection that was applied over a period of years. If selection goals changed with time or selection did not closely approximate a truncation type of selection for a particular goal, the index in retrospect could not be expected to be an accurate description of the selection practiced. Dickerson et al. (1954) warned that if all traits which were actually included in the selection program were not also included in the index in retrospect, the index might be an inadequate tool in characterizing the selection program.

As previously noted, there was apparently no definitive method involved in selecting female replacements. Annual realized selection differentials for boars tended to fluctuate somewhat, depending on the trait involved and

breed in question. For those traits which received considerable attention in a particular breed, boar selection was fairly consistent from one year to the next.

Expected Genetic Gain

Lush (1954) showed that the expected annual rate of genetic change could be computed as:

$$\Delta G = i \sigma_A r_{XA} / \bar{T},$$

where i is selection intensity, σ_A is the standard deviation of breeding values, r_{XA} is the accuracy with which breeding value is estimated by phenotype and \bar{T} is the generation interval of the population.

Harvey and Bearden (1962) have shown that the expected genetic progress from selection on the index in retrospect in standard measure is:

$$\begin{aligned} \Delta g_j &= \Delta G_j / \sigma_{X_j} \\ &= i_I r_{A_j I} \sigma_{A_j} / \sigma_{X_j} \\ &= i_I (\sum_k B_k r_{x_k A_j}) \sigma_{A_j} / \sigma_I \sigma_{X_j} \\ &= i_I (\sum_k B_k r_{x_k A_j} h_j) / \sigma_I \end{aligned}$$

however, since $i_I = \sigma_I$;

$$\Delta g_j = \sum_k B_k r_{x_k A_j} h_j .$$

The annual rate of genetic change in standard measure that might have been expected to result from selection on

the "idealized" index was computed as follows:

$$\begin{aligned}
 \Delta g_j &= \Delta G_j / \sigma_{X_j} \\
 &= i_{\max} \sigma_{A_j} r_{"I" A_j} / \bar{T} \sigma_{X_j} \\
 &= i_{\max} \sigma_{A_j} (\sum_k b_k r_{x_k A_j}) / \bar{T} \sigma_{X_j} \sigma_{"I"} \\
 &= i_{\max} (\sum_k b_k r_{x_k A_j} h_j) / \bar{T} \sigma_{"I"} .
 \end{aligned}$$

The expected genetic progress of the j th trait in the population was computed as the unweighted average of the expected genetic gain resulting from sire and dam selection.

The expected genetic progress in terms of an aggregate breeding value, H , under the average realized selection described by the index in retrospect can be compared with that which might have been achieved had selection been based on an "idealized" index. This comparison can be accomplished by computing Δg_j for all traits under each index. Note that the same age structure has been assumed for selection under both indexes. Multiplying Δg_j and e_j , the standardized economic value, and summing across all traits gives ΔH for each index and provides the basis for comparison. The relationship between ΔH and Δg_j is shown

by the following formula:

$$\begin{aligned}
 \Delta H &= i r_{IH} \sigma_H / \bar{T} \\
 &= i \sigma_I^2 \sigma_H / \sigma_H \sigma_I \bar{T} \\
 &= i \sigma_I^2 / \sigma_I \bar{T} \\
 &= i (\sum_j \sum_k b_k b_j \sigma_{x_k x_j} / \sigma_{x_k} \sigma_{x_j}) / \sigma_I \bar{T} \\
 &= i (\sum_k b_k \sum_j e_j \sigma_{A_k A_j} / \sigma_{x_k} \sigma_{x_j}) / \sigma_I \bar{T} \\
 &= \sum_j e_j [i (\sum_k b_k r_{x_k A_j} h_j) / \sigma_I \bar{T}] \\
 &= \sum_j e_j \Delta g_j
 \end{aligned}$$

, equivalently;

$$\begin{aligned}
 \Delta H &= \sum_j a_j \sigma_{x_j} \Delta g_j \\
 &= \sum_j a_j \sigma_{x_j} \Delta G_j / \sigma_{x_j} \\
 &= \sum_j a_j \Delta G_j
 \end{aligned}$$

Note that ΔH is expressed in actual measure (\$).

The expected annual genetic gain both in standard measure (σ) and in actual units for each trait and in the aggregate breeding value under the selection scheme actually practiced, as described by the index in retrospect, is contrasted with that which might have been achieved had selection been based on an "idealized" selection index in Tables 41 through 45.

The interpretation of Tables 41 through 45 is contingent

Table 41. Expected annual genetic gain by trait and selection scheme for the Duroc breed

Trait	Unit of measure	Realized selection			"Idealized" selection		
		sires	dams	net	sires	dams	net
Number weaned	σ	0.059	0.048	0.054	0.161	0.137	0.149
	pigs	0.138	0.113	0.127	0.378	0.322	0.350
56-day weight	σ	0.047	0.034	0.041	0.175	0.074	0.124
	lb.	0.422	0.305	0.368	1.571	0.664	1.123
154-day weight	σ	0.210	0.122	0.166	0.780	0.410	0.595
	lb.	6.229	3.619	4.924	23.137	12.162	17.649
Carcass backfat	σ	-.078	-.024	-.051	-.352	-.061	-.206
	in.	-.014	-.004	-.009	-.065	-.011	-.038
Ham and loin percentage	σ	0.035	0.006	0.020	-.022	-.002	-.012
	%	0.061	0.010	0.035	-.038	-.003	-.021
Loin eye area	σ	0.158	0.074	0.116	0.223	0.208	0.215
	sq.in.	0.095	0.044	0.069	0.133	0.124	0.129
Aggregate breeding value	σ			0.154			0.503
	\$			0.82			2.68

Table 42. Expected annual genetic gain by trait and selection scheme for the Hampshire breed

Trait	Unit of measure	Realized selection			"Idealized" selection		
		sires	dams	net	sires	dams	net
Number weaned							
	σ	-.000	0.000	0.000	0.001	0.001	0.001
	pigs	-.000	0.000	0.000	0.002	0.002	0.002
56-day weight							
	σ	0.099	0.052	0.075	0.341	0.186	0.263
	lb.	0.839	0.441	0.636	2.891	1.577	2.230
154-day weight							
	σ	0.214	0.070	0.142	0.729	0.401	0.565
	lb.	5.941	1.943	3.942	20.239	11.133	15.868
Carcass backfat							
	σ	-.043	-.004	-.024	-.020	0.036	0.008
	in.	-.006	-.001	-.003	-.003	0.005	0.001
Ham and loin percentage							
	σ	-.092	-.036	-.064	-.410	-.289	-.350
	%	-.140	-.055	-.097	-.623	-.439	-.532
Loin eye area							
	σ	0.020	0.028	0.024	-.163	-.137	-.150
	sq.in.	0.012	0.017	0.015	-.100	-.084	-.092
Aggregate breeding value	σ			0.080			0.313
	\$			0.40			1.56

Table 43. Expected annual genetic gain by trait and selection scheme for the Poland breed

Trait	Unit of measure	Realized selection			"Idealized" selection		
		sires	dams	net	sires	dams	net
Number weaned	σ	-.001	0.006	0.003	0.068	0.080	0.074
	pigs	-.002	0.012	0.006	0.140	0.165	0.152
56-day weight	σ	-.026	0.004	-.011	0.113	0.044	0.078
	lb.	-.218	0.033	-.092	0.946	0.368	0.653
154-day weight	σ	0.018	0.018	0.018	0.348	0.161	0.254
	lb.	0.458	0.458	0.458	8.845	4.092	6.456
Carcass backfat	σ	-.178	-.072	-.125	0.440	0.099	0.269
	in.	-.027	-.011	-.019	0.068	0.015	0.041
Ham and loin percentage	σ	0.288	0.091	0.190	-.226	-.065	-.146
	%	0.438	0.138	0.289	-.344	-.099	-.222
Loin eye area	σ	0.297	0.059	0.178	-.190	-.060	-.125
	sq.in.	0.185	0.037	0.111	-.119	-.037	-.078
Aggregate breeding value	σ			0.037			0.237
	\$			0.15			0.97

Table 44. Expected annual genetic gain by trait and selection scheme for the Yorkshire breed

Trait	Unit of measure	Realized selection			"Idealized" selection		
		sires	dams	net	sires	dams	net
Number weaned	σ	-.027	-.000	-.014	-.005	0.025	0.010
	pigs	-.061	-.000	-.032	-.011	0.056	0.023
56-day weight	σ	0.004	-.022	-.009	0.960	0.491	0.726
	lb.	0.034	-.186	-.076	8.120	4.153	6.141
154-day weight	σ	0.038	-.004	0.017	0.556	0.292	0.424
	lb.	1.030	-.108	0.461	15.065	7.912	11.489
Carcass backfat	σ	-.187	-.070	-.128	0.147	0.192	0.170
	in.	-.033	-.012	-.023	0.026	0.034	0.030
Ham and loin percentage	σ	0.008	-.018	-.005	-.744	-.363	-.554
	%	0.013	-.028	-.008	-1.165	-.568	-.867
Loin eye area	σ	-.153	-.018	-.085	-1.074	-.516	-.795
	sq.in.	-.087	-.010	-.048	-.613	-.294	-.454
Aggregate breeding value	σ			-.004			0.259
	\$			-.02			1.05

Table 45. Expected annual genetic gain by trait and selection scheme for the pooled analysis

Trait	Unit of measure	Realized selection			"Idealized" selection		
		sires	dams	net	sires	dams	net
Number weaned	σ	0.010	0.010	0.010	0.058	0.057	0.058
	pigs	0.022	0.022	0.022	0.127	0.125	0.127
56-day weight	σ	-.008	0.034	0.013	0.228	0.122	0.175
	lb.	-.068	0.290	0.111	1.950	1.044	1.497
154-day weight	σ	0.108	0.053	0.080	0.473	0.257	0.365
	lb.	2.948	1.447	2.184	12.913	7.016	9.964
Carcass backfat	σ	-.100	-.019	-.060	0.090	0.068	0.079
	in.	-.017	-.003	-.010	0.015	0.011	0.013
Ham and loin percentage	σ	0.127	0.021	0.074	-.259	-.156	-.207
	%	0.201	0.033	0.117	-.410	-.247	-.328
Loin eye area	σ	0.204	0.038	0.121	-.106	-.056	-.081
	sq.in.	0.123	0.023	0.073	-.064	-.034	-.049
Aggregate breeding value	σ			0.069			0.275
	\$			0.32			1.26

upon certain assumptions. The phenotypic and genetic parameters used in constructing these tables were taken to be reasonable estimates of population parameters. It is assumed that the relative differences in the economic values of traits as taken from Robison, Chapman and Self (1960) realistically describe the importance of these traits to the commercial swine industry. An identical age structure was assumed under both systems of selection. Presumably the potentially maximum selection intensity could have been achieved under "idealized" selection.

Measurements that were taken and used, yet went unrecorded and information which may have been used from foundation animals and replacements brought in from outside the herd were not included in the computation of realized selection differentials. As a consequence, computed realized selection differentials may somewhat underestimate selection actually practiced.

The differences expected in ΔH under realized and "idealized" selection are striking. If the actual selection practiced had been exclusively for meatiness; i.e. ham and loin percentage, the differences would have been even more pronounced in favor of the "idealized" selection index. The present economic incentive for producing leaner, meatier hogs and the genetic factors which allow this change to be rather easily made are not great enough to counterbalance

the overwhelming economic importance of reproductive performance and growth rate.

