Master of Science Animal Science

ABSTRACT

Brian Wayne Kennedy

COMPARISON OF TECHNIQUES FOR EVALUATION OF SIRES AND MATING SYSTEMS IN SWINE

The effects of sire and mating system on growth and carcass traits in swine were investigated using within litter (double mating), within dam (sequential mating), random mating and field data evaluation techniques. Data involving 80 double mated litters (697 pigs), 312 sequential mated litters, 718 random mated litters and 622 field litters were analyzed by least squares methods. Sire effects were important for post-weaning growth and carcass traits while mating system effects were important only for post-weaning growth. Based on the number of litters required to detect significant differences, double mating was the most efficient evaluation technique.

The practical application of blood group markers for a double mating program and the effects of double mating on litter size and sex ratio were evaluated. The relationship of blood group factors to economic traits also was investigated.

Suggested short title

SIRE AND MATING SYSTEM EVALUATION

IN SWINE

COMPARISON OF TECHNIQUES FOR EVALUATION OF SIRES AND MATING SYSTEMS IN SWINE

by

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A thesis submitted to the Faculty of Graduate Studies and Research in partial fulfilment of the requirements for the degree of Master of Science.

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July 1970

ACKNOWLEDGEMENTS

The author wishes to express his deepest gratitude to Dr. J. E. Moxley for his encouragement and guidance throughout this study. Also special thanks go to Miss Ruth Saison of the Ontario Veterinary College for her co-operation and assistance.

The willing technical help of Mr. R. M. Channon and Mr. A. Sutherland, both of the Animal Science Department, is gratefully appreciated. The author wishes to thank also his parents, Mr. and Mrs. D. R. Kennedy, and Miss Maria Therese Boris for typing the manuscript.

The support of the Quebec Agricultural Research Council through its financial assistance to this project is appreciated.

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I. INTRODUCTION

In livestock production, the expression of any quantitative trait is a function of both genotype and environment. A substantial portion of the variation observed in most economic traits is not, however, attributable to specific genetic and environmental factors but is of nonspecific origin and as such is often called uncontrollable variation.

Complexities involved in the identification and reduction of this variation have prevented animal breeders from attaining the progress that has been achieved by plant breeders and laboratory geneticists. Difficulties, often peculiar to large animal experiments, such as long generation intervals, the high cost of maintaining large livestock populations and the problems of non-homogeneous material, frequently result in experiments lacking adequate population size, replication and precision to yield conclusive results. More effective control over 'uncontrollable' variation could permit animal geneticists to obtain substantive results with smaller numbers of animals and thus reduce the time and cost of experimentation.

Genetic improvement in livestock is achieved through the exploitation of the genetic variation that exists between individual animals and mating systems. Our ability to effectively assess genetic differences lies in our ability to develop evaluation techniques capable of reducing the 'uncontrollable' variation that often masks true genetic differences.

We cannot assume that all animals located on the same farm or experimental station function under uniform conditions. Animals which share a common dam, housing unit and time of birth exhibit less variation than do those which have only general location and management practices in common. The use of litter mates in swine affords us the opportunity to develop techniques which can control some of these sources of variation and thus provide more efficient evaluation of the genetic merit of sires and mating systems.

The purpose of this project was to compare the effectiveness of several techniques designed for the evaluation of sires and mating systems in swine. Inherent with these techniques are differential abilities to control variation generally attributed to the effects of dam and litter differences. The techniques are

i) the use of random matings, using both field and experimental data, to compare sires and mating systems on a between litter basis,

ii) the use of sequential matings to provide between litter within dam comparisons and

iii) the use of double matings (mixed litter technique) to provide within litter within dam comparisons.

The double mating technique requires the use of mixed inseminations and the accurate matching of pigs from mixed litters with their respective sires. Paternity or sire identification is established through the use of color or blood group genetic markers. As an auxiliary study, this project considered also

i) some biological effects of double mating or mixed insemination and

ii) the relationship of some blood group factors to economic traits in swine.

II. REVIEW OF LITERATURE

1. Selection and Sire Evaluation

"In the genetic improvement of swine man is concerned with replacing an existing population of genotypes with another which is superior in some particular feature or features of economic merit. Selection is generally conceded to be the main force at man's command for accomplishing this purpose and is most simply defined as a non-random designation of the individuals to be the parents of the next generation." (Fredeen, 1958).

A substantial amount of experimental knowledge relative to the effects of selection on most economic traits in swine has been accumulated over the past few decades. Theoretical and experimental considerations of the modes of gene action upon which selection techniques can best capitalize have also received wide attention.

Comstock and Winters (1944) and Rempel and Winters (1952) reported effective selection for both litter size and growth in inbred Poland China lines. Fine and Winters (1952) observed similar results selecting for litter size in Minnesota No. 1 and Minnesota No. 2 lines. In a study using two non-inbred Chester White and Duroc herds, Damon and Winters (1955) reported that selection was effective, although slow, for improvement in the number of pigs farrowed and average weaning weight.

In contradiction, Dickerson (1951) disclosed at a symposium on the effectiveness of selection that selection conducted in 49 strains from five research projects showed negligible improvement in litter size and growth rate. In support of Dickerson's view, Bradford et al. (1958) found that selection practiced for performance traits with inbred Chester White and Yorkshire lines during their development was ineffective. Fredeen (1958), however, pointed out that most of these selection studies were subjected to inbreeding and attributed the conflicting interpretations on the effectiveness of selection for litter size and early growth to difficulties in the accurate estimation of inbreeding decline.

Reports on the effect of selection on post-weaning traits are more consistent. Krider *et al.* (1946) reported the effective separation of rapid and slow growing Hampshire lines in four generations. Dickerson and Grimes (1947) successfully selected for high and low feed requirements in two strains of Duroc swine for five generations.

Another experiment, conducted by Craig *et al.* (1956), split a Hampshire foundation stock into two lines for large and small body size which, after ten generations, differed by 50 pounds at 180 days of age. Dettmers *et al.* (1965) selected for small size to develop a miniature pig for research purposes and over an eleven year period reduced body size at 140 days of age by 29 percent.

The introduction of the live backfat probe by Hazel and Kline (1952) has facilitated research in effective selection for backfat thickness. Hetzer and Harvey (1967) have reported on selection for both high and low backfat thickness in two Duroc and two Yorkshire lines while maintaining an unselected control in each breed. After ten generations, there was a 68 percent differential in backfat thickness between the two Duroc lines and in the Yorkshire lines a difference of 44 percent after eight generations of selection was observed. In one-directional selection work conducted in Missouri, Zoellner *et al.* (1963) practiced effective selection for thinner backfat and Gray *et al.* (1968) reported a 20 percent decrease in the backfat thickness of a Poland China line after five generations of selection.

Most selection experiments have involved selection for only one trait or closely correlated traits and are of limited relevance to the commercial pig producer who must select for a variety of productive and reproductive characteristics. Three methods - tandem selection involving selection for one trait at a time, selection for several characteristics at a time through independent culling levels and selecting several traits on the basis of a total score or selection index - have been proposed where selection for several traits is to be practiced. Hazel and Lush (1942) and Young (1961) demonstrated that the selection index method is theoretically superior to the method of independent culling levels which in turn is never inferior to tandem selection.

Several swine selection indexes have been proposed in the literature (Hazel, 1943; Bernard *et al.*, 1954; Robison *et al.*, 1960; and others).

The relative effectiveness of selection for the improvement of a trait is largely contingent upon the degree of heritability exhibited by that trait; heritability being an estimation of the consequence of additive genetic inheritance in the expression of that trait.

A detailed examination of theoretical considerations and methods of heritability estimation has been provided by Lush (1948). Extensive reviews of heritability estimates from the literature have been presented by Craft (1953) and Fredeen (1953). Estimates, for any given trait, show considerable variation which can be attributed to several causes - population differences, the mating system used may deviate from random more than anticipated, sampling errors, and differences in the relative effectiveness of various estimation procedures in excluding environmental and non-additive genetic influences from the estimate (Lush, 1940; Fredeen, 1958).

Craft (1958) and Hazel (1963) have prepared composite averages of heritability estimates for several productive and reproductive criteria in swine. Some average heritabilities, selected from Hazel (1963), are presented as follows:

AVERAGE HERITABILITIES OF ECONOMIC TRAITS

Trait	Approx. % Heritability
Litter size	10
Birth weight	15
Weaning weight	15
Post-weaning growth rate	30
Feed efficiency	30
Backfat thickness	50
Percent lean in carcass	50
Area of *longissimus dorsi*	50
Length of body	60

Evident from this illustration is the fact that heritabilities are highest for traits expressed later in life and that reproductive and pre-weaning growth traits are of low heritability. This is consistent with the inconclusive experimental evidence experienced in selection for traits expressed at birth or early in life and general experimental success in selecting for post-weaning growth and carcass traits, particularly where measurement on the live animal is feasible.