Great differences among breeding groups in their potential for improving profitability through selection are apparent. The Duroc line had a potential for annual improvement in net merit of \$2.68, nearly 3 times as great as the Poland line. Had selection been based on the "idealized" index it is expected that the reproductive performance and growth rate of Duroc pigs would have shown marked improvement. Carcasses of Duroc pigs would have become leaner, with larger loin eyes, but very little change would have been made in ham and loin percentage. In contrast to this, while selection based on the "idealized" index in the Yorkshire line would have resulted in heavier pigs at 56 and 154 days, a marked decrease in carcass meatiness would also have occurred. A similar pattern of response would have been expected in the Hampshire line, although the decrease in carcass meatiness would probably not have been as pronounced as in the Yorkshire line. Poland pigs selected on the "idealized" index would have become faster growing but fatter.

Differences among the breeds in their expected response to the selection that was actually practiced are also evident. The selection described by the selection index in retrospect for the Duroc breed results in a positive response

in all traits studied and an increase in net merit of \$.82 per year. In contrast, a decrease in profit potential of \$.02 per year is the anticipated result of selection realized within the Yorkshire line. The expectation of leaner Yorkshire pigs is the only significantly positive response to selection actually practiced in the Yorkshire breed. The anticipated response to realized selection in the Hampshire breed is faster growth with little change in other traits. Leaner, meatier Poland pigs are expected as a result of selection described by the index in retrospect for the Poland breed.

One of the objectives of this research project was to obtain estimates of the rate of genetic improvement in meatiness resulting from individual, family and progeny selection in purebred seedstocks. Expected genetic gain can be partitioned into that resulting from individual, sib and progeny selection by using the technique previously described in partitioning realized selection intensity into that due to different sources of information.

Genetic gain is predicted from an index which was constructed using only data from individual records, deleting sib and progeny information. This step gives the expected genetic gain due to selection on individual records. Another index is constructed using data from both individual and sib sources, deleting progeny information. The difference

between the expected genetic gain predicted from the index containing both individual and sib information and that containing only individual data is the expected genetic gain due to selection on sib records after having accounted for individual selection. The expected genetic progress due to selection on progeny records after having accounted for individual and sib selection is the difference between predicted genetic gain from the full index which includes information from all sources and the expected genetic gain predicted to result from combined individual and sib selection.

The expected genetic gain under both the realized and "idealized" selection schemes has been partitioned into that attributable to different sources of information and is presented for each breed in Tables 46 through 50.

Virtually all of the genetic improvement in carcass meatiness resulting from selection described by the index in retrospect comes from selection on sib information. With the exception of the Yorkshire breed, genetic improvement in the aggregate breeding value under realized selection resulted primarily from selection on data collected directly on the individual. Comparison of the expected genetic gain from realized and "idealized" selection in Tables 46 through 50 indicates that more efficient use could have been made of progeny test records.

Table 46. Expected genetic gain (in standard measure) due to selection on different sources of information for realized and "idealized" selection in the Duroc breed

Trait	Realized selection			"Idealized" selection		
	individual	sib	progeny	individual	sib	progeny
Number weaned	0.035	0.012	0.006	0.079	0.004	0.067
56-day wt.	0.065	-.048	0.024	0.066	0.004	0.054
154-day wt.	0.180	-.027	0.012	0.454	0.012	0.130
Carcass backfat	-.082	0.017	0.014	-.106	-.054	-.046
Ham and loin %	-.021	0.082	-.040	-.035	0.026	-.003
Loin eye area	0.020	0.172	-.076	0.124	0.044	0.047
Aggregate breeding value	0.141	0.003	0.009	0.348	0.013	0.142

Table 47. Expected genetic gain (in standard measure) due to selection on different sources of information for realized and "idealized" selection in the Hampshire breed

Trait	Realized selection			"Idealized" selection		
	individual	sib	progeny	individual	sib	progeny
Number weaned	-.060	0.060	0.000	-.000	0.000	0.001
56-day wt.	0.095	-.026	0.006	0.178	0.011	0.074
154-day wt.	0.170	-.041	0.013	0.375	0.033	0.157
Carcass backfat	0.007	-.038	0.008	-.002	0.025	-.015
Ham and loin %	-.104	0.058	-.018	-.232	-.042	-.076
Loin eye area	-.046	0.071	-.001	-.108	-.052	0.010
Aggregate breeding value	0.094	-.020	0.007	0.207	0.017	0.089

Table 48. Expected genetic gain (in standard measure) due to selection on different sources of information for realized and "idealized" selection in the Poland breed

Trait	Realized selection			"Idealized" selection		
	individual	sib	progeny	individual	sib	progeny
Number weaned	-.003	0.001	0.005	0.044	0.002	0.028
56-day wt.	0.022	-.026	-.007	0.051	-.001	0.029
154-day wt.	0.048	-.026	-.005	0.214	0.000	0.040
Carcass backfat	-.027	-.089	-.009	0.140	0.032	0.097
Ham and loin %	-.005	0.163	0.031	-.152	0.012	-.006
Loin eye area	-.023	0.145	0.056	-.141	0.006	0.009
Aggregate breeding value	0.029	0.002	0.006	0.177	0.004	0.057

Table 49. Expected genetic gain (in standard measure) due to selection on different sources of information for realized and "idealized" selection in the Yorkshire breed

Trait	Realized selection			"Idealized" selection		
	individual	sib	progeny	individual	sib	progeny
Number weaned	-.008	0.001	-.007	0.007	-.006	0.008
56-day wt.	0.144	-.169	0.016	0.036	0.339	0.350
154-day wt.	0.046	-.083	0.054	0.169	0.110	0.145
Carcass backfat	-.073	-.058	0.002	0.255	0.015	-.100
Ham and loin %	-.030	0.080	-.055	-.233	-.077	-.244
Loin eye area	0.082	0.140	-.143	-.322	-.174	-.299
Aggregate breeding value	0.021	-.050	0.025	0.106	0.065	0.088

Table 50. Expected genetic gain (in standard measure) due to selection on different sources of information for realized and "idealized" selection in the pooled breed analysis

Trait	Realized selection			"Idealized" selection		
	individual	sib	progeny	individual	sib	progeny
Number weaned	0.003	0.003	0.004	0.025	0.004	0.029
56-day wt.	0.040	-.025	-.002	0.130	-.000	0.044
154-day wt.	0.107	-.024	-.002	0.292	-.000	0.073
Carcass backfat	-.042	-.024	0.006	0.059	0.000	0.019
Ham and loin %	-.011	0.088	-.004	-.141	-.019	-.047
Loin eye area	-.008	0.124	0.005	-.103	-.001	0.023
Aggregate breeding value	0.072	-.004	0.002	0.201	0.002	0.073

Response to Selection

Theoretical expectations of genetic change resulting from selection are not always realized. Since no designed method for measuring actual genetic gain was used in this project it may be quite difficult to compare theoretical expectations of genetic gain with that actually realized. As Dickerson (1951) noted, the confounding of time trends in nutrition, disease, management, climate, inbreeding and other factors may make the evaluation of selection effectiveness inextricable.

Since no planned control populations were carried nor were special attempts made to make repeat matings, other methods for estimating the actual genetic change realized in these data must be used. Henderson et al. (1959) and Smith (1962) have proposed methods for obtaining estimates of genetic gain from field data.

The method proposed by Henderson et al. (1959) estimates genetic and environmental trends by a maximum likelihood procedure. It requires; however, that either repeatability be known without error or an iterative technique be used which provides no guarantee of a unique answer. Additionally they assume that age correction factors are perfectly known. The unpalatability of necessary assumptions and computational perplexity of the method proposed by Henderson et al. (1959) have led to the use of Smith's (1962) techniques for esti-

mating actual genetic gain.

Smith (1962) noted that if sires were mated to a random sample of dams in two successive years, the difference between the performance of his progeny in those two years would be $\Delta G/2$, where ΔG represents the annual genetic change in the population. The overlap in time of progeny from different boars provides the basis for estimating genetic change.

Smith (1962) proposed two regression methods of estimation. Smith Method 1 is based on the difference between the linear regression of population performance on years and the pooled within-sire regression of progeny performance on years, i.e. $\Delta G = 2(b_{PT} - b_{ST})$. Smith Method 2 or twice the pooled within-sire regression on years of the difference between population and sire progeny performance; i.e. $\Delta G = 2b_{(P-S)T}$, is more appealing in that it removes year to year fluctuations in environment from the estimate of genetic change.

Several aspects of the structure of these data complicate the use of Smith's (1962) regression methods. Age of dams and age of sires are confounded. Boars in their first year-season of use were mated almost exclusively to first litter gilts. Older boars were very rarely mated to first litter gilts. To avoid bias resulting from this confounding all regressions were computed on a within-age of dam basis. As

a consequence sampling errors of the regression coefficients are increased. It has been assumed that boars were mated to a random sample of dams within an age of dam class.

Smith (1962) noted that bias can result from selection of sires on the basis of their early progeny. If progeny from sires used for a short period of time and then culled are included in the pooled within sire regression on time, genetic change will be underestimated. To avoid this source of bias and increase the likelihood that progenies from several year-seasons of a boar's use contributed to the within-age of dam regression of progeny performance on time for that boar, only boars which had progeny in 3 or more year-seasons were included in actual computations. Relatively few of the boars used to compute Smith's regression estimates made significant contributions to the early and late year-seasons involved in this study. As a consequence the within-sire regressions of progeny performance on time are rather poorly estimated and subject to large sampling errors.

All data were adjusted to a zero inbreeding of dam, zero inbreeding of pig, male basis using least squares regressions and constants reported in Tables 67 through 74 of the appendix. Carcass data were adjusted to a 145-pound carcass weight basis using partial regression coefficients from the aforementioned tables. Regression estimates of actual genetic gain from Smith's (1962) Methods 1 and 2 and the

within-age of dam regressions of population performance on time were computed on a year-season basis and then converted to an annual basis. Dickerson (1951) noted that although subject to confounding with many factors, the regression of population performance on time could be regarded as an estimate of genetic change. Estimates of the actual annual genetic gain from Smith's Method 2 ($2b_{(P-S)T}$), Smith's Method 1 ($2[b_{PT} - b_{ST}]$), and the within-age of dam regression of population performance on time are presented by trait for each breed in Tables 51 through 55.

Standard deviations of estimates from both of Smith's methods were quite similar. They ranged from 1.07 to 1.27 pigs, 1.20 to 1.87 lb., 4.04 to 6.33 lb., 0.05 to 0.06 in., 0.44 to 0.64 %, and 0.15 to 0.22 sq. in. for number weaned, 56-day weight, 154-day weight, carcass backfat, ham and loin percentage and loin eye area, respectively, in the different breeds. The regressions of population performance on time are much more precisely estimated, having sampling errors approximately 1/20th the size of those accompanying estimates from Smith's methods.

The most intuitively appealing of Smith's regression techniques for estimating genetic gain, Method 2, is subject to large sampling errors. However, the fact that it yields consistently more conservative estimates than Method 1 suggests that year to year environmental fluctuation may have

Table 51. Estimates of actual annual genetic gain by trait for the Duroc breed

Trait	Unit of measure	$2B_{(P-S)T}$	$2(B_{PT} - B_{ST})$	B_{PT}
Number weaned				
	σ	-.179	-.222	-.091
	pigs	-.421	-.522	-.214
56-day wt.				
	σ	0.157	0.733	-.048
	lb.	1.412	6.577	-.428
154-day wt.				
	σ	0.210	0.781	-.003
	lb.	6.242	23.164	-.078
Carcass backfat				
	σ	-.468	-.588	-.076
	in.	-.086	-.108	-.014
Ham and loin %				
	σ	0.406	1.048	0.358
	%	0.707	1.823	0.623
Loin eye area				
	σ	-.069	0.851	0.242
	sq.in.	-.041	0.509	0.145

Table 52. Estimates of actual annual genetic gain by trait for the Hampshire breed

Trait	Unit of measure	$2B_{(P-S)T}$	$2(B_{PT} - B_{ST})$	B_{PT}
Number weaned				
	σ	-.073	-.874	-.007
	pigs	-.153	-1.837	-.014
56-day wt.				
	σ	-.027	-.540	-.041
	lb.	-.226	-4.575	-.346
154-day wt.				
	σ	0.395	0.293	0.023
	lb.	10.959	8.125	0.647
Carcass backfat				
	σ	-.028	0.042	-.173
	in.	-.004	0.006	-.025
Ham and loin %				
	σ	-.347	0.274	0.266
	%	-.528	0.416	0.405
Loin eye area				
	σ	-.646	0.486	0.211
	sq.in.	-.398	0.299	0.130

Table 53. Estimates of actual annual genetic gain by trait for the Poland breed

Trait	Unit of measure	$2B_{(P-S)T}$	$2(B_{PT} - B_{ST})$	B_{PT}
Number weaned	σ	0.295	0.666	0.077
	pigs	0.608	1.372	0.159
56-day wt.	σ	-.016	0.351	-.016
	lb.	-.131	2.941	-.135
154-day wt.	σ	0.005	0.530	0.010
	lb.	0.137	13.467	0.242
Carcass backfat	σ	-.006	-.532	-.208
	in.	-.001	-.082	-.032
Ham and loin %	σ	0.037	0.660	0.397
	%	0.057	1.003	0.603
Loin eye area	σ	0.240	0.287	0.279
	sq.in.	0.150	0.179	0.174

Table 54. Estimates of actual annual genetic gain by trait for the Yorkshire breed

Trait	Unit of measure	$2B_{(P-S)T}$	$(B_{PT} - B_{ST})$	B_{PT}
Number weaned	σ	-.642	-.725	0.019
	pigs	-1.447	-1.633	0.043
56-day wt.	σ	0.116	0.256	-.153
	lb.	0.982	2.163	-1.293
154-day wt.	σ	0.312	0.402	-.092
	lb.	8.441	10.899	-2.492
Carcass backfat	σ	0.393	0.224	-.129
	in.	0.070	0.040	-.023
Ham and loin %	σ	-.447	-.232	0.245
	%	-.700	-.363	0.384
Loin eye area	σ	0.352	0.301	0.181
	sq.in.	0.201	0.172	0.103

Table 55. Estimates of actual annual genetic gain by trait for the pooled breed analysis

Trait	Unit of measure	$2B_{(P-S)T}$	$2(B_{PT} - B_{ST})$	B_{PT}
Number weaned				
	σ	-.183	-.289	0.002
	pigs	-.400	-.632	0.005
56-day wt.				
	σ	0.063	0.249	-.056
	lb.	0.536	2.128	-.478
154-day wt.				
	σ	0.238	0.514	-.010
	lb.	6.492	14.040	-.276
Carcass backfat				
	σ	0.018	-.188	-.145
	in.	0.003	-.031	-.024
Ham and loin %				
	σ	-.107	0.431	0.332
	%	-.169	0.682	0.525
Loin eye area				
	σ	0.010	0.465	0.238
	sq.in.	0.006	0.281	0.144

had an important effect on these data. The fairly consistent differences between the within-age of dam regression of population performance on time and estimates of genetic change in growth rate and carcass measurements support the argument that non-genetic time trends may have been quite important in these data.

Expectations of genetic gain predicted from the index in retrospect do not consistently agree with any of the estimates of actual genetic change presented in Tables 51 through 55. Underestimation of realized selection differentials due to the practice of assigning zero selection differentials on preprogeny test traits to foundation boars and boars brought into the herd from outside sources may have forced the theoretical predictions of genetic gain to be too small. Foundation boars sired 17.5%, 11.4%, 17.2% and 11.7% of all pigs weaned in the Duroc, Hampshire, Poland and Yorkshire breeds, respectively. Boars from outside sources sired 1.0%, 7.1%, 0.3% and 22.0% of all weaned pigs in the aforementioned breeds.

The actual genetic response to realized selection cannot be accurately assessed from these data with existing methods for estimating genetic change.

DISCUSSION

The poor consumer image of pork has been a major factor in the declining per capita consumption of pork during the past several decades. To counter this image, the pork industry has led in the development of high quality, convenient to use meat products. The premium paid producers of leaner, meatier hogs is a direct reflection of the industry's attempt to satisfy consumer demands for leaner retail cuts.

The downward trend of per capita pork consumption has not yet been reversed. High quality, conveniently used pork products are readily available to today's consumer, but at a higher price. It appears likely that more than just a better product must be offered to meet the competition of the pork industry; that product must be lower priced as well. More efficient swine production methods must be developed to enable producers to sell pigs at lower prices and still receive an adequate income.

The impressive increase in the means of traits from central boar testing stations have provided producers with an example of how genetic principles can be utilized to make pigs more efficient and meatier. However, as Brinks (1960) noted the observed change in test station averages is greater than might be expected from genetic theory.

The present project was conducted to measure the rate

at which genetic change in meatiness could be made to occur in purebred swine populations through a program of intense selection. In effect, this was an attempt to genetically direct the metabolic pathways of feed utilization towards protein deposition. Because of the relative energy content of fat and protein it has been theorized that lean, meaty pigs should more efficiently use feedstuffs than fat pigs. It was expected that leaner, meatier pigs would not only produce a product that was more acceptable to the consumer, but would be more economical to produce because of more efficient feed utilization.

Early in the course of the analysis of these data it was determined that the four breed groups used in the study represented distinctly different populations. Differences in the means and variances were not the only distinctions noted. There were, apparently, differences in the genetic and phenotypic relationships between performance and carcass characteristics among the breeds.

Recall that the literature presents a confusing picture about the genetic relationships between performance and carcass traits. Part of this discord may well be due to the fact that breeds or even lines of breeding can be dissimilar with respect to genetic relationships between traits. It is of interest to note the generally good agreement in the literature of correlation estimates among carcass traits.

This suggests that the sampling errors of the divergent correlation estimates between growth rate and carcass characteristics would not be great enough to account for the conflicting differences in those estimates. Environmental differences could account for some of the disparity of estimates, but enough estimates from similar environmental conditions are available to suggest that this explanation lacks sufficiency.

The breed differences noted in these data may reflect characteristics of the lines of breeding sampled, rather than real breed differences. However, differences among these breeding groups suggest that formulation of unique plans for genetic improvement may be necessary to maximize genetic change in genetically divergent populations.

Using the distinctive parameter estimates from each line of breeding, "idealized" selection indexes were constructed to compare the genetic response that might have been expected in individual breeding groups with the genetic response expected to result from selection actually practiced. The "idealized" selection indexes were constructed from constituent indexes, using a method proposed by Henderson (1963). The constituent indexes for ham and loin percentage can be used to describe the selection that should have been practiced for increasing meatiness (as indicated by ham and loin percentage) in these breeding groups. None

of these indexes are proposed for general use, as they are applicable only to the particular characteristics of these data.

The selection program outlined at the onset of the project was to be based upon initial selection of boars for minimum backfat probe at 200 pounds; further attention was to be given to littermate carcass data with later culling to be based on progeny carcass cutout. The same selection scheme was to be practiced in each breed.

A selection index in retrospect was computed for each sex within each breed to characterize the selection actually practiced. Dickerson et al. (1954) noted that the index in retrospect describes only the average selection practiced over a period of time. Inspection of the annual realized selection differentials indicate some variation in selection practices, but the only consistent trend was for more intense selection on 56 and 154-day weights and ham and loin percentage as numbers of pigs in the herd increased with time.

The indexes in retrospect indicate that selection was actually practiced differently in each breed and that in no breed was the predetermined criterion for selection (meatiness as indicated by ham and loin percentage) given foremost attention.

Female selection procedures were not outlined at the

initiation of this project. There is little evidence that much female selection was actually practiced. From 17 to 20 percent of all females weaned entered the breeding herd but the intensity of selection on female indexes in retrospect correspond to culling only the poorest 25 percent based on truncation selection from a normal distribution. Obviously a great opportunity for selection was unrealized. Over 60 percent of the potential from boar selection could have been realized from more attention to selection of female replacements. Utilization of female selection opportunity was uniformly poor across all breeds.

The index in retrospect on Duroc boars indicates that more attention was given to littermate loin eye area average than any other trait. This may have been an attempt to correct a deficiency in this particular line of breeding as Duroc loin eyes were characteristically smaller than in other lines. Weight at 154 days received considerable emphasis, but relatively little attention was given backfat probe at 200 pounds which was to have been a major tool for estimating leanness on individual boars. It is of interest to note the comparison of the index in retrospect and constituent index for ham and loin percentage of Duroc boars in Table 30. Had the goal of improving ham and loin percentage been strictly adhered to, very little attention should have been given any observations other than litter-

mate averages for ham and loin percentage and loin eye area and progeny loin eye area average. The very low heritability estimate for ham and loin percentage in Durocs (0.15) indicated that in this line it may have been more effective to pay attention to the closely related but more highly heritable indicator of meatiness, loin eye area. The constituent index for ham and loin percentage specifies that genetic improvement in ham and loin percentage of Durocs is to be made as a correlated response to selection for larger loin eyes. Table 30 also indicates that progeny test data were poorly utilized. While approximately 4 percent of the Duroc boars weaned were used in the herd they were representative of only the best 34 percent based on the index in retrospect.

Weight at 154 days was the major criterion of selection practiced in the Hampshire line. Again this would appear to have been an attempt to correct a deficiency in the line. Littermate ham and loin percentage averages received appreciable attention but were countered by an effective negative weighting to progeny ham and loin averages. Little attention was given to backfat probes. Contrasting the index in retrospect and constituent index for ham and loin percentage of Hampshire boars in Table 32 indicates that too much attention was given to 154 day weight to effect genetic improvement in ham and loin percentage. Additionally,

use of progeny test data was less than optimal. Based on the index in retrospect, Hampshire boars saved were typical of the best 43 percent; however, less than 5 percent were used.

Appreciable genetic improvement in ham and loin percentage would be realized only from the selection practiced in the Poland line. Relatively more attention was given the littermate ham and loin percentage averages of Polands than any other breed group. Yet more attention was paid to the 154-day weight of Poland boars than was given their littermate ham and loin percentage averages. Progeny and littermate loin eye area averages account for a substantial portion of the selection intensity applied to Poland boars. Little emphasis was given to backfat probes. The constituent index for ham and loin percentage of Poland boars presented in Table 34 indicates that too much attention was given weight at 154 days to maximize the rate of genetic improvement in ham and loin percentage. The selection intensity on the index in retrospect indicates that Poland boars were representative of the best 49 percent; however, only 4 percent entered the breeding herd.

Littermate loin eye area averages and weight at 154 days were the principal criteria for selecting Yorkshire boars. Backfat probes were a more important part of the realized selection in Yorkshires than in any of the other

breeds. Relatively more attention was given to the progeny performance of Yorkshire boars. However, this may have been an artifact resulting from the procedure of assigning zero selection differentials to boars coming from sources outside of the Napier herd. Since relatively more outside boars were used in the Yorkshire breed, preprogeny test selection differentials for Yorkshires were probably underestimated. This would result in more weight being given to progeny test traits in the index in retrospect. Table 36 indicates that littermate loin eye area averages and 154-day weight were overstressed in Yorkshire selection, given the goal of genetic improvement in ham and loin percentage. In contrast to the Duroc line, it would have been more effective to concentrate selection efforts directly on measures of ham and loin percentage in the Yorkshire line. Approximately 4 percent of the boars weaned in the Yorkshire breed were used for breeding but were typical of only the top 39 percent based on the index in retrospect.