According to Hazel (1963), mass selection is limited in its effectiveness to selection for increased growth and other traits which can be measured directly on the animals to be selected. Progeny testing and family selection, however, have proved useful in the improvement of carcass composition traits. Cunningham (1965) has also advocated progeny testing as useful when the heritability of the trait under selection is low.

The best documented evidence for substantial field improvement through the use of progeny testing has been recorded in Denmark. Lush (1936) has explained the system and described the subsequent changes in characteristics of Danish Landrace and Large White swine from the program's inception in 1907 until 1935. Fredeen (1958) traced population improvement in Danish pigs, based on Danish progeny test data, from 1926 to 1956. Over the thirty year period, effective field selection was practiced for rate of growth, efficiency of gain, carcass length, depth of backfat and belly thickness.

A more recent report by Smith (1963) has shown that backfat thickness in Danish Landrace decreased an average of 5.7 mm, or over 13 percent, during the period 1952-60. Smith estimated, however, that only one-fifth of this improvement represented genetic change with the balance being attributed to environmental causes.

In the United States, the effectiveness of selection in the field has received comment by several workers. Christians (1969) attributed herd and breed improvement in the Minnesota swine population to on farm and central evaluation testing programs. The improvement made in productive and carcass traits through two testing stations over a ten year period is shown in the following summaries:

PRODUCTION SUMMARY

Spring Season	Average Daily Gain (lbs./day)	Age at 200 lbs. (days)	Feed Efficiency (lbs./cwt. gain)
1958	1.85	152	303
1963	1.88	149	296
1968	1.91	142	283

CARCASS SUMMARY

Spring Season	Length (in.)	Backfat (in.)	Loin Eye Area (sq. in.)	% Ham and Loin (live wt. basis)
1958	29.3	1.54	3.52	22.8
1963	29.6	1.52	4.02	26.2
1968	29.5	1.33	4.51	28.7

Hazel (1963) reviewed information obtained from the central testing station at Ames, Iowa, between 1956 and 1962 and noticed a marked and consistent improvement which he attributed to genetic change. After the seven year period, during which attempts were made to provide standard environmental conditions, improvements of greater than 20 and 30 percent respectively were recorded for percent trimmed ham and loin and for area of eye of lean. Hazel concluded that sufficient genetic variability still existed to permit considerable additional change in fat-lean proportions.

In contrast, Cox and Smith (1968) contested the validity of considering improvements in pig performance measured at testing stations as evidence of the effectiveness of testing schemes in producing genetic change. Using data obtained from Iowa stations during 1956-66, they reported estimates of genetic change in daily gain and backfat depth much smaller than trends in performance from testing stations would indicate. This appeared consistent with the findings of Smith (1963) on performance tests with Danish Landrace.

A national pig progeny testing service was instituted in Great Britain in 1958. Smith (1965) reported on performance trends for daily gain, feed efficiency, backfat depth and carcass length to 1962 and concluded that progeny testing had made little impact on swine improvement in Great Britain. Similar findings in Canada have been reported by Fredeen (1953) who found, after 20 years of performance testing, no material change in the mean of any traits evaluated.

Despite these reservations, the eventual widespread use of artificial insemination in swine breeding will see added emphasis placed on progeny testing programs. Through artificial insemination, the distribution of a single boar's progeny over a wide geographic area will exclude environmental differences that are often interpreted as differences in genetic merit between sires (Haring and Smidt, 1966).

Melrose (1966) has estimated that, through artificial insemination, one boar could service at least 2,000 sows per annum with the resultant potential of over 20,000 progeny. The use of fewer sires for reproduction will result in greater selection pressure being applied through the sire. Increased emphasis will be placed on the testing of sires for use in artificial insemination centers and on the effect of sire on economic traits.

Baker et al. (1943) in a study of six Duroc lines reported that the effect of sire was significant ($P<.05$) on 56 day weight and highly significant ($P<.01$) on four measures of weight taken between 56 and 168 days of age. Sire did not significantly affect birth or 21 day weight.

In a comparison of Large White boars, each on the basis of 20 progeny from five litters, Duckworth et al. (1961) reported that boar differences were significant ($P<.01$) for age at 60 pounds, age at market, daily gain, feed efficiency, weight at market, carcass length, three measures of backfat depth and belly thickness. Sire had no effect on weight at 8 weeks.

Roache (1964) also reported that sire, within both the Yorkshire and Landrace breeds, significantly ($P<.05$) affected loin eye area and percent ham, shoulder, loin and belly.

Bereskin et al. (1968) reported on the effect of sire on carcass traits in Durocs and Yorkshires and noted significant differences among boars of both breeds for all traits considered. A summary of the analysis of variance for carcass traits is illustrated on the next page.

THE EFFECTS OF SIRE AND BREED ON CARCASS TRAITS

Source of Variance	Degrees of Freedom	Carcass Trait					
		Length	Back-fat	% Ham	% Loin	% Ham and Loin	Loin Eye Area
		Mean Squares					
Breed of Sire	1	5.05**	.03	.30	.85	.18	.12
Boars/Breed of Sire	30	.64**	.08**	1.25**	1.55**	4.66*	.74**
Duroc Boars	15	.65*	.05**	1.15**	2.00**	5.48**	.88**
York Boars	15	.64*	.11**	1.35**	1.09**	3.85**	.59**
Breed of Dam	1	16.79**	.16**	3.57**	15.77**	35.22**	9.98**
Breed of Sire x Breed of Dam	1	.14	.14**	6.76**	.15	4.66**	.02
Breed of Dam x Boars/Breed of Sire	30	.22	.02	.46	.26	.93	.14
Residual	112	.30	.02	.52	.35	.87	.16
Total	175						

* Significant at the 5% level of probability.
** Significant at the 1% level of probability.

From Bereskin _et_ _al._ (1968).

These reports would indicate that the effect of sire is greatest for post-weaning growth and carcass traits and is of lesser importance for traits expressed early in life which are under greater maternal influence and are of low heritability.

2. Mating Systems

"Perhaps the greatest change in animal breeding procedures of recent decades has been the increase in systematic crossbreeding and crossing between lines and strains as an alternative to purebreeding." (Lerner and Donald, 1966).

Fredeen (1957) has listed two principal advantages accruing from crossbreeding - one as a method of introducing new genetic variability into an existing gene pool and the other to capitalize on hybrid vigor or heterosis. Heterosis is attributed to one or more forms of non-additive genetic action.

Lush *et al.* (1939) considered superiority in performance of hybrid progeny over the mean of parental performance as evidence of the heterosis phenomenon. In contrast, Carroll and Roberts (1942) have regarded heterosis as hybrid superiority over the better parent. The latter approach, as pointed out by Fredeen (1957), may be adequate when performance is expressed in terms of a single value, but the consideration of several traits leads to a situation in which the hybrid is expected to excel the performance of a non-existent composite parent.

In an article reviewing fifty years of progress in swine breeding, Craft (1958) reported that little meaningful research in crossbred swine had been conducted prior to 1920. "Early trials", wrote Craft, "were with small numbers of animals, and the design of trials was decidedly inadequate... It was not until after 1920 that such trials included numbers large enough to indicate clearly that crosses were actually superior in certain respects."

Hammond (1922), in a ten year study of British show records, compared twelve single crosses from eight British breeds with parental means for growth. Hammond noted that in many cases crossbreds were heavier than the parental mean and found only one instance where the parental mean exceeded the crossbred for body weight.

An early Canadian experiment by Shaw and MacEwan (1936) measured six breeds and their reciprocal single crosses for rate and economy of gain. Crossbreds, when compared to one parental breed, gained more rapidly and consumed less feed.

The report of Winters _et al._ (1935) compared the performance of backcrosses, three-breed crosses, as well as single crosses, to that of purebreds. Three-breed crosses generally performed best. Almost two more pigs were farrowed per litter and litters averaged 96 pounds heavier at weaning than did purebreds. Weaning weights were 63 pounds heavier for backcross litters, but no superiority over purebreds was observed for numbers of pigs farrowed. Single cross litters averaged one additional pig and were 37 pounds heavier at weaning. Considering post-weaning growth, backcross pigs gained most rapidly and attained a weight of 220 pounds 22 days before purebreds. Both three-breed and single crosses reached this weight 17 days earlier than purebreds.

Lush _et al._ (1939) reported similar relative superiority for single cross, backcross and three-breed cross pigs for growth and survival. The Iowa researchers also noted the pre-eminence of crossbred dams for maternal ability.

In the same year, a similar study by Roberts and Carroll (1939) compared single crossbreds with purebred Duroc Jersey and Poland China. Crossbreds had a small, although non-significant, advantage for rate of gain, feed efficiency and age at market.

Trials by Robison (1948) compared four mating systems - purebred, single cross, backcross and three-breed cross - for rate of growth with similar results. However, as with the work of Shaw and MacEwan (1936), comparisons were based on only one parental breed, rendering it difficult to determine the degree, if any, of heterosis exhibited.

The importance of hybrid vigor in swine was questioned in early reports. The Illinois Agricultural Experimental Station Annual Report of 1928, commenting on work by Carroll and Roberts, reported that there was no crossbred advantage for rate or economy of gain. In a formal report, Carroll and Roberts (1942) concluded from a study of over 50,000 animals that hybrid vigor cannot be expected in the majority of crosses. Nonetheless, the superiority of crossbreds, particularly those farrowed from hybrid dams, has been experimentally established for survival and growth characteristics.

Bradford _et al._ (1953) demonstrated that litters from crossbred dams had a significantly lower mortality to 154 days than litters from straightbred dams. Similarly, Gaines and Hazel (1957) investigated the merits of crossbred sows and reported that crossbred Landrace-Poland China sows were superior to purebred sows for litter size at all ages.

A British study of close to 35,000 litters by Smith and King (1964) found that crossbred sows exhibited considerable heterosis, farrowing and weaning 5 and 8 percent more pigs respectively than purebreds when compared on an within herd basis. Litters farrowed from crossbred dams also had an 11 percent advantage in total weight at weaning.

The following summary of the merits of three mating systems - purebred, single cross, and three-breed cross - relative to survival and growth traits has been presented by Hazel (1963). The size and weight figures are given in terms of 100 percent for purebreds.

MATING SYSTEM SUMMARY

Characteristic	Pure-bred	Single cross	3-breed cross
Litter size at birth	100	101	111
Litter size at 8 weeks	100	107	125
Pig weight at 8 weeks	100	108	110
Pig weight at 154 days	100	114	113
Pork produced per litter	100	122	141

Single cross pigs showed better livability and faster growth than purebreds and yielded 22 percent more pork per litter. Three-breed crosses had an additional advantage in litter size and viability and produced 41 percent more pork per litter than purebreds.

Reports on the effects of crossbreeding on characteristics expressed in later life are less numerous as fewer crossbreeding experiments have provided information beyond the age of weaning.

Hammond (1922) was one of the first workers to attempt to compare purebreds and single crosses on the basis of carcass merit but concluded that the numbers involved in his study were too small to supply a definitive answer. Hazel (1963) indicated that crossbred pigs are usually intermediate between parental performance for carcass traits. Roache (1964) reported that mating system had no discernible effect on carcass traits.

Kirsch et al. (1963), in a comparison between Landrance, Pietrains and their F_1 crosses, found little evidence of heterosis for the carcass characteristics studied. Skarman (1965) reported only slight and generally non-significant differences between purebred and crossbred pigs for carcass traits but did report a significant ($P<.05$) crossbred advantage for area of eye of lean.

Bereskin et al. (1968) compared purebred Durocs and Yorkshires and their reciprocal crosses for carcass length, backfat thickness, weight and percent ham, loin, ham and loin, and loin eye area, as illustrated on the following page.

Total litters numbered 260 and provided 172 error degrees of freedom. Significant interaction of the two breeds indicated some possible heterotic effects on backfat thickness, weight and percent ham and percent ham and loin. This may also be considered as specific combining ability by breeds. No evidence of heterosis was observed for carcass length, weight and percent loin or loin eye area.

In general, heterotic response appears to be greatest for traits expressed early in life and is less important for traits expressed in later stages of development (Fredeen, 1957).

Comstock (1960) stated that all breeds of swine, or sets of breeds, are not equally fit for use in crossing and advocated selection for combining ability. Experimental work for specific combining ability in poultry has enjoyed a degree of success (Merritt and Gowe, 1960) but results to date in swine have been largely negative.

Studies on six lines of inbred swine by Bradford et al. (1958) failed to show specific combining ability for either weaning weight or weight at five months.

In another trial involving six inbred lines, Hetzer et al. (1961) found specific combining effects unimportant for growth and carcass traits. A more recent report by O'Ferrall et al. (1968) showed little or no difference in specific combining effects for pre-weaning

THE EFFECTS OF MATING SYSTEM ON CARCASS TRAITS

Statistic	Carcass Trait (Least Squares Estimates)							
	Length (in.)	Backfat (in.)	Ham (lbs.)	Loin (lbs.)	Ham (%)	Loin (%)	Ham and Loin (%)	Loin Eye Area (sq.in.)
Breed of Sire (D)	-.21**	-.01	.11	-.16	.05	-.07	-.03	-.03
Breed of Dam (D)	-.34**	.04**	-.33**	-.57**	-.15**	-.27**	-.43**	-.27**
Interaction (D-D, Y-Y)	-.02	-.04**	.40**	-.13	.20**	-.06	.13*	-.01
Overall Least Squares Mean	29.51	1.59	29.83	25.42	14.20	12.11	26.31	3.76
Least Squares Breed Group Means								
♂ ♀								
D - D	28.95	1.57	30.02	24.56	14.30	11.70	25.99	3.45
Y - Y	30.03	1.53	30.45	26.02	14.50	12.39	26.90	4.06
D - Y	29.67	1.57	29.86	25.96	14.21	12.36	26.58	4.02
Y - D	29.40	1.68	28.99	25.13	13.80	11.97	25.78	3.54

* Significant at the 5% level of probability.
** Significant at the 1% level of probability.
(D) Duroc
(Y) Yorkshire

From Bereskin _et al._ (1968)

traits. Bereskin _et_ _al._ (1968), although suggesting possible evidence for specific combining ability by breeds relative to carcass traits, failed to observe specific combining ability for individual boars within breeds.

3. Evaluation Techniques

"Statistically significant differences between purebreds and crossbreds have seldom been observed in individual experiments. The variability encountered in measuring performance traits of swine is so great that the number of animals employed must be prohibitively large in order to show statistical significance." (Fredeen, 1957). Efforts have been made, however, to develop mating techniques, appropriate for sire and mating system evaluation, which would control this variability and hence reduce the number of observations required to show significance.

The effects of maternal influences on progeny testing can be reduced by diallel mating (Johansson and Rendel, 1968). Descriptions of the diallel mating technique for use in sire evaluation have been presented by Lush (1945) and Johansson and Rendel (1968).

Sows are randomly divided into two groups of equal size. One group is mated to boar 1 and the other to boar 2. For the next litter the boars are exchanged between the two groups. As both boars produced a litter with each sow, the term for the dam differences is eliminated and environmental differences are diminished due to the contemporaneous use of boars.

Kudrjawzew (1933) extended the diallelic mating technique to permit the simultaneous comparison of more than two boars. The following is an illustration of this polyallelic mating technique as reported by Lush (1945).

POLYALLELIC MATING PLAN

	Boar Number			
	1	2	3	4
First season	A and B	C and D	E and F	G and H
Second season	H and C	B and E	D and G	F and A

A comparison between four boars employs eight sow groups which are lettered from A to H. Boars 1 and 2 are compared by litters from sow groups

B and C. The progeny from sow groups D and E are used to compare boars 2 and 3, and so on along the chain. Although no direct comparison between boars 1 and 3 is available, indirect comparisons can be made as each of these boars is compared directly with both boars 2 and 4.

Kudrjawzew (1934) used polyallelic matings to compare the performance of four boars for total litter weight at six months. Liebenberg and Gollnitz (1966) successfully ranked boars on the basis of diallelic and polyallelic matings.

The diallel mating technique has also been applied to mating system comparisons. Kirsch _et al._ (1963) used diallel matings to compare purebred Landrace and Pietrains with their single crosses for rate and economy of gain and carcass characteristics. In another European experiment, Blendl (1965) employed a type of diallel mating to compare purebreds and crossbreds for carcass composition.

In plant and poultry breeding diallel matings have received considerable attention. Theoretical considerations have been presented by Hayman (1954), Kempthorne (1956) and others. Griffing (1956) also has discussed the use of diallel matings relative to specific combining ability.

Diallel matings, however, have not been used extensively with swine. Difficulties often are encountered in analyzing the data when some matings are unsuccessful but Lauprecht _et al._ (1967) have reported a method to circumvent this problem. Nonetheless, diallelic and polyallelic mating techniques have received little attention in swine research outside of Europe.