The disparity between the intensity of selection described by the index in retrospect and the proportion of the population used in the breeding herd could have several explanations. The index in retrospect may not fully describe the selection actually practiced. Considerable attention may have been given to soundness, conformation and other attributes which were not included in the index in retro-

spect. As previously noted there was some fluctuation in the annual realized selection differentials of each trait. This suggests some vacillation of selection goals. Also, selection of individual boars on different criteria may have occurred.

A factor which limited the opportunity for selection in these populations was the poor survival rate of pigs farrowed. Only 59, 63, 68 and 68, percent, of the Duroc, Hampshire, Poland and Yorkshire pigs born survived until 154 days of age. While these percentages include both living and dead pigs at birth, most of the death loss occurred between birth and weaning.

As Dickerson and Hazel (1944a) noted, "A regular plan of progeny testing is unlikely to increase, and may reduce progress unless (1) the progeny-test information becomes available early in the tested animal's lifetime, (2) the reproductive rate is low, and (3) the basis for making early selections is relatively inaccurate." While progeny test data were collected in this project, they were not efficiently utilized. Because of the relatively few progeny tested boars maintained in each line, chance death or injury of outstanding sires could have limited effective use of progeny records. A contributing factor to the inefficient use of progeny test data was the lack of physical facilities for housing boars at the Napier farm.

Undoubtedly several good boars were culled on the basis of incomplete progeny test data just to make room for more promising young boars.

The usefulness of the backfat probe is difficult to determine from these data, since only a select group of animals were probed. Even then relatively little attention was given to probe data in any but the Yorkshire breed. Martin and Fredeen (1967) concluded that genetic change in percent lean cuts would be more effectively achieved by indirect selection for minimum backfat probe than by slaughtering littermate samples. The constituent indexes for ham and loin percentage computed from these data indicate that estimates of backfat on the live animal may not be of equal value for all lines of breeding.

Too much attention may have been given to littermate carcass data in this selection project. The index in retrospect indicates that more weight was given to littermate carcass records than deemed appropriate by the constituent indexes for ham and loin percentage in all but the Poland breed. Holland and Hazel (1958) noted that among the disadvantages of using littermate samples for carcass data were, "...that the slaughtered pigs may be biased samples of the groups they represent, that the slaughtering reduces the intensity of selection which might otherwise be practiced, and that the information is not immediately available when

selection usually will be practiced." All of these disadvantages would be particularly applicable to this study where only 5.4, 5.4, 5.5 and 7.0, pigs per litter, survived until 154 days in the Duroc, Hampshire, Poland and Yorkshire lines, respectively, while nearly 2 pigs per litter were sacrificed for carcass data.

Estimates were made of the genetic gain expected to result from selection described by the indexes in retrospect. In Tables 41 through 44 it is shown that 0.02, -.06, 0.19 and 0.005, standard deviation units, increase per year in ham and loin percent would result from the selection practiced in the Duroc, Hampshire, Poland and Yorkshire lines, respectively. Certainly only a small fraction of the potential change in ham and loin percentage could have resulted from selection described by the index in retrospect of each breed.

Contrary to conclusions reached while reviewing the literature, genetic antagonisms between performance and carcass cutability traits found in the Hampshire and Yorkshire lines would frustrate selection efforts to genetically improve both performance and meatiness. Efforts to effect simultaneous genetic improvement in the performance and carcass characteristics of the Poland line would likely be only moderately successful. Potential genetic improvement of the Duroc strain would not be limited by genetic

antagonisms between economically important traits.

An attempt was made to estimate the actual genetic response to selection using regression methods proposed by Smith (1962). While estimates of the actual genetic response to selection were obtained, their sampling errors were quite large. No designed method of estimating the actual genetic change in meatiness was planned as an integral part of this project. The structure of the data was not well suited for obtaining good estimates of actual genetic change.

While Smith's (1962) regression methods did not yield reliable estimates of the genetic change that occurred in these populations, they do contain valuable information. Recall that year to year environmental fluctuations can influence estimates from Smith's Method 1. The tendency for estimates of actual genetic change from Smith's Method 2 to be more conservative than estimates obtained by Smith's Method 1 suggests that year to year environmental fluctuations could have affected these data. Estimates of the actual genetic gain in 154-day weight agree in sign with the genetic improvement anticipated from realized selection; however, the within-age of dam regressions of population performance on time indicate little or no improvement occurred. The phenotypic time trends indicate considerable improvement occurred in carcass meatiness, a result that would not have been anticipated from realized selection as described by the indexes in retrospect. These observations

suggest that nongenetic time trends had an important effect on these data.

As noted earlier there was no significant linear time trend in the inbreeding of dams or pigs for any breed. While increasing levels of inbreeding were shown to be generally detrimental to performance traits, they do not explain the discrepancy between the estimates of phenotypic and genetic time trends.

A deteriorative environment could account for declining performance from pigs with greater genetic potential for growth. Estimates of phenotypic and genetic correlations indicate that slower growing pigs tend to have leaner, meatier carcasses. Increasing disease problems with time might be expected in an SPF herd. It should be noted that the Napier herd doubled in size over the 8 years included in this study without appreciable growth in the facilities to house it or labor force to care for it.

While the measured selection criteria indicate it unlikely, the phenotypic time trends may actually reflect genetic changes made in these populations.

The major objective of this project, measurement of the rate of genetic improvement in meatiness that can be obtained from intense individual, family and progeny selection in purebred swine populations, cannot be directly obtained from these data. The intended criterion of selec-

tion, ham and loin percentage, was not in fact used as the major criterion of selection. Further, the structure of the data was not well suited to obtaining accurate estimates of actual genetic change.

There is, however, an indirect means for estimating the rate of genetic improvement in meatiness that theoretically could have been obtained in these purebred swine populations. Using the constituent indexes for ham and loin percentage in Tables 30 through 39, the potential maximum selection intensities from Table 24 and the average generation intervals reported in Table 26, estimates can be obtained of the potential annual genetic gain in ham and loin percentage that theoretically could have occurred in these populations had ham and loin percentage been the sole criterion of selection. Recall that

$$\Delta g_j = i r_{IA_j} \sigma_{A_j} / \bar{T} = i \sigma_{I_j} / \bar{T} \quad .$$

Additionally, this expected genetic change can be partitioned into that resulting from use of individual, sib and progeny information using a previously described technique. The results in Table 56 show a tremendous potential for genetic improvement in ham and loin percentage.

It is interesting to note that the lines differ both with respect to the amount of genetic improvement expected and the importance of different sources of information in attaining that improvement. In the Duroc line where

Table 56. Percent of the potential annual genetic gain in ham and loin percentage attributable to different sources of information by breed

Breed	Potential annual genetic gain in ham and loin percentage		Percent attributable to use of information on		
	Δg^a	ΔG^b	Individual	Sibs	Progeny
			percent		
Duroc	0.294	0.511	27.5	12.6	59.9
Hampshire	0.555	0.844	45.1	21.1	33.8
Poland	0.724	1.100	18.6	55.0	26.4
Yorkshire	0.779	1.218	50.3	21.6	28.1
Pooled	0.507	0.802	27.5	40.6	31.9

^aIn standard deviation units.

^bIn percent.

heritability was estimated to be low, most of the improvement in ham and loin percent would have resulted from progeny testing with sib data contributing relatively little. Selection on individual records would be the expectant major source of genetic improvement in ham and loin percentage for the Yorkshire and Hampshire breeds. In contrast to the above situations selection on sib records would have accounted for more than half of the genetic improvement in ham and loin percentage of the Poland line. Clearly, no general set of recommended selection practices is appro-

priate to all genetic groups.

It should be pointed out that selection for meatiness as proposed in the project outline may not be the most effective means of increasing the efficiency with which high quality pork is produced. The literature indicates that heavily muscled pigs have a higher frequency of pale, soft exudative muscle tissue. Field reports suggest that in addition to the tendency to produce lower quality pork, meatier strains have a higher incidence of the porcine stress syndrome which results in higher mortality rates.

Carcass characteristics are not the only economically important factors in swine production. To gain insight into the effectiveness of meatiness as a means of increasing the efficiency of pork production, "idealized" selection indexes were constructed using economic values reported by Robison, Chapman and Self (1960). These indexes, presented in Tables 30 through 39, indicate that selection for meatiness would not have maximized the rate of genetic improvement in profitability of the populations included in this study. It should be realized that the expected genetic gain the aggregate breeding values presented in Tables 41 through 45 is limited by the age structure of these populations which may not have been optimal.

"Idealized" selection in the Duroc line would have been expected to result in larger litters and faster growing,

leaner pigs with larger loin eyes. Hampshires would expectantly respond to selection on the "idealized" index by growing faster, but developing poorer carcass cutability characteristics. An increase of 0.15 pigs per litter per year with an improved potential to grow but having poorer carcasses would have been the anticipated response to "idealized" selection in the Poland breeding group. More profitable, faster growing Yorkshires with fatter, less heavily muscled carcasses would have been the expectant result of selection on their "idealized" selection index. The genetic antagonisms noted in the Hampshire, Poland and Yorkshire lines would restrict their potential for genetic improvement in the aggregate breeding value to less than half that anticipated in the Duroc line.

In genetic groups where strong genetic antagonisms between carcass and performance traits exist the genetic response to any type of intense selection may be great enough to invert the relative economic importance of the different traits. Kempthorne and Nordskog (1959) have developed an indexing method which permits no genetic change in a chosen attribute. This in effect limits the intensity of selection practiced for net merit but maintains an economically acceptable level of the restricted element. A restricted selection index may be necessary in certain genetic groups of swine to maintain the level of carcass

merit attained from past selection efforts, yet allow genetic improvement to occur in other economically important traits.

To facilitate a comparison of their response to selection, the same set of economic values, a_i , were used for all the lines of breeding included in this study. However, as Harris (1970) points out, "...the a_i values depend on the population means. Thus a different set of a_i values are probably needed for each genetic group." It should also be pointed out that the relative economic importance of traits may differ substantially for different management systems and for different agricultural and marketing areas.

Weight at 154 days may not be as important to the producer who is farrowing twice a year and finishing pigs on pasture as it is in a continuous farrowing operation where pigs are grown and finished in an artificially controlled environment. Hodson (1970) reported that it costs about 4¢ a day per pig to cover the cost of labor, interest and equipment. His information indicates that each 0.1 pound increase in growth rate corresponds to 5 fewer days for a pig to reach a market weight of 200 pounds or \$.20 savings per pig. For pigs gaining 1.5 pounds a day an increase of 1 pound in 154-day weight would increase net profit by about \$.025. Since his objective was to provide a guide for purchasing boars from central testing stations

where feed efficiency data is available, Hodson's economic value for growth rate does not include that increase in profitability resulting from increased feed efficiency as a correlated response to selecting for faster growth rate. Nevertheless, Hodson's figures may roughly characterize the economic importance of growth rate in less intensive swine production systems. The current trend in swine production is towards relatively expensive confinement systems. Under intensive swine production systems, the rate at which pigs can be grown to market weight is critical to the producer's profit potential.

Reproductive efficiency or the number of pigs marketed per litter is certainly the economically most important trait in any commercial swine enterprise. However, because of its relatively low heritability swine producers have not been encouraged to utilize the additively genetic variability that does exist in this important trait. The "idealized" selection indexes for Durocs and Polands and the genetic response theoretically obtainable from their use indicate the considerable potential for genetic improvement in reproductive performance.