Perhaps the most promising approach to efficient sire and mating system evaluation is through double mating. Successful double mating produces mixed litters, with progeny representing two sires and/or mating systems.

The organization of a double mating plan for mating system evaluation, as presented by Roberts and Carroll (1939), is illustrated as follows:

DOUBLE MATING PLAN

Sows		Boars
Duroc Jersey	X	Duroc Jersey Poland China
Poland China	X	Duroc Jersey Poland China

Double mating provides comparative data between two sires or mating systems by effectively controlling dam differences in pre- and post-natal maternal environments (Fredeen, 1957). Unlike the diallel mating technique, it permits comparisons to be made in a single breeding season.

Early studies restricted use of the double mating technique to mating system comparisons. Hays (1919), in one of the first experiments with double mating in swine, concluded that crossbreds were superior to purebreds for the production of feeder hogs. Small scale tests using double matings were performed by Shaw and MacEwan (1936) who recognized the potential of double mating for obtaining reliable results with a small number of litters.

A more detailed experiment by Lush et al. (1939) double mated Duroc, Poland China and Yorkshire stock, and their crosses, to investigate purebred, single cross, backcross and three-breed cross performance. Crossbred pigs were more vigorous at birth, exhibited greater survival to weaning and made more rapid post-weaning gains. Crossbred dams, which produced backcross and three-breed cross litters, were superior to purebreds. Other early mating system comparisons using the double mating technique include the reports of Roberts and Carroll (1939) and Robison (1948) which have been discussed previously.

Paternity in double mated litters has normally been established through the inheritance of color markers. The inheritance of color patterns for six breeds, when crossed with Durocs, has been outlined by Sumption (1961) and Searle (1968) has examined the genetic basis of coat color inheritance in swine and other mammals. The imperative use of color markers for sire identification has limited the application of the double mating technique to mating system evaluation involving breeds and crosses of contrasting color. The double mating technique has been inadequate for the comparison of sires and mating systems of like color and for sire evaluation within the same breed. The introduction of blood group markers for paternity identification (Buschmann, 1964; Widdowson and Newton, 1964; Newton and Widdowson, 1965; Saison and Moxley, 1966) has eliminated this restriction and has greatly expanded the practicability of the double mating technique.

Paternity usually is established on the basis of blood group factor inheritance within one or more closed systems; a closed system being defined as one in which all animals in a population react to one or more of the known antisera for that system. A method for sire identification, using the L system, as presented by Saison and Moxley (1966) is illustrated as follows:

DOUBLE MATING SIRE IDENTIFICATION PLAN
(L SYSTEM)

Sow Genotype		Boar Genotype	Progeny Phenotype From Each Boar
L^a/L^a	X	Boar 1 L^a/L^a	L (a+ b-)
		Boar 2 L^b/L^b	L (a+ b+)
L^b/L^b	X	Boar 1 L^b/L^b	L (a- b+)
		Boar 2 L^a/L^a	L (a+ b+)

Matings are arranged in which one boar is homozygous for either the a or b factor and the second boar and sow are both negative for this factor. In the upper mating, progeny with L_a are attributable to Boar 1, those which are L_{ab} are ascribed to Boar 2. Double matings are not limited to specific systems. Paternity identification is possible whenever a boar is found to be homozygous for a factor lacking in a second boar and sow.

Recently, on the basis of double matings using both color and blood group markers, Howard (1968) concluded that both mating system and sire comparisons can be made more efficiently on a within litter basis than on a between litter basis.

Three decades ago, Lush _et al._ (1939) noted an oddity intrinsic to the double mating technique whereby certain boars sire more progeny than do others in double mated litters. This phenomenon of unequal numbers appeared to be independent of order of service or breed of sow or boar. Sumption and Adams (1961a) added support to the view that order of service does not influence the distribution of progeny by sire and suggested multiple mating as a method of selecting for mating efficiency. Sumption _et al._ (1959) and Sumption and Adams (1961b) embodied this theory in the development of the Minnesota No. 3 breed. Additional evidence for preferential fertilization, using both natural matings and mixed artificial inseminations, has been presented by Saison and Moxley (1966).

The simultaneous introduction of semen of both boars into the sow was suggested by Roberts and Carroll (1939) as a method of increasing the frequency of mixed litters and balancing the proportion of progeny attributable to each sire. This has become possible through the artificial insemination of mixed semen and Howard (1968) has reported that mixed inseminations tend to produce more equal progeny distribution than do separate natural matings.

Reports of other consequences of double mating are of some interest also. Roberts and Carroll (1939) noted that double mated litters averaged two pigs more per litter than single mated litters. In experiments conducted in the Soviet Union, Sokolovskaja _et al._ (1964) observed higher conception rates and lower embryonic mortality through the use of mixed inseminations. A similar report by Hlebov (1965) disclosed that conception rate, embryo weight and litter size were all increased through mixed inseminations. Sokolovskaja _et al._ (1966), however, reported that insemination with mixed semen did not improve the rate of conception but did increase embryo survival.

In contrast, the Yugoslav workers Cerne and Salehar (1964), in a study incorporating 61 double and 292 single mated sows, reported that the number of pigs born alive was significantly reduced by almost two pigs per litter when mixed inseminations were made.

4. Blood Groups and Economic Traits

"An obvious question in the minds of livestock breeders is whether or not the blood groups are correlated with any morphological or physiological characteristics of economic importance." (Irwin and Stone, 1961). The use of blood groups for paternity identification in a double mating program adds pertinence to this question.

Ford (1945, 1957) reasoned that no gene is neutral in selective value and as a consequence blood groups must react to natural selection. Relationships which have been established between blood groups and diseases in man lend credence to this argument (Levine et al., 1941; Aird et al., 1953; Buckwalter et al., 1956).

Evidence of an association between blood groups and economic traits in farm animals was first advanced by Briles et al. (1953) who reported apparent heterozygote superiority within the B blood group system in chickens. Reviews of the relationships of blood groups to economic traits in poultry have been presented by Briles (1960), Merat and Perramon (1967) and others. In addition, Oosterlee (1965) has reviewed the effects of blood groups in both chickens and cattle. Stone and Irwin (1963) attributed the association between blood groups and other traits to any one, or combinations, of four mechanisms - linkage, pleiotropy, heterosis and incompatibility between mother and fetus.

Information on blood groups in swine is, however, less extensive than that available on poultry and cattle. An early review on swine blood groups was published by Andresen (1962) and subsequent reports of Saison and Ingram (1962), Andresen and Baker (1964) and Saison (1966) have presented supplemental information on the A-O, C, E, K and N systems. A more current review of the status of blood group polymorphism in swine has been presented by Moustgaard and Hesselholt (1966).

Reports on the association of blood groups and economic characters in swine have, nonetheless, been limited. The first report appears to be by Baltzer (1964) who indicated a possible relationship between 17 blood group factors and production traits in German Landrace. Kristjansson (1964) found differences in return to service rates between different mating types as to the transferrin locus in the serum protein series and attributed this difference to higher embryonic mortality in BB x AB transferrin matings. Tikhonov (1968) reported that pigs of G^a/G^a genotype experience higher embryonic mortality than do homozygous G^b/G^b or heterozygous G^a/G^b pigs. Litter size was also increased by mating to provide heterozygous progeny (G^a/G^a x G^b/G^b) perhaps indicating a heterotic response.

In an extensive two-part study, Smith _et al._ (1968) and Jensen _et al._ (1968) tested the effects of 15 blood group and seven serum protein systems on viability and 12 blood group and four serum protein systems on reproductive and productive traits among over 16,000 Duroc and Hampshire pigs. Blood type and survival to 154 days were significantly ($P<.05$) associated in only 14 out of 275 mating types. In the cases which showed significance, results were inconsistent between breeds and among mating type.

The second phase of the study, which considered ten productive and reproductive traits, reported that 13 percent of 300 F-tests showed significant relationships, indicating a possible association between blood and serum systems and the traits under consideration. As in the first study, most effects were not consistent between breeds but some similarities were noted. Although less than two percent of the variance in productive traits was accounted for by blood group, up to twelve percent of the reproductive variance was attributed to the systems studied. A major and consistent effect of the H system on reproductive performance also was found.

Smith (1967) stated that the value of simple Mendelian loci, such as blood group factors, in improving quantitative traits depends on the proportion of additive genetic variance contributed by the known loci relative to the heritability of the metric trait in question and the form of selection practiced. If normal selection is ineffective, such as for traits of low heritability, or if indirect selection must be applied, as in the case with sex-limited traits and traits that cannot be evaluated on the live animal, then specific loci may significantly contribute to the rate of improvement possible. Smith concluded, however, "that at present there appears to be no loci that could be used with confidence in the improvement of economic traits of farm animals".

III. THEORETICAL CONSIDERATIONS

The purpose of developing mating techniques for sire and mating system evaluation is to establish sensitive methods which can detect real genetic differences with relatively few animals and within a short period of time. This can be accomplished through the use of mating plans designed to reduce 'uncontrollable' variation and the error term. The three mating techniques used in this study - random, sequential (a variation of polyallelic mating) and double mating - are considered on a theoretical basis for relative effectiveness, germane to sire evaluation, in achieving this end.

The analysis of variance for the random mating technique is illustrated as follows:

RANDOM MATING ANALYSIS OF VARIANCE

Source of Variation	Composition of Mean Squares
Between sires	$\sigma^2_{pig} + k_2\sigma^2_{lit.} + k_3\sigma^2_{sire}$
Between litters within sires	$\sigma^2_{pig} + k_1\sigma^2_{lit.}$
Between pigs within litters	σ^2_{pig}

The pig mean square contains that portion of the total variation attributable to environmental differences between pigs within litters. The term also contains ONE-HALF of the additive genetic variance plus some variation due to dominance and epistatic deviations. The litter mean square consists of the pig component plus a component due to environmental differences between litters within sires. The sire mean square contains components due to the effects of pig, litter and sire differences. The ratio of the sire mean square to the litter mean square is, therefore, the appropriate test for sire differences.

The sequential mating technique is a variation on the polyallelic mating plan. Only the first two litters from each dam are considered but the litters are sired by different boars. The analysis of variance for the sequential mating technique is illustrated as follows:

SEQUENTIAL MATING ANALYSIS OF VARIANCE

Source of Variation	Composition of Mean Squares
Between sires	$\sigma^2_{pig} + k_4\sigma^2_{lit.} + k_5\sigma^2_{sire}$
Between dams	$\sigma^2_{pig} + k_2\sigma^2_{lit.} + k_3\sigma^2_{dam}$
Between litters	$\sigma^2_{pig} + k_1\sigma^2_{lit.}$
Between pigs within litters	σ^2_{pig}

The composition of the pig mean square in the sequential mating analysis is similar to that described for random mating but differs in that variation due to dam differences has been removed and the term contains only one-half the additive genetic variance. The litter mean square, as with the random mating analysis, constitutes the error term and the ratio of the sire mean square to the litter mean square again is the appropriate test for sire differences. The theoretical refinement over the random mating analysis rests in the removal of dam effects from the ratio.

The double mating technique permits maternal half-sib comparisons on a within litter basis. The analysis of variance for the double mating technique is illustrated as follows:

DOUBLE MATING ANALYSIS OF VARIANCE

Source of Variation	Composition of Mean Squares
Between litters	$\sigma^2_{pig} + k_2\sigma^2_{sire} + k_3\sigma^2_{lit.}$
Between sires within litters	$\sigma^2_{pig} + k_1\sigma^2_{sire}$
Between pigs within sires	σ^2_{pig}

With double mating, as with sequential mating, the pig mean square contains between pig environmental deviations, a half of the additive genetic variance plus some variation due to dominance and epistatic deviations. However, in the double mating analysis, the sire mean square contains only pig and sire components as deviations due to litter differences have been removed. With the removal of the litter component from the sire mean square, the appropriate test for sire differences simply becomes the ratio of the sire mean square to the pig mean square.

IV. METHODS OF ANALYSIS

1. General Analysis

Under conditions of equal subclass frequencies, the analysis of variance is a straightforward procedure. However, disproportionate subclass numbers cause the different classes of effects to be non-orthogonal and effects cannot be directly separated without confounding. This often is the case in animal breeding trials concerned with litter size and sex. The method of fitting constants through least squares analysis can be used to free these effects from entanglement.

Harvey (1960) has outlined appropriate models for performing least squares analysis of data with unequal subclass numbers and they form the basis for the models used in this study.

As an illustration, the following model was used for the estimation of variance components of the random mated data:

$$Y_{ijklmop} = \mu + a_i + b_{ij} + c_{ijk} + d_{ijkl} + f_{ijklm} + g_o + e_{ijklmop} \qquad (1)$$

$$\begin{aligned} i &= 1, 2 \ldots\ldots q \\ j &= 1, 2 \ldots\ldots r_i \\ k &= 1, 2 \ldots\ldots s_{ij} \\ l &= 1, 2 \ldots\ldots t_{ijk} \\ m &= 1, 2 \ldots\ldots v_{ijkl} \\ o &= 1, 2 \ldots\ldots w \end{aligned}$$

where:

$Y_{ijklmop}$ represents the p^{th} pig of the o^{th} sex from the $ijklm^{th}$ litter of the $ijkl^{th}$ dam of the ijk^{th} breed of dam and the ij^{th} sire of the i^{th} breed of sire

μ = the population mean

a_i = the effect of the i^{th} breed of sire

b_{ij} = the effect of the j^{th} sire within the i^{th} breed of sire

c_{ijk} = the effect of the k^{th} breed of dam within the ij^{th} sire

d_{ijkl} = the effect of the l^{th} dam within the ijk^{th} breed of dam

f_{ijklm} = the effect of the m^{th} litter within the $ijkl^{th}$ dam

g_o = the effect of the o^{th} sex

$e_{ijklmop}$ = the random error assumed to be N.I.D. $(0,\sigma_e^2)$.

Interactions are assumed to be absent. This is a mixed model with the random effects, breed of sire, sire, breed of dam, dam and litter, forming a nested classification. Sex effects are regarded as fixed. Nesting of the random effects permits the model to be simplified as follows:

$$Y_{ijk} = \mu + f_i' + g_j + e_{ijk} \qquad (2)$$

$$i = 1, 2 \dots p$$

$$j = 1, 2 \dots q$$

where:

Y_{ijk} represents the k^{th} pig of the j^{th} sex in the i^{th} litter

μ = the population mean

f_i' = the effect of the i^{th} litter nested within dam, breed of dam, sire and breed of sire

g_j = the effect of the j^{th} sex

e_{ijk} = the random error assumed to be N.I.D. $(0,\sigma_e^2)$.

The least squares equations for the simplified model are represented in tabular form as follows:

$$\begin{array}{llcccccc} & & \hat{\mu} & \hat{f}'_i & \hat{g}_j & & \text{R.H.M.} \\ \hline \mu & : & n_{\bullet\bullet} & n_{i\bullet} & n_{\bullet j} & = & Y_{\bullet\bullet} \\ f'_i & : & n_{i\bullet} & n_{i\bullet} & n_{ij} & = & Y_{i\bullet} \\ g_j & : & n_{\bullet j} & n_{ij} & n_{\bullet j} & = & Y_{\bullet j} \end{array}$$

Restrictions imposed:

$$\hat{\mu} + \hat{f}'_i = f'_i$$

and

$$\sum_j g_j = 0$$

by deletion and subtraction of the q row and column from the 1 to q-1 rows and colums permit solution of the equations.

The matrix notation of the reduced least squares equations can be presented as follows:

$$\begin{bmatrix} A & B \\ B' & C \end{bmatrix} \begin{bmatrix} \alpha \\ \gamma \end{bmatrix} = \begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix}$$

where:

A = diagonal $n_{i\bullet}$ matrix

B = n_{ij} matrix

B' = transpose n_{ij} matrix

C = diagonal $n_{\bullet j}$ matrix

α = matrix of nested litter effects to be estimated

γ = matrix of sex effects to be estimated

Y_1 and Y_2 = appropriate right-hand member matrices of the sums of observations for the equations.

Because of the large number of equations, $\mu + f'_i$ sets of equations are absorbed into the equations for g_j as follows:

$$(C - B'A^{-1}B)\gamma = Y_2 - B'A^{-1}Y_1$$

where A^{-1} represents the inverse of the A matrix.

Letting $D = C - B'A^{-1}B$

and $Z = Y_2 - B'A^{-1}Y_1$

then $D\gamma = Z$

and the fixed effect can be estimated from the equation:

$$\gamma = D^{-1}Z$$

The litter effects are then adjusted for the sex effects and the adjusted sums of squares for the random effects are calculated.