The results obtained in this study indicate the need for individual consulting with producers in designing breeding programs that suit the genetic properties of the swine populations they are dealing with and the economic

characteristics of their swine production operation. If genetic antagonisms between economically important traits are as important as these data indicate they may be in some swine populations, rather complicated selection programs may be needed to genetically improve the efficiency of swine production. It appears likely that more efficient swine production is needed to improve the competitiveness of pork products on the consumer level.

SUMMARY

A selection project was conducted to measure the rate of genetic improvement in meatiness expected to result from intense selection in purebred swine populations. Of particular interest was the utility of individual, family and progeny information in effecting genetic change in ham and loin percentage.

The selection program called for primary selection of boars for minimum backfat probe at 200 pounds. Additional selection was to be based on littermate carcass records with final culling on progeny test data. The intensity, effectiveness and criteria of selection were investigated.

Performance and carcass data were collected over an 8-year period on 460, 414, 661 and 394 purebred Duroc, Hampshire, Poland and Yorkshire litters, respectively.

An index in retrospect was computed for each sex within each genetic group to characterize the selection actually practiced. The indexes in retrospect indicated that the predetermined criteria for selection were not strictly adhered to. Weight at 154 days played an unexpectedly prominent role in the selection practiced within all breeds.

The realized intensity of selection was limited by a high mortality rate among pigs born, lack of utilization of the opportunity for female selection, inefficient use of progeny test data and failure to practice truncation

selection on boars for some predetermined index of merit.

The effectiveness of selection for ham and loin percentage was restricted by the failure to actually use ham and loin percentage as the criterion of selection, failure to achieve the potential intensity of selection and genetic antagonisms between performance and carcass characteristics.

Only a fraction of the potential rate of genetic improvement in ham and loin percentage could have been achieved from the selection actually practiced. Had ham and loin percentage been used as the sole criterion of selection, a potential 0.51, 0.84, 1.10 and 1.22 percent increase per year could theoretically have been achieved in the Duroc, Hampshire, Poland and Yorkshire lines of breeding, respectively.

Phenotypic and genetic parameter estimates indicated that each genetic group would have a characteristic response to selection and that unique selection programs would be required to maximize the rate of genetic improvement in ham and loin percentage. Partitioning of the potential genetic gain in ham and loin percentage into that due to selection on information from individual, family and progeny sources substantiated the conclusion that a common selection program would not be appropriate for the divergent genetic groups included in this study.

Conflicting estimates of the genetic and phenotypic response to selection suggested that nongenetic time trends had an important influence on these data.

The choice of ham and loin percentage as a criterion for selection to genetically improve the efficiency of producing high quality pork was discussed. Sophisticated selection indexes of net merit were judged to be more satisfactory selection criteria. Specialized breeding programs are indicated for dissimilar swine production operations.

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APPENDIX

Table 57. Number of litters and means of inbreeding of dam (%) by breed and year-season

Year-season	Duroc		Hampshire		Poland		Yorkshire		Pooled	
	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}
62S	23	1.89	19	0.00	36	2.19	12	6.39	90	2.32
62F	18	3.12	12	0.00	32	0.49	8	2.56	70	1.56
63S	27	6.11	30	6.51	44	7.39	16	2.21	117	6.09
63F	18	2.89	18	1.97	29	9.28	9	0.00	74	4.32
64S	32	7.46	31	4.20	59	8.88	25	2.24	147	6.28
64F	26	6.64	26	9.90	45	6.08	21	0.00	118	5.81
65S	32	9.92	26	12.50	40	7.59	28	2.81	126	7.56
65F	27	9.71	12	0.77	35	4.00	25	3.42	99	4.90
66S	48	7.71	25	8.84	45	9.15	35	2.68	153	6.87
66F	35	8.86	18	3.78	31	3.66	22	1.80	106	4.72
67S	30	10.25	35	3.43	26	3.78	32	2.96	123	4.76
67F	21	5.64	22	3.74	27	6.31	28	4.34	98	4.97
68S	34	11.79	43	5.23	47	7.68	41	5.86	165	7.36
68F	33	11.57	38	5.93	56	6.61	26	2.48	153	6.55
69S	32	9.70	33	5.14	47	6.16	41	3.13	153	5.76
69F	24	13.59	26	3.77	62	9.54	25	4.38	137	7.98
Overall	460	8.08	414	5.27	661	6.61	394	3.20	1,929	5.83

Table 58. Number of pigs and means of inbreeding of pig (%) by breed and year-season

Year-season	Duroc		Hampshire		Poland		Yorkshire		Pooled	
	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}
62S	165	11.99	117	10.82	194	17.53	90	0.00	566	11.74
62F	132	8.07	54	10.07	152	14.23	39	1.28	377	10.14
63S	176	13.74	207	13.30	269	14.85	113	1.33	765	12.18
63F	94	10.62	89	8.75	130	22.26	70	0.00	383	12.20
64S	184	13.46	165	13.53	361	19.16	201	5.39	911	13.95
64F	140	8.11	154	8.24	280	7.75	142	6.42	176	7.66
65S	135	16.33	115	20.92	200	18.06	188	5.97	638	14.65
65F	143	9.90	63	1.48	208	8.32	162	2.22	576	6.25
66S	285	12.60	172	9.21	324	11.52	313	10.82	1,094	11.24
66F	183	14.67	72	10.76	186	10.57	168	12.01	609	12.22
67S	153	17.70	189	9.35	178	12.79	230	7.40	750	11.27
67F	130	16.69	136	9.46	152	13.20	196	7.69	614	11.35
68S	218	11.27	251	5.24	305	6.05	351	3.00	1,125	5.93
68F	164	12.96	212	6.95	336	9.29	174	6.00	886	8.76
69S	186	14.14	194	5.72	258	11.07	273	7.03	911	9.35
69F	113	15.11	136	7.32	325	11.15	158	5.75	732	9.88
Overall	2,601	12.98	2,326	9.31	3,858	12.52	2,868	6.00	11,653	10.38

Table 59. Number of litters and means of number born per litter by breed and year-season

Year-season	<u>Duroc</u>		<u>Hampshire</u>		<u>Poland</u>		<u>Yorkshire</u>		<u>Pooled</u>	
	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}
62S	23	9.26	19	8.68	36	6.94	12	11.33	90	8.49
62F	18	10.00	12	6.83	32	7.00	8	8.88	70	7.96
63S	27	10.78	30	9.10	44	8.23	16	10.44	117	9.34
63F	18	9.89	18	8.89	29	6.83	9	11.67	74	8.66
64S	32	10.19	31	9.19	59	8.12	25	10.48	147	9.20
64F	26	9.31	26	8.69	45	8.62	21	10.81	118	9.18
65S	32	8.62	26	7.81	40	7.35	28	10.75	126	8.52
65F	27	8.96	12	8.58	35	8.83	25	9.72	99	9.06
66S	48	9.27	25	9.28	45	9.36	35	11.66	153	9.84
66F	35	9.11	18	6.22	31	9.00	22	10.59	106	8.90
67S	30	7.33	35	8.43	26	9.54	32	9.72	123	8.83
67F	21	8.67	22	8.64	27	8.22	28	9.21	98	8.69
68S	34	9.24	43	8.86	47	8.47	41	11.32	165	9.44
68F	33	7.91	38	8.24	56	8.29	26	10.65	153	8.59
69S	32	8.56	33	8.15	47	7.77	41	9.68	153	8.53
69F	24	8.33	26	8.69	62	7.42	25	8.64	137	8.04
Overall	460	9.08	414	8.49	661	8.11	394	10.35	1,929	8.88

Table 60. Number of litters and means of number weaned per litter by breed and year-season

Year-season	<u>Duroc</u>		<u>Hampshire</u>		<u>Poland</u>		<u>Yorkshire</u>		<u>Pooled</u>	
	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}
62S	23	7.17	19	6.11	36	5.36	12	7.50	90	6.27
62F	18	7.28	12	4.50	32	4.75	8	4.62	70	5.34
63S	27	6.59	30	6.90	44	6.07	16	7.06	117	6.54
63F	18	5.17	18	4.89	29	4.38	9	7.78	74	5.11
64S	32	5.72	31	5.29	59	6.08	25	8.04	147	6.17
64F	26	5.38	26	5.88	45	6.20	21	6.71	118	6.04
65S	32	4.16	26	4.38	40	4.98	28	6.68	126	5.02
65F	27	5.22	12	5.25	35	5.91	25	6.48	99	5.79
66S	48	5.94	25	6.84	45	7.18	35	8.91	153	7.13
66F	35	5.20	18	4.00	31	5.97	22	7.59	106	5.72
67S	30	5.10	35	5.40	26	6.85	32	7.09	123	6.07
67F	21	6.19	22	6.14	27	5.59	28	6.96	98	6.23
68S	34	6.41	43	5.79	47	6.49	41	8.56	165	6.81
68F	33	4.94	38	5.53	56	5.93	26	6.69	153	5.75
69S	32	5.72	33	5.85	47	5.28	41	6.59	153	5.84
69F	24	4.62	26	5.23	62	5.18	25	6.32	137	5.30
Overall	460	5.63	414	5.59	661	5.79	394	7.25	1,929	6.01

Table 61. Number of pigs and means of 56-day weight (lb.) by breed and year-season

Year-season	<u>Duroc</u>		<u>Hampshire</u>		<u>Poland</u>		<u>Yorkshire</u>		<u>Pooled</u>	
	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}
62S	165	42.88	116	39.50	192	38.77	90	42.67	563	40.75
62F	131	44.27	54	40.39	152	41.59	37	44.38	374	42.63
63S	176	44.49	207	40.00	267	41.98	113	44.37	763	42.37
63F	93	49.30	88	42.23	127	43.51	70	47.46	378	45.37
64S	183	44.66	164	40.76	359	42.92	201	45.66	907	43.49
64F	140	44.41	153	40.91	279	42.37	141	41.50	713	42.28
65S	133	45.86	114	39.24	199	41.75	187	44.57	633	43.00
65F	141	44.45	63	43.03	207	43.77	162	46.19	573	44.54
66S	285	46.58	171	40.89	323	42.31	312	43.84	1,091	43.64
66F	182	41.74	72	36.22	185	41.82	167	41.17	606	40.95
67S	153	45.78	188	37.85	178	41.92	228	40.27	747	41.18
67F	130	42.82	135	39.56	151	47.50	195	40.04	611	42.36
68S	218	41.11	249	38.78	304	40.62	351	39.83	1,122	40.06
68F	163	41.66	210	38.65	332	40.57	174	37.92	879	39.79
69S	183	42.73	193	40.03	256	37.86	270	41.59	902	40.43
69F	111	37.28	136	35.30	321	34.16	158	36.04	726	35.26
Overall	2,587	43.76	2,313	39.45	3,832	41.13	2,856	41.91	11,588	41.57

Table 62. Number of pigs and means of 154-day weight (lb.) by breed and year-season

Year- season	<u>Duroc</u>		<u>Hampshire</u>		<u>Poland</u>		<u>Yorkshire</u>		<u>Pooled</u>	
	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}
62S	158	196.3	111	172.6	186	171.6	84	191.8	539	182.2
62F	126	190.5	49	170.3	150	179.7	34	192.1	359	183.4
63S	169	200.9	201	177.9	257	189.9	108	205.5	735	191.4
63F	86	215.3	88	188.4	119	189.0	70	204.1	363	198.0
64S	177	203.0	151	179.5	351	187.1	200	203.5	879	192.7
64F	135	182.7	149	173.7	273	183.3	137	176.6	694	179.8
65S	131	207.0	109	180.0	191	191.1	185	205.2	616	196.8
65F	138	205.4	62	197.9	203	200.8	160	207.1	563	203.4
66S	275	199.9	168	194.5	310	195.6	307	197.9	1,060	197.2
66F	171	188.5	70	173.6	182	192.8	163	194.1	586	189.6
67S	152	209.6	188	187.8	172	197.2	223	198.3	735	197.7
67F	122	189.7	135	182.4	149	200.9	187	189.4	593	190.7
68S	209	203.0	241	188.7	292	192.3	341	193.6	1,083	194.0
68F	147	185.9	199	170.5	305	177.5	157	168.1	808	175.5
69S	177	192.0	185	178.3	238	172.8	249	190.8	849	183.3
69F	93	158.4	113	151.5	263	170.2	137	161.3	606	162.9
Overall	2,466	196.4	2,219	179.8	3,641	186.5	2,742	193.0	11,068	189.0

Table 63. Number of carcasses and means of carcass backfat (in.) by breed and year-season

Year-season	Duroc		Hampshire		Poland		Yorkshire		Pooled	
	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}
62S	69	1.52	33	1.31	58	1.45	21	1.49	181	1.46
62F	26	1.47	5	1.40	21	1.46	4	1.64	56	1.47
63S	43	1.48	44	1.30	58	1.45	24	1.44	169	1.42
63F	33	1.40	37	1.28	54	1.51	21	1.50	145	1.42
64S	54	1.51	53	1.37	122	1.44	55	1.57	284	1.47
64F	54	1.50	58	1.31	107	1.59	54	1.54	273	1.50
65S	39	1.52	41	1.39	76	1.53	66	1.51	222	1.50
65F	65	1.40	30	1.25	103	1.45	76	1.48	274	1.43
66S	114	1.39	57	1.23	109	1.37	96	1.40	376	1.36
66F	66	1.43	25	1.30	79	1.45	51	1.49	221	1.44
67S	57	1.46	84	1.32	63	1.35	92	1.48	296	1.40
67F	43	1.46	60	1.26	61	1.48	67	1.52	231	1.43
68S	76	1.46	88	1.23	104	1.33	97	1.38	365	1.34
68F	59	1.42	76	1.18	108	1.36	44	1.46	287	1.34
69S	45	1.42	46	1.28	56	1.31	48	1.45	195	1.36
69F	31	1.30	39	1.18	97	1.32	35	1.32	202	1.29
Overall	874	1.44	776	1.27	1,276	1.42	851	1.47	3,777	1.41

Table 64. Number of carcasses and means of ham and loin percentage (%) by breed and year-season

Year-season	Duroc		Hampshire		Poland		Yorkshire		Pooled	
	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}
62S	69	35.22	33	37.74	58	37.19	21	36.66	181	36.48
62F	26	36.69	5	38.56	21	38.36	4	37.67	56	37.55
63S	43	36.79	44	39.85	58	38.29	24	38.25	169	38.31
63F	33	37.84	37	40.19	54	38.65	21	38.95	145	38.90
64S	54	37.32	53	40.05	122	39.41	55	37.71	284	38.80
64F	54	37.89	58	40.03	107	38.55	54	38.89	273	38.80
65S	39	38.11	41	40.00	76	38.99	66	37.99	222	38.72
65F	65	40.13	30	41.45	103	40.59	76	40.66	274	40.59
66S	114	39.31	57	41.10	109	40.91	96	39.69	376	40.14
66F	66	39.09	25	41.12	79	40.17	51	39.44	221	39.78
67S	57	39.52	84	40.78	63	41.34	92	40.42	296	40.42
67F	43	39.70	60	41.38	61	40.24	67	39.62	231	40.25
68S	76	39.57	88	40.92	104	41.01	97	39.49	365	40.29
68F	59	39.49	76	41.31	108	41.23	44	39.75	287	40.66
69S	45	38.79	46	39.98	56	41.36	48	38.75	195	39.80
69F	31	40.49	39	42.13	97	41.96	35	40.61	202	41.53
Overall	874	38.59	776	40.60	1,276	40.08	851	39.30	3,777	39.67

Table 65. Number of carcasses and means of loin eye area (sq. in.) by breed and year-season

Year-season	<u>Duroc</u>		<u>Hampshire</u>		<u>Poland</u>		<u>Yorkshire</u>		<u>Pooled</u>	
	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}
62S	69	3.32	33	4.15	58	3.91	21	3.78	181	3.71
62F	26	3.64	5	4.39	21	4.41	4	4.00	56	4.02
63S	43	3.47	44	4.61	58	4.15	24	4.04	169	4.08
63F	33	3.91	37	4.84	54	4.52	21	4.48	145	4.46
64S	54	3.54	53	4.57	122	4.51	55	3.93	284	4.22
64F	54	3.95	58	4.82	107	4.65	54	4.34	273	4.48
65S	39	3.79	41	4.61	76	4.43	66	3.86	222	4.18
65F	65	4.55	30	5.43	103	4.94	76	4.81	274	4.87
66S	114	4.05	57	4.97	109	4.72	96	4.19	376	4.42
66F	66	4.07	25	5.29	79	4.97	51	4.40	221	4.61
67S	57	4.19	84	4.89	63	5.05	92	4.40	296	4.64
67F	43	4.49	60	5.36	61	5.09	67	4.50	231	4.88
68S	76	4.45	88	5.02	104	5.18	97	4.48	365	4.80
68F	59	4.49	76	5.41	108	5.33	44	4.83	287	5.10
69S	45	4.43	46	4.86	56	5.23	48	4.52	195	4.79
69F	31	4.34	39	5.01	97	5.13	35	4.54	202	4.88
Overall	874	4.06	776	4.94	1,276	4.81	851	4.36	3,777	4.56

Table 66. Number of probed boars and means of backfat probe (in.) by breed and year-season

Year-season	Duroc		Hampshire		Poland		Yorkshire		Pooled	
	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}	n	\bar{X}
62S	18	1.09	14	1.00	16	1.07	6	1.22	54	1.07
62F	21	0.99	7	0.89	18	1.06	8	1.11	54	1.02
63S	12	1.07	11	0.86	27	1.00	19	1.02	69	1.00
63F	16	0.96	9	0.81	10	1.03	9	0.85	44	0.92
64S	19	0.92	14	0.89	21	0.99	25	0.96	79	0.94
64F	22	0.89	23	0.84	33	0.94	18	0.88	96	0.89
65S	25	1.03	14	0.94	26	0.99	30	1.02	95	1.00
65F	9	0.92	12	0.66	17	0.89	14	0.78	52	0.81
66S	13	0.86	19	0.60	17	0.78	20	0.74	69	0.73
66F	16	0.86	13	0.62	20	0.83	26	0.77	75	0.78
67S	12	0.81	10	0.64	14	0.83	10	0.79	46	0.77
67F	9	0.94	11	0.60	8	0.89	11	0.73	39	0.77
68S	14	1.04	21	0.97	26	0.98	18	1.05	79	1.00
68F	6	0.98	35	0.84	32	0.91	9	1.01	82	0.90
69S	0		0		0		0		0	
69F	0		0		0		0		0	
Overall	212	0.96	213	0.81	285	0.95	223	0.91	933	0.91

Table 67. Number of observations (n) and least squares constants (c) for total litter weight at 56 days by breed and year-season

Factor	Duroc		Hampshire		Poland		Yorkshire	
	n	c	n	c	n	c	n	c
$\hat{\mu}$	307	254.9	317	194.2	402	281.1	278	270.3
Year-season								
62S	20	-46.8	14	-40.7	22	22.6	9	-226.8
62F	6	132.0	9	-60.4	23	-26.8	6	-226.3
63S	17	-75.2	25	0.4	34	55.6	10	6.3
63F	14	-78.8	16	-62.4	14	-4.5	9	25.0
64S	18	-42.5	24	-49.0	25	66.6	18	38.5
64F	20	-61.8	23	-16.9	34	14.4	19	-100.7
65S	23	-48.6	26	-52.9	34	3.1	16	-46.9
65F	24	20.2	12	37.8	15	53.1	22	-33.1
66S	39	82.8	25	67.1	45	65.0	33	86.3
66F	28	40.9	17	-51.4	28	-40.0	17	86.2
67S	24	36.4	35	1.1	24	-2.6	28	117.8
67F	20	77.2	22	61.6	25	-48.3	28	66.4
68S	31	33.4	40	65.6	41	-70.5	41	149.6
68F	23	-69.4	29	100.1	38	-87.6	22	57.6
Age of dam								
1 yr.	130	-21.5	144	-17.3	180	-45.0	99	-36.4
1 1/2 yr.	86	-13.4	75	-17.1	105	12.3	89	-7.2
2 yr.	57	39.5	53	36.3	70	17.2	56	20.1
2 1/2 yr. and older	34	-4.6	45	-1.9	47	15.4	34	23.5
Regression F dam		-.76		-.86		-1.97		-2.50
Regression F pig		-2.49		-.61		-2.22		-2.54

Table 68. Number of observations (n) and least squares constants (c) for number weaned by breed and year-season

Factor	Duroc		Hampshire		Poland		Yorkshire	
	n	c	n	c	n	c	n	c
$\hat{\mu}$	307	5.89	317	5.33	402	6.44	278	6.14
Year-season								
62S	20	-.67	14	0.17	22	0.11	9	-5.00
62F	6	2.21	9	-0.68	23	-1.12	6	-5.21
63S	17	-1.09	25	1.06	34	0.63	10	0.10
63F	14	-1.73	16	-0.71	14	-0.95	9	0.08
64S	18	-.73	24	-0.41	25	1.00	18	0.16
64F	20	-.99	23	0.19	34	-0.00	19	-2.31
65S	23	-.98	26	1.50	34	-0.20	16	-1.67
65F	24	.58	12	0.18	15	1.26	22	-1.57
66S	39	1.56	25	1.24	45	1.83	33	1.55
66F	28	1.05	17	-1.55	28	-0.47	17	1.96
67S	24	.44	35	-0.64	24	0.38	28	2.45
67F	20	1.66	22	0.51	25	-0.88	28	2.55
68S	31	.88	40	0.66	41	-0.51	41	4.33
68F	23	-2.19	29	1.48	38	-1.07	22	2.60
Age of dam								
1 yr.	130	-.34	144	-0.32	180	-0.64	99	-0.37
1 1/2 yr.	86	-.38	75	-0.27	105	0.28	89	0.07
2 yr.	57	..90	53	0.71	70	0.10	56	0.20
2 1/2 yr. and older	34	-.18	45	-0.12	47	0.26	34	0.10
Regression F dam		-.018		-.014		-.047		-.058
Regression F pig		-.036		-.017		-.035		-.052

Table 69. Number of observations (n) and least squares constants (c) for 56-day weight by breed and year-season