Considering the original model (1), the composition of the adjusted mean squares of the random effects can be presented as follows:

Source	df	Composition of Mean Squares
Breed of sire	q'	$k_{11}\sigma^2_e + k_{12}\sigma^2_f + k_{13}\sigma^2_d + k_{14}\sigma^2_c + k_{15}\sigma^2_b + k_{16}\sigma^2_a$
Sire	r'	$k_{21}\sigma^2_e + k_{22}\sigma^2_f + k_{23}\sigma^2_d + k_{24}\sigma^2_c + k_{25}\sigma^2_b$
Breed of Dam	s'	$k_{31}\sigma^2_e + k_{32}\sigma^2_f + k_{33}\sigma^2_d + k_{34}\sigma^2_c$
Dam	t'	$k_{41}\sigma^2_e + k_{42}\sigma^2_f + k_{43}\sigma^2_d$
Litter	v'	$k_{51}\sigma^2_e + k_{52}\sigma^2_f$
Error		σ^2_e

where: $q' = q - 1$

$$r' = \sum_i r_i - q$$

$$s' = \sum_i \sum_j s_{ij} - \sum_i r_i$$

$$t' = \sum_i \sum_j \sum_k t_{ijk} - \sum_i \sum_j s_{ij}$$

$$v' = \sum_i \sum_j \sum_k \sum_l v_{ijkl} - \sum_i \sum_j \sum_k t_{ijk}$$

The computations of the coefficients, except those associated with σ^2_e, can be performed directly as follows:

$$k_{52} = \frac{1}{v'}\left(n_{\cdot\cdot\cdot\cdot\cdot\cdot} - \sum_i\sum_j\sum_k\sum_l \frac{\sum_m n^2_{ijklm\cdot}}{n_{ijkl\cdot\cdot}} \right)$$

$$k_{42} = \frac{1}{t'}\left(\sum_i\sum_j\sum_k\sum_l \frac{\sum_m n^2_{ijklm\cdot}}{n_{ijkl\cdot\cdot}} - \frac{\sum_i\sum_j\sum_k\sum_l\sum_m n^2_{ijklm\cdot}}{n_{\cdot\cdot\cdot\cdot\cdot\cdot}} \right)$$

$$k_{43} = \frac{1}{t'}\left(n_{\cdot\cdot\cdot\cdot\cdot\cdot} - \sum_i\sum_j\sum_k \frac{\sum_l n^2_{ijkl\cdot\cdot}}{n_{ijk\cdot\cdot\cdot}} \right) \qquad \text{etc.}$$

The calculations required in the computation of the coefficients associated with σ^2_e (k_{11}, k_{21}, k_{31}, k_{41} and k_{51}) are somewhat more involved but can be computed from values obtained during absorption and inversion of the reduced matrix.

$$k_{51} = 1 + \frac{1}{v'} \sum_i\sum_j\sum_k\sum_l\sum_m D^{ijklm}(P'''''_{ijklm} - P''''_{ijklm})$$

$$k_{41} = 1 + \frac{1}{t'} \sum_i\sum_j\sum_k\sum_l\sum_m D^{ijklm}(P''''_{ijklm} - P'''_{ijklm}) \qquad \text{etc.}$$

where:

D^{ijklm} = $(C - B'A^{-1}B)^{-1}$

P'''''_{ijklm} = $B'A^{-1}B$ values obtained in the absorption of $\mu + a_i + b_{ij} + c_{ijk} + d_{ijkl} + f_{ijklm}$ equations

P''''_{ijklm} = values obtained from $B'A^{-1}B$ multiplication after the f_{ijklm} effects are deleted and $\mu + a_i + b_{ij} + c_{ijk} + d_{ijkl}$ equations are absorbed

P'''_{ijklm} = values obtained from $B'A^{-1}B$ multiplication after d_{ijkl} effects are deleted and $\mu + a_i + b_{ij} + c_{ijk}$ equations are absorbed.

Computational work was done on I.B.M. 1620 and 360/75 computers.

2. Enumeration Data

Certain aspects of this study involved enumeration data and these data were analyzed by chi-square tests for randomness. Where only one degree of freedom was available, Yates' (1934) correction for continuity was applied. Cases which showed borderline significance were tested by the Fisher (1954) exact probability method where it was computationally feasible.

V. SOURCES AND CHARACTERISTICS OF THE DATA

Two sources of data were used in this study. Field data were obtained from Newfoundland during the period 1965-66 and experimental data, which included random, sequential and double matings, were obtained from the Macdonald College swine herd during the twelve year period 1957-68.

1. Newfoundland Field Data

Growth and carcass measurements were available on 2304 pigs from 734 litters representing 43 sires. The study used three breeds - Landrace, Yorkshire and Lacombe - in various combinations. Matings were made on a random basis. The distribution of litters by mating type is illustrated in Table 1.

Of a total of 734 litters farrowed, 622 were considered suitable for sire and mating system evaluation. The 37 litters sired by crossbred boars and litters farrowed by dams classified as 'others' were included only for the variance component analysis and these litters are enclosed in parentheses.

Purebred dams farrowed 307 litters of which 205 were purebred, as indicated with a superscript 'a', and the balance of 102 litters were single crosses. The purebred litters were almost exclusively Landrace.

Of the 315 litters farrowed by crossbred dams, 91 were classified as backcrosses and are indicated with a superscript 'b'. The remainder of 224 litters were designated as three-breed crosses.

The herd was heavily influenced by the Landrace breed. Landrace boars sired approximately two-thirds of the litters and about 45 percent of the litters were farrowed by Landrace dams.

All pigs employed in this study were farrowed at the Newfoundland

TABLE 1: THE DISTRIBUTION OF NEWFOUNDLAND LITTERS BY MATING TYPE

Type of Dam	Breed of Dam	Breed of Sire Yorkshire	Landrace	Lacombe	Crossbred[c]	Total
Purebred	Yorkshire	5[a]	1	0	(0)	6
	Landrace	78	200[a]	23	(19)	320
	Total	83	201	23	19	326
Crossbred	York-Land	6[b]	22[b]	1	(0)	29
	York-Lac	5[b]	6	0[b]	(2)	13
	Land-Lac	7	17[b]	0[b]	(0)	24
	Land-Backcross	0	41[b]	0	(1)	42
	York-Crisscross	7	24	0	(0)	31
	Land-Crisscross	15	27	1	(0)	43
	Lac-Crisscross	25	55	1	(0)	81
	Lac-Tricross	14	40	1	(7)	62
	Total	79	232	4	10	325
	Others[c]	(26)	(46)	(3)	(8)	83
	Grand Total	188	479	30	37	734

[a] Purebred litter. Single cross litters are unscripted.

[b] Backcross litter. Three-breed cross litters are unscripted.

[c] Litters in parentheses were not considered for sire or mating system evaluation.

Central Swine Testing Station. Baby pigs were weaned at approximately eight weeks and shipped to farmers co-operating with the program. The participating farmers raised the pigs to market weight and shipped the finished hogs to a central abattoir where maximum loin and shoulder backfat, carcass weight, weight of trimmed loin and shipping date were recorded.

2. Experimental College Data

A total of 6000 pigs from 798 litters comprised the experimental data. Five breeds in various combinations were used in the program but only Yorkshire and Landrace were employed in the first five years. The Lacombe breed was introduced to the herd in 1962. In late 1966 Large Black breeding stock were also introduced and a year later a Hampshire boar entered service. All five breeds were represented in 1968. Matings were by natural service or artificial insemination.

Male pigs were castrated within two weeks following birth and baby pigs were weaned at 21 days and raised on the college farm to a market weight normally ranging between 180 and 200 pounds liveweight. Market pigs were usually slaughtered and measured for carcass traits at Canada Packers in Montreal but in some instances slaughter and measurement occurred at the college.

a. Random Matings

A total of 5303 pigs was produced from 718 random mated litters. The litters were sired by 61 boars. Random mated litters were farrowed during all years of the study. Their distribution by mating type is illustrated in Table 2.

Purebred dams farrowed 450 litters of which 251 were purebred and 199 were single crosses. The purebred litters are indicated by a super-

TABLE 2: THE DISTRIBUTION OF RANDOM MATED LITTERS BY MATING TYPE

Type of Dam	Breed of Dam	Breed of Sire					
		Yorkshire	Landrace	Lacombe	Large Black	Hampshire	Total
Purebred	Yorkshire	147[a]	84	18	2	7	258
	Landrace	45	79[a]	18	3	0	145
	Lacombe	14	4	23[a]	4	0	45
	Large Black	0	0	0	2[a]	0	2
	Total	206	167	59	11	7	450
Crossbred	York-Land	58[b]	58[b]	22	3	8	149
	York-Lac	19[b]	14	8[b]	3	1	45
	Land-Lac	8	5[b]	4[b]	1	0	18
	York-L.B.	0[b]	2	0	0[b]	1	3
	Land-L.B.	7	3[b]	1	0[b]	0	11
	Lac-L.B.	1	4	0[b]	0[b]	0	5
	York-Backcross	3[b]	16[b]	7	0	0	26
	Land-Backcross	10[b]	0[b]	1	0	0	11
	Total	106	102	43	7	10	268
	Total	312	269	102	18	17	718

[a] Purebred litter. Single cross litters are unscripted.