Factor	Duroc		Hampshire		Poland		Yorkshire	
	n	c	n	c	n	c	n	c
$\hat{\mu}$	1698	43.08	1733	37.41	2380	43.55	2047	43.59
Year-season								
62S	132	-2.58	80	-2.82	116	1.24	65	-.69
62F	55	1.02	42	-.87	119	1.66	26	0.28
63S	112	-3.27	169	-5.77	209	3.06	65	-.11
63F	68	-.31	83	-5.84	63	5.35	70	1.38
64S	103	-2.06	118	-5.29	146	3.93	152	3.93
64F	102	-3.51	132	-3.30	217	2.48	126	-.98
65S	104	-1.33	109	1.92	161	1.62	109	3.48
65F	128	-1.55	62	5.12	100	-.24	144	4.52
66S	229	2.93	168	2.82	310	-1.47	286	1.95
66F	130	-.39	68	0.09	166	-2.54	131	-.60
67S	115	3.77	188	3.97	152	-2.30	205	-2.26
67F	121	2.24	135	5.38	143	-.45	187	-2.47
68S	193	4.08	225	5.11	257	-6.63	341	-3.28
68F	106	0.96	154	5.48	221	-5.71	140	-5.15
Sex								
Males	778	0.23	885	0.36	1202	0.19	1063	0.22
Females	920	-.23	848	-.36	1178	-.19	984	-.22
Age of dam								
1 yr.	655	-1.42	734	-1.17	992	-2.48	651	-2.59
1 1/2 yr.	463	0.89	400	-.46	642	0.05	676	-.93
2 yr.	382	-.27	350	1.27	441	1.87	469	1.26
2 1/2 yr. and older	198	0.80	249	0.36	305	0.57	251	2.26
Regression F dam		0.011		-.060		-.005		-.018
Regression F pig		-.156		0.023		-.128		-.066

Table 70. Number of observations (n) and least squares constants (c) for 154-day weight by breed and year-season

Factor	Duroc		Hampshire		Poland		Yorkshire	
	n	c	n	c	n	c	n	c
$\hat{\mu}$	1698	192.54	1733	185.47	2380	192.20	2047	198.68
Year-season								
62S	132	-6.75	80	10.80	116	-0.39	65	17.17
62F	55	-16.57	42	5.12	119	3.75	26	6.55
63S	112	-1.63	169	2.75	209	14.46	65	3.52
63F	68	5.60	83	-7.98	63	18.98	70	11.63
64S	103	-3.83	118	-10.93	146	7.17	152	11.06
64F	102	-27.00	132	-18.71	217	-6.50	126	-16.06
65S	104	11.16	109	8.31	161	9.10	109	9.62
65F	128	1.21	62	11.28	100	5.16	144	8.99
66S	229	8.04	168	16.01	310	0.87	286	2.04
66F	130	0.08	68	-6.30	166	-5.81	131	-2.16
67S	115	21.01	188	11.10	152	-2.08	205	-0.07
67F	121	4.44	135	-0.26	143	-6.25	187	-11.62
68S	193	11.44	225	0.62	257	-11.91	341	-7.84
68F	106	-7.19	154	-21.81	221	-26.59	140	-32.82
Sex								
Males	778	7.85	885	8.37	1202	8.20	1063	10.25
Females	920	-7.85	848	-8.37	1178	-8.20	984	-10.25
Age of dam								
1 yr.	655	1.40	734	-5.41	992	-4.45	651	-7.83
1 1/2 yr.	463	2.85	400	1.57	642	0.68	676	-1.86
2 yr.	382	-2.00	350	2.63	441	2.25	469	-0.45
2 1/2 yr. and older	198	-2.25	249	1.21	305	1.52	251	10.14
Regression F dam		0.14		-.17		.01		-.04
Regression F pig		-.85		-.29		-.70		-.67

Table 71. Number of observations (n) and least squares constants (c) for carcass backfat by breed and year-season

Factor	Duroc		Hampshire		Poland		Yorkshire	
	n	c	n	c	n	c	n	c
\bar{L}	635	1.44	628	1.35	842	1.43	673	1.53
Year-season								
62S	62	0.01	24	0.22	39	0.06	19	0.51
62F	11	-.07	5	0.25	16	0.03	3	0.44
63S	28	-.01	36	0.10	40	-.00	12	-.17
63F	24	-.01	35	0.03	32	0.06	21	-.01
64S	32	0.12	40	0.14	54	-.01	42	0.04
64F	41	0.10	52	0.03	87	0.07	51	0.04
65S	29	0.08	41	0.07	61	0.06	40	-.00
65F	58	0.05	30	-.07	43	0.01	68	-.03
66S	95	-.06	57	-.03	109	-.07	90	-.08
66F	51	0.01	25	-.05	73	-.04	41	-.05
67S	49	-.02	84	-.07	58	-.05	82	-.13
67F	42	-.07	60	-.15	59	0.02	67	-.14
68S	70	0.06	82	-.16	91	-.09	97	0.22
68F	43	-.01	57	-.30	80	-.06	40	0.21
Sex								
Males	414	0.03	448	0.01	618	0.04	526	0.07
Females	221	-.03	180	-.01	224	-.04	147	-.07
Age of dam								
1 yr.	265	0.03	282	-.01	362	0.00	221	-.05
1 1/2 yr.	169	-0.01	139	0.00	215	0.00	216	0.00
2 yr.	132	-0.01	111	-.02	160	0.00	154	0.03
2 1/2 yr. and older	69	-0.01	96	0.03	105	-.01	82	0.02
Regression F dam		-.001		-.001		-.000		0.001
Regression F pig		-.001		-.001		-.000		-.001
Regression carcass wt.		-.007		0.006		0.007		0.008

Table 72. Number of observations (n) and least squares constants (c) for ham and loin percentage by breed and year-season

Factor	Duroc		Hampshire		Poland		Yorkshire	
	n	c	n	c	n	c	n	c
$\bar{\mu}$	635	38.92	628	40.44	842	40.05	673	38.82
Year-season								
62S	62	-1.64	24	-2.67	39	-1.01	19	-3.18
62F	11	0.07	5	-1.62	16	-.27	3	-2.11
63S	28	-.06	36	-.93	40	0.17	12	-.44
63F	24	-.18	35	-.68	32	0.44	21	-.53
64S	32	-.80	40	-.72	54	-.09	42	-1.15
64F	41	-.82	52	-.68	87	-.78	51	-.53
65S	29	-.41	41	-.90	61	-.47	40	-1.05
65F	58	1.48	30	1.07	43	0.09	68	1.84
66S	95	0.77	57	0.42	109	0.59	90	0.75
66F	51	0.19	25	1.51	73	0.37	41	0.62
67S	49	0.49	84	1.03	58	0.86	82	1.01
67F	42	0.71	60	1.71	59	0.22	67	1.55
68S	70	0.06	82	1.14	91	0.44	97	1.61
68F	43	0.14	57	1.30	80	0.67	40	1.61
Sex								
Males	414	-.23	448	-.32	618	-.67	526	-.74
Females	221	0.23	180	0.32	224	0.67	147	0.74
Age of dam								
1 yr.	265	-.28	282	-.14	362	-0.07	221	0.35
1 1/2 yr.	169	0.07	139	-.10	215	0.06	216	-.05
2 yr.	132	0.18	111	0.21	160	-.08	154	-.22
2 1/2 yr. and older	69	0.02	96	0.03	105	0.08	82	-.08
Regression F dam		0.006		0.001		0.011		0.002
Regression F pig		0.026		0.009		-.010		0.018
Regression carcass wt.		-.040		-.040		-.034		-.030

Table 73. Number of observations (n) and least squares constants (c) for loin eye area by breed and year-season

Factor	Duroc		Hampshire		Poland		Yorkshire	
	n	c	n	c	n	c	n	c
$\bar{\mu}$	635	4.20	628	5.04	842	4.85	673	4.59
Year-season								
62S	62	0.19	24	0.03	39	-.00	19	-.22
62F	11	0.38	5	0.01	16	-.21	3	-.01
63S	28	0.15	36	-.14	40	-.12	12	0.26
63F	24	0.07	35	-.07	32	-.09	21	0.27
64S	32	-.28	40	-.19	54	-.17	42	-.15
64F	41	-.26	52	0.01	87	-.28	51	0.07
65S	29	-.32	41	-.68	61	-.21	40	-.34
65F	58	0.19	30	0.46	43	-.02	68	0.56
66S	95	-.06	57	-.08	109	0.09	90	-.03
66F	51	-.09	25	0.21	73	0.13	41	0.06
67S	49	0.02	84	-.16	58	0.21	82	-.14
67F	42	0.13	60	0.26	59	0.21	67	0.01
68S	70	-.07	82	0.05	91	0.20	97	0.19
68F	43	-.22	57	0.29	80	0.27	40	0.14
Sex								
Males	414	-.22	448	-.18	618	-.26	526	-.27
Females	221	0.22	180	0.18	224	0.26	147	0.27
Age of dam								
1 yr.	265	-.04	282	-.06	362	0.03	221	-.06
1 1/2 yr.	169	0.03	139	0.05	215	0.04	216	-.06
2 yr.	132	0.05	111	-.05	160	-.05	154	-.00
2 1/2 yr. and older	69	-.04	96	0.06	105	-.01	82	0.12
Regression F dam		0.004		0.003		0.001		0.003
Regression F pig		0.009		0.004		0.000		-.000
Regression carcass wt.		0.017		0.017		0.020		0.017

Table 74. Number of observations (n) and least squares constants (c) for backfat probe by breed and year-season

Factor	Duroc		Hampshire		Poland		Yorkshire	
	n	c	n	c	n	c	n	c
$\hat{\mu}$	201	0.98	206	0.71	228	0.97	216	0.97
Year-season								
62S	21	0.52	16	0.11	14	0.06	11	1.67
62F	17	0.29	5	-.13	17	-.02	8	1.39
63S	12	0.27	10	0.06	24	0.12	19	-.07
63F	15	-.09	9	0.13	4	0.14	9	-.06
64S	19	-.13	11	0.07	9	0.07	21	-.06
64F	17	-.19	20	0.02	22	0.10	17	-.16
65S	25	0.06	14	-.04	22	0.12	31	-.15
65F	9	-.11	13	-.22	7	-.08	13	-.32
66S	12	-.13	19	-.27	17	-.17	20	-.26
66F	12	-.18	12	-.22	20	-.18	24	-.22
67S	12	-.22	10	-.10	12	-.18	8	-.06
67F	9	-.15	11	-.06	7	-.19	11	-.04
68S	14	0.01	21	0.36	25	-.08	15	-.97
68F	7	0.05	35	0.30	28	-.15	9	-.91
Age of dam								
1 yr.	80	-.04	80	0.07	86	-.02	72	0.03
1 1/2 yr.	68	0.01	53	-.01	60	0.01	65	-.01
2 yr.	33	0.06	39	-.01	47	0.01	46	0.00
2 1/2 yr. and older	20	-.03	34	-.04	35	0.00	33	-.02
Regression F dam		-.001		-.000		-.002		-.001
Regression F pig		-.000		0.002		0.001		-.004

Table 75. Summary of analysis of variance for Duroc breed^a

<u>Total litter wt.</u>			<u>Number weaned</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	33,119 **	Year	6	13.46 *
Season	1	7,800	Season	1	0.76
Y X S	6	44,299 **	Y X S	6	21.32 **
Age of dam	3	26,161	Age of dam	3	14.82 *
Reg. F dam	1	16,889	Reg. F dam	1	9.01
Reg. F pig	1	142,229 **	Reg. F pig	1	30.16 *
Sires	27	17,345 *	Sires	27	6.87
Residual	261	10,818	Residual	261	5.33

k = 10.77
 \bar{F} pig = 14.19

k = 10.77
 \bar{F} pig = 14.19

<u>56-day weight</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	100.4
Season	1	50.7
Y X S	6	306.3 **
Sex	1	88.0
Age of dam	3	215.4 *
Reg. F dam	1	15.4
Reg. F pig	1	2891.5 **
Sires	27	262.6 **
Residual	1,651	69.7

k = 59.47
 \bar{F} pig = 12.99

<u>154-day weight</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	7,142 **
Season	1	19,825 **
Y X S	6	3,832 **
Sex	1	101,661 **
Age of dam	3	1,328
Reg. F dam	1	2,790
Reg. F pig	1	86,913 **
Sires	27	5,631 **
Residual	1,651	750

k = 59.47
 \bar{F} pig = 12.99

^a ** P < 0.01 .
 * P < 0.05 .

Table 75 (Continued)

<u>Carcass backfat</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	0.0586 *
Season	1	0.0687
Y X S	6	0.0665 *
Sex	1	0.4376 **
Age of dam	3	0.0137
Reg. F dam	1	0.0482
Reg. F pig	1	0.0168
Reg. carcass wt.	1	2.2239 **
Sires	27	0.0758 **
Residual	587	0.0261

k = 22.32
 \bar{F} pig = 13.32

<u>Ham and loin percentage</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	7.39 *
Season	1	9.59
Y X S	6	11.84 **
Sex	1	214.83 **
Age of dam	3	1.87
Reg. F dam	1	1.71
Reg. F dam	1	27.12 **
Reg. carcass wt.	1	64.53 **
Sires	27	5.32 **
Residual	587	2.68

k = 22.32
 \bar{F} pig = 13.32

<u>Loin eye area</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	0.395
Season	1	0.157
Y X S	6	0.865 **
Sex	1	23.949 **
Age of dam	3	0.157
Reg. F dam	1	0.821
Reg. F pig	1	3.198 **
Reg. carcass wt.	1	11.023 **
Sires	27	1.772 **
Residual	587	0.267

k = 22.32
 \bar{F} pig = 13.32

<u>Backfat probe</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	0.0854 **
Season	1	0.1730 *
Y X S	6	0.0569
Age of dam	3	0.0315
Reg. F dam	1	0.0253
Reg. F pig	1	0.0011
Sires	27	0.0305
Residual	155	0.0271

k = 6.97
 \bar{F} pig = 11.96

Table 76. Summary of analysis of variance for Hampshire breed^a

<u>Total litter wt.</u>			<u>Number weaned</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	3,690	Year	6	2.50
Season	1	120	Season	1	0.59
Y X S	6	39,589 **	Y X S	6	20.53 **
Age of dam	3	27,255 *	Age of dam	3	9.80
Reg. F dam	1	13,762	Reg. F dam	1	3.55
Reg. F pig	1	5,940	Reg. F pig	1	4.43
Sires	27	9,428	Sires	27	5.79
Residual	271	10,080	Residual	271	6.12

$k = 11.15$
 $\bar{F} \text{ pig} = 10.29$

$k = 11.15$
 $\bar{F} \text{ pig} = 10.29$

<u>56-day weight</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	249.8 **
Season	1	109.6
Y X S	6	117.1
Sex	1	212.3
Age of dam	3	218.0 *
Reg. F dam	1	318.2 *
Reg. F pig	1	45.3
Sires	27	266.0 **
Residual	1,686	60.8

$k = 60.74$
 $\bar{F} \text{ pig} = 9.57$

<u>154-day weight</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	5,230 **
Season	1	13,671 **
Y X S	6	2,636 **
Sex	1	118,065 **
Age of dam	3	1,869 *
Reg. F dam	1	2,658 *
Reg. F pig	1	7,319 **
Sires	27	4,637 **
Residual	1,686	667

$k = 60.74$
 $\bar{F} \text{ pig} = 9.57$

^a ** $P < 0.01$.
 * $P < 0.05$.

Table 76 (Continued)

<u>Carcass backfat</u>			<u>Ham and loin percentage</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	0.0611 **	Year	6	3.71
Season	1	0.2081 **	Season	1	20.52 **
Y X S	6	0.0279	Y X S	6	4.40 *
Sex	1	0.0316	Sex	1	46.81 **
Age of dam	3	0.0411	Age of dam	3	1.95
Reg. F dam	1	0.0198	Reg. F dam	1	0.07
Reg. F pig	1	0.0376	Reg. F pig	1	2.78
Reg. carcass wt.	1	1.2658 **	Reg. carcass wt.	1	55.32 **
Sires	27	0.0372 **	Sires	27	6.21 **
Residual	580	0.0163	Residual	580	1.86

$k = 22.14$
 $\bar{F} \text{ pig} = 9.87$

$k = 22.14$
 $\bar{F} \text{ pig} = 9.87$

<u>Loin eye area</u>			<u>Backfat probe</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	0.127	Year	6	0.1605 **
Season	1	4.084 **	Season	1	0.0340
Y X S	6	1.120 **	Y X S	6	0.0481 **
Sex	1	15.007 **	Age of dam	3	0.0186
Age of dam	3	0.272	Reg. F dam	1	0.0001
Reg. F dam	1	0.258	Reg. F pig	1	0.0231
Reg. F pig	1	0.468	Sires	27	0.0279 **
Reg. carcass wt.	1	10.429 **	Residual	160	0.0110
Sires	27	1.431 **			
Residual	580	0.322			

$k = 22.14$
 $\bar{F} \text{ pig} = 9.87$

$k = 7.21$
 $\bar{F} \text{ pig} = 7.49$

Table 77. Summary of analysis of variance for Poland

<u>Total litter wt.</u>			<u>Number weaned</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	9,848	Year	6	2.79
Season	1	65,383 *	Season	1	34.90 *
Y X S	6	21,243	Y X S	6	11.94 *
Age of dam	3	32,235 *	Age of dam	3	7.66
Reg. F dam	1	115,594 **	Reg. F dam	1	66.26 **
Reg. F pig	1	196,197 **	Reg. F pig	1	48.46 **
Sires	27	13,761	Sires	27	7.52
Residual	356	10,020	Residual	356	5.26
<hr/>			<hr/>		
$k = 14.30$			$k = 14.30$		
$\bar{F} \text{ pig} = 13.79$			$\bar{F} \text{ pig} = 13.79$		
<hr/>			<hr/>		
<u>56-day weight</u>			<u>154-day weight</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	438.8 **	Year	6	8,171 **
Season	1	5.7	Season	1	5,511 **
Y X S	6	132.4 *	Y X S	6	3,687 **
Sex	1	84.2	Sex	1	158,171 *
Age of dam	3	736.3 **	Age of dam	3	1,883 *
Reg. F dam	1	3.6	Reg. F dam	1	22
Reg. F pig	1	3472.0 **	Reg. F pig	1	103,184 **
Sires	27	181.0 **	Sires	27	2,974 **
Residual	2,333	62.8	Residual	2,333	531
<hr/>			<hr/>		
$k = 84.70$			$k = 84.70$		
$\bar{F} \text{ pig} = 12.35$			$\bar{F} \text{ pig} = 12.35$		

^a ** $P < 0.01$.
 * $P < 0.05$.

Table 77 (Continued)

<u>Carcass backfat</u>			<u>Ham and loin percentage</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	0.0489 *	Year	6	2.04
Season	1	0.0521	Season	1	0.12
Y X S	6	0.0371	Y X S	6	5.17 *
Sex	1	0.8236 **	Sex	1	257.83 **
Age of dam	3	0.0019	Age of dam	3	0.89
Reg. F dam	1	0.0049	Reg. F dam	1	7.70 *
Reg. F pig	1	0.0022	Reg. F pig	1	7.76 *
Reg. carcass	1	2.6013 **	Reg. carcass	1	64.94 **
wt.			wt.		
Sires	27	0.1056 **	Sires	27	13.38 **
Residual	794	0.0191	Residual	794	1.85

k = 29.92
 \bar{F} pig = 12.98

k = 29.92
 \bar{F} pig = 12.98

<u>Loin eye area</u>			<u>Backfat probe</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	0.269	Year	6	0.0400 *
Season	1	0.002	Season	1	0.0359 *
Y X S	6	0.230	Y X S	6	0.0180
Sex	1	38.402 **	Age of dam	3	0.0050
Age of dam	3	0.240	Reg. F dam	1	0.0360
Reg. F dam	1	0.076	Reg. F pig	1	0.0059
Reg. F pig	1	0.000	Sires	27	0.0364 **
Reg. carcass	1	23.199 **	Residual	182	0.0151
wt.					
Sires	27	2.173 **			
Residual	794	0.297			

k = 29.92
 \bar{F} pig = 12.98

k = 8.05
 \bar{F} pig = 11.41

Table 78. Summary of analysis of variance for Yorkshire breed^a

<u>Total litter wt.</u>			<u>Number weaned</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	38,058 *	Year	6	25.04 **
Season	1	23,934	Season	1	8.23
Y X S	6	23,960	Y X S	6	8.63
Age of dam	3	17,909	Age of dam	3	1.84
Reg. F dam	1	74,926 *	Reg. F dam	1	39.59 *
Reg. F pig	1	64,596 *	Reg. F pig	1	27.02
Sires	27	16,757	Sires	27	8.88
Residual	232	13,847	Residual	232	7.74
<hr/>			<hr/>		
$k = 9.82$			$k = 9.82$		
$\bar{F} \text{ pig} = 6.32$			$\bar{F} \text{ pig} = 6.32$		
<hr/>			<hr/>		
<u>56-day weight</u>			<u>154-day weight</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	348.5 **	Year	6	6,555 **
Season	1	147.6	Season	1	20,428 **
Y X S	6	209.1 *	Y X S	6	6,598 **
Sex	1	99.1	Sex	1	209,619 **
Age of dam	3	793.8 **	Age of dam	3	9,476 **
Reg. F dam	1	25.5	Reg. F dam	1	116
Reg. F pig	1	275.9 *	Reg. F pig	1	28,323 **
Sires	27	340.8 **	Sires	27	2,835 **
Residual	2,000	62.5	Residual	2,000	668
<hr/>			<hr/>		
$k = 72.29$			$k = 72.29$		
$\bar{F} \text{ pig} = 6.05$			$\bar{F} \text{ pig} = 6.05$		

^a ** $P < 0.01$.
 * $P < 0.05$.

Table 78 (Continued)

<u>Carcass backfat</u>			<u>Ham and loin percentage</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	0.0954 **	Year	6	6.08 **
Season	1	0.0105	Season	1	20.73 **
Y X S	6	0.0312	Y X S	6	14.73 **
Sex	1	1.7717 **	Sex	1	218.32 **
Age of dam	3	0.0806 *	Age of dam	3	3.57
Reg. F dam	1	0.0150	Reg. F dam	1	0.10
Reg. F pig	1	0.0231	Reg. F pig	1	6.90
Reg. carcass wt.	1	3.0789 **	Reg. carcass wt.	1	47.60 **
Sires	27	0.0978 **	Sires	27	10.82 **
Residual	625	0.0249	Residual	625	2.09

$\bar{k} = 23.76$
 $\bar{F} \text{ pig} = 6.44$

$\bar{k} = 23.76$
 $\bar{F} \text{ pig} = 6.44$

<u>Loin eye area</u>			<u>Backfat probe</u>		
<u>Source</u>	<u>df</u>	<u>M.S.</u>	<u>Source</u>	<u>df</u>	<u>M.S.</u>
Year	6	0.360	Year	6	0.2349 *
Season	1	1.991 **	Season	1	0.0400
Y X S	6	1.328 **	Y X S	6	0.0343
Sex	1	29.765 **	Age of dam	3	0.0035
Age of dam	3	0.414	Reg. F dam	1	0.0030
Reg. F dam	1	0.270	Reg. F pig	1	0.0766
Reg. F pig	1	0.004	Sires	27	0.1680
Reg. carcass wt.	1	15.641 **	Residual	170	0.1092
Sires	27	1.501 **			
Residual	625	0.251			

$\bar{k} = 23.76$
 $\bar{F} \text{ pig} = 6.44$

$\bar{k} = 7.58$
 $\bar{F} \text{ pig} = 4.54$