[b] Backcross litter. Three-breed cross litters are unscripted.

script 'a'. Crossbred dams produced 268 litters. Backcrosses, which are indicated by a superscript 'b', comprised 184 of these litters while three-breed crosses made up the balance of 84 litters.

All Yorkshire-backcross dams were one-fourth Landrace (Yorkshire x Yorkshire-Landrace) and, as only a few litters were involved, their litters were classified as backcrosses when mated to either a Yorkshire or Landrace boar. Similarly all Landrace-backcross dams were one-fourth Yorkshire and their litters, when mated to a Yorkshire boar, also were considered as backcrosses.

b. Sequential Matings

A total of 2315 pigs, from 312 sequential mated litters, were farrowed over the 12 year period. The sequential mating program involved a variation on the polyallelic mating technique. Only the first and second litters from each dam were considered and to be regarded as sequential matings these litters must have been sired by different boars. Forty-four boars were used in the program. The distribution of sequential mated litters by mating type is illustrated in Table 3.

Purebred dams farrowed 184 litters of which 152, as indicated with a superscript 'a', were suitable for mating system evaluation. By design, 76 were purebreds and 76 were single crosses. The balance of 32 litters were included for sire comparisons.

Crossbred dams farrowed 128 litters but only 42 were suitable for backcross and three-breed cross comparison and are so designated with a superscript 'b'. As with the purebred dams, the remainder were used for sire evaluation.

TABLE 3: THE DISTRIBUTION OF SEQUENTIAL MATED LITTERS BY MATING TYPE

Breed of Alternate Sires	Breed of Dam										
	Purebred			Crossbred							
	Yorkshire	Landrace	Lacombe	York-Land	York-Lac	Land-Lac	York-Backcross	Land-Backcross	Land-L.B.	Lac-L.B.	Total
Yorkshire Landrace	74[a]	38[a]	0	58	2[b]	2[b]	2	0	2[b]	2	180
Yorkshire Lacombe	10[a]	8	8[a]	14[b]	4	4[b]	0[b]	0[b]	2	0[b]	50
Landrace Lacombe	2	10[a]	4[a]	4[b]	6[b]	0	2[b]	0[b]	0[b]	0[b]	28
Landrace Large Black	0	2[a]	0	0[b]	2	2[b]	0[b]	0[b]	0	0[b]	6
Yorkshire Hampshire	6[a]	0	0	2[b]	2[b]	0	0[b]	0[b]	0	0	10
Landrace Hampshire	2	0[a]	0	0[b]	0	0	0[b]	0[b]	0[b]	0	2
Others[c]	14	6	0	4	2	0	6	2	2	0	36
Total	108	64	12	82	18	8	10	2	6	2	312

[a] Suitable sequential mating for purebred vs. single cross comparison.

[b] Suitable sequential mating for backcross vs. three-breed cross comparison.

[c] Alternate sire combinations designated 'others' involved sires of the same breed and the matings were suitable for sire evaluation only.

c. Double Matings

The double mating study extended from 1965-68 and involved 697 pigs from a total of 80 litters. A litter was classified as double mated if progeny from two sires were represented. Twenty boars were used in the double mating program. The distribution of double mated litters by mating type is illustrated in Table 4.

Forty-seven litters, totalling 404 pigs, were farrowed by purebred dams. However, only 24 litters, as indicated with a superscript 'a', were suitable for mating system evaluation. The remaining 23 litters involved boar pair and dam combinations which produced only single cross progeny but were included in the study for sire evaluation purposes. Purebred and single cross progeny numbered 102 and 302 pigs respectively.

Crossbred dams farrowed 293 pigs in 33 litters of which 26 contributed to mating system differences. These are indicated by a superscript 'b'. Backcrosses numbered 160 pigs while three-breed crosses totalled 133 pigs.

Most matings were made by the artificial insemination of semen mixed from two boars although a limited number of natural matings were performed. In such cases, artificial insemination of semen from the second boar immediately followed natural service by the first boar.

Semen collection was by the gloved-hand technique as described by Herrick and Self (1962). Semen was mixed on the basis of equal volumes of semen or equal concentrations of sperm based on a motile sperm count. Inseminations made in the latter stages of the study were all by equal volumes after Howard (1968) established this method to be as effective as equal concentrations in producing mixed litters.

TABLE 4: THE DISTRIBUTION OF DOUBLE MATED LITTERS BY MATING TYPE

	Breed of Dam									
	Purebred				Crossbred					
Breed of Sire Pairs	Yorkshire	Landrace	Lacombe	Total	York-Land	York-Lac	Land-Lac	Lac-L.B.	Total	Grand Total
Yorkshire Landrace	5[a]	6[a]	2	13	2	2[b]	1[b]	0	5	18
Yorkshire Lacombe	3[a]	3	1[a]	7	2[b]	3	2[b]	0[b]	7	14
Landrace Lacombe	8	2[a]	1[a]	11	2[b]	3[b]	0	0[b]	5	16
Yorkshire Large Black	4[a]	2	2	8	3[b]	1[b]	2	2[b]	8	16
Landrace Large Black	4	0[a]	0	4	3[b]	0	0[b]	0[b]	3	7
Lacombe Large Black	0	0	0[a]	0	0	2[b]	0[b]	0	2	2
Yorkshire Hampshire	1[a]	0	0	1	0[b]	2[b]	0	0	2	3
Landrace Hampshire	2	1[a]	0	3	1[b]	0	0[b]	0	1	4
Total	27	14	6	47	13	13	5	2	33	80

[a] Suitable mating for purebred vs. single cross comparison.

[b] Suitable mating for backcross vs. three-breed cross comparison.

The progeny of each sire were identified by color marker or blood type. Breeding stock were blood typed at a minimum for the L and N systems and some animals were typed for up to 35 factors from 14 blood group systems. Sires of baby pigs were generally identified on the basis of inheritance of the L or N systems and specifically factors L_g and L_d or N_a and N_b were used. In a limited number of cases other blood group systems were used for sire identification.

The numbers of breeding stock and baby pigs typed for each blood group factor are illustrated in Table 5. A total of 24 sires, 168 dams and 653 baby pigs were blood typed for some or all factors. All blood typing was done under the generous direction of Miss Ruth Saison of the Ontario Veterinary College at Guelph.

Most of the 653 baby pigs were from double mated litters, although a small number of single mated litters were blood typed in the early phases of the study.

TABLE 5: THE NUMBER OF SIRES, DAMS AND BABY PIGS TYPED FOR EACH OF 35 BLOOD GROUP FACTORS

System	Factor	Sires	Dams	Baby Pigs
A-O	A	4	12	0
	O	11	58	0
B	a	4	8	97
	b	4	8	97
C	a	22	138	364
D	a	22	145	521
E	a	22	145	521
	b	22	145	514
	d	22	145	514
	e	13	88	194
	f	22	148	517
	g	4	40	113
F	a	22	145	521
G	a	4	1	0
	b	22	145	521
H	a	22	143	498
	c	4	1	18
I	a	4	8	97
	b	4	8	97
K	a	22	145	521
	b	19	82	198
	e	19	143	521
	e_1	20	145	476
	d	19	145	521
L	a	19	117	459
	b	4	8	97
	c	4	8	97
	d	24	168	592
	e	24	8	97
	g	24	168	564
M	a	3	8	97
N	a	24	168	605
	b	24	168	605
	c	22	166	584
R	a	13	84	184
Total Number Typed		24	168	653

3. Traits Studied

Fourteen growth and carcass traits were available for study in the Macdonald College experimental data. Pig weight was recorded at birth, 21 days (weaning), 56 days and 154 days of age. Two additional growth traits - age at market and gain per day expressed as pounds liveweight per day of age - also were recorded.

Following slaughter, eight carcass traits were recorded. These included maximum depth of backfat as measured at the shoulder and loin, carcass length and area of eye of lean (m. longissimus dorsi) as calculated with a planometer from acetate tracings. The left side of the carcass was butchered into trimmed commercial cuts and the weights of trimmed ham, shoulder and loin were individually recorded. The sum of the weights of the three left-side trimmed cuts were doubled to provide an estimate of total lean cut yield.

A rhinitis score also was established for use in the blood group studies. Carcasses were rated from one to five on a subjective scale by visual estimation of nasal turbinate degeneration attributable to atrophic rhinitis.

The Newfoundland field data provided two growth and three carcass traits for study. Growth was measured as age at market and gain per day expressed in pounds carcass weight per day of age. The carcass traits studied were maximum depth of shoulder and loin backfat and the weight of commercially trimmed loin (left-side).

Means and standard errors of the growth and carcass traits obtained from the Macdonald College experimental data and the Newfoundland field data are illustrated in Table 6. All field data traits and experimental data carcass traits have been adjusted for sex and carcass weight differences. Experimental data growth traits have been adjusted for sex differences only.

TABLE 6: MEANS AND STANDARD ERRORS OF GROWTH AND CARCASS TRAITS

Trait	Experimental Data[a] (Macdonald College) Mean	± S.E.	d.f.	Field Data[b] (Newfoundland) Mean	± S.E.	d.f.
Birth Weight (lbs.)	2.86	.40	4585			
21 Day Weight (lbs.)	11.91	2.17	4585			
56 Day Weight (lbs.)	31.4	6.1	4585			
154 Day Weight (lbs.)	163.6	18.4	2764			
Age at Market (days)	174.9	14.0	2764	193.9	15.1	1568
Daily Gain (lbs./day)[c]	1.118	.092	2764	.823	.064	1568
Length (in.)	30.52	.55	2244			
Shoulder Backfat (in.)	1.54	.18	2244	1.57	.16	1568
Loin Backfat (in.)	1.29	.16	2244	1.33	.17	1568
Area of Eye of Lean (sq.in.)	4.116	.399	2244			
Trimmed Ham (lbs.)	15.55	.80	2244			
Trimmed Shoulder (lbs.)	12.80	.96	2244			
Trimmed Loin (lbs.)	11.50	.89	2244	15.25	.79	1568
Lean Cut Yield (lbs.)	79.68	3.88	2244			

[a] Growth traits are adjusted for sex differences. Carcass traits are adjusted for sex and carcass weight differences.

[b] All field data traits are adjusted for sex and carcass weight differences.

[c] Daily gain is expressed as pounds carcass weight per day of age in the Newfoundland field data.

VI. LINEAR MODELS AND RESULTS

1. Preliminary Considerations

As the double mating program involved the selection of breeding stock, in part, on the basis of blood group factors, preliminary studies were conducted to investigate the relationship between blood group factors and economic traits. The effects of double mating on litter size and sex ratio were investigated also.

a. Blood Group Factor Frequencies

A total of 653 pigs were typed for up to 32 blood group factors involving 13 systems. The frequency of each factor was determined as the ratio of the number of pigs which were typed positive to the total number of pigs blood typed for the factor. The distribution of blood group factor frequencies by sex is illustrated in Table 7.

Factors with frequencies of less than .100 and greater than .900 were categorized as rare and common respectively. Rare factors included B_b, C_a, E_a, F_a and M_a. B_b was absent in the population studied. Factors classified as common were B_a, E_d, E_e, E_g, G_b, I_a, L_b, L_c, L_e, L_g and N_b. Two of the common factors, L_g and N_b, were used for sire identification in the double mating program.

The distribution of blood group factor frequencies by sex was tested for randomness by adjusted chi-square. Male pigs had higher frequencies ($P<.05$) of the C_a, F_a, L_c and L_e factors while females more frequently ($P<.05$) possessed factors K_e and K_{e1}. None of these factors were used for sire identification.

TABLE 7: THE DISTRIBUTION OF BLOOD GROUP FACTOR FREQUENCIES BY SEX

System	Factor	All Pigs No. Typed	No. Pos.	No. Neg.	Freq.	Males No. Typed	No. Pos.	No. Neg.	Freq.	Females No. Typed	No. Pos.	No. Neg.	Freq.
B	a	97	97	0	1.000	59	59	0	1.000	38	38	0	1.000
	b	97	0	97	.000	59	0	59	.000	38	0	38	.000
C	a	364	14	350	.038	202	12	190	.059*	162	2	160	.012
D	a	521	150	371	.288	291	83	208	.285	230	67	163	.291
E	a	521	50	471	.096	291	26	265	.089	230	24	206	.104
	b	514	277	237	.539	289	164	125	.567	225	113	112	.502
	d	514	514	0	1.000	289	289	0	1.000	225	225	0	1.000
	e	194	176	18	.907	110	101	9	.918	84	75	9	.893
	f	517	326	191	.631	290	175	115	.603	227	151	76	.665
	g	113	110	3	.973	66	65	1	.985	47	45	2	.957
F	a	521	49	472	.094	291	35	256	.120*	230	14	216	.061
G	b	521	480	41	.921	291	267	24	.918	230	213	17	.926
H	a	498	131	367	.263	280	78	202	.279	218	53	165	.243
	c	18	15	3	.833	12	9	3	.750	6	6	0	1.000
I	a	97	96	1	.990	59	59	0	1.000	38	37	1	.974
	b	97	52	45	.536	59	36	23	.611	38	16	22	.421
K	a	521	260	261	.499	291	134	157	.460	230	126	104	.545
	b	198	165	33	.833	111	89	22	.802	87	76	11	.874
	e	521	221	300	.424	291	111	180	.381	230	110	120	.478*
	e_1	476	195	281	.410	267	98	169	.367	209	97	112	.464*
	d	521	53	468	.102	291	32	259	.110	230	21	209	.091
L	a	459	162	297	.353	252	90	162	.357	207	72	135	.346
	b	97	97	0	1.000	59	59	0	1.000	38	38	0	1.000
	c	97	89	8	.918	59	57	2	.966*	38	32	6	.842
	d	592	275	317	.465	330	153	177	.464	262	122	140	.466
	e	97	89	8	.918	59	57	2	.966*	38	32	6	.842
	g	564	537	27	.952	317	301	16	.950	247	236	11	.955
M	a	97	8	89	.082	59	4	55	.068	38	4	34	.105
N	a	605	196	409	.324	341	110	231	.323	264	86	178	.326
	b	605	595	10	.983	341	334	7	.979	264	261	3	.989
	c	584	117	467	.200	329	62	267	.188	255	55	200	.216
R	a	184	19	165	.103	107	12	95	.112	77	7	70	.091

* Differences between sexes significant at the 5% level of probability.

b. Blood Group Factors and Productive Traits

The following model was used to investigate the effects of blood group factors on productive traits:

$$Y_{ijklm} = \mu + l_i + s_j + m_k + b_l + e_{ijklm}$$

where:

μ = the population mean
l_i = the effect of the i^{th} litter
s_j = the effect of the j^{th} sex
m_k = the effect of the k^{th} mating system
b_l = the effect of the l^{th} blood group factor
e_{ijklm} = the random error associated with the m^{th} pig assumed to be N.I.D. $(0,\sigma^2_e)$.

Equations for the mean and litter effects were absorbed. Sex, mating system and blood group factor effects were regarded as fixed. In an attempt to separate the effects of breed of dam, purebred Yorkshire and Landrace pigs were assigned to separate mating system classes. Similarly, single crosses out of Yorkshire dams were considered separately from single crosses out of Landrace dams. The small number of pigs from Lacombe dams were classified with those from Landrace dams. Carcass data were adjusted also for carcass weight differences.

The effects of 27 blood group factors, comprising 12 systems, on growth traits, carcass traits and rhinitis score are illustrated in Tables 8 and 9. The effects are expressed as the probability of obtaining the observed F-value for each factor-trait combination by chance alone. The row means reflect the average influence of a specific blood group factor on the traits studied while the column means reflect the average influence of all factors on a specific trait. The row and column means were tested

TABLE 8: THE EFFECT OF BLOOD GROUP FACTOR ON GROWTH
(EXPRESSED AS THE PROBABILITY OF OBTAINING OBSERVED F-VALUE BY CHANCE ALONE)

System	Factor	No. of Pigs	Birth Weight	21 Day Weight	56 Day Weight	No. of Pigs	154 Day Weight	Row Means
C	a	239	.336	.231	.533			.367
D	a	342	.863	.920	.953	202	.578	.828
E	a	342	.022	.262	.105	202	.321	.178**
	b	338	.186	.647	.538	200	.060	.358
	e	169	.951	.188	.578	68	.580	.574
	f	342	.522	.143	.538	200	.440	.411
	g	96	.984	.232	.051	35	.183	.362
F	a	342	.729	.105	.113	202	.050	.249*
G	b	342	.493	.354	.003	202	.503	.339
H	a	325	.655	.266	.842	191	.604	.592
	c	17	.989	.275	.396	7	.144	.451
I	b	80	.619	.449	.982	28	.418	.617
K	a	342	.150	.417	.220	202	.946	.433
	b	158	.352	.009	.778	72	.974	.528
	e	342	.467	.699	.306	202	.690	.540
	e_1	339	.407	.689	.304	192	.792	.548
	d	342	.070	.610	.752	202	.681	.528
L	a	267	.584	.578	.920	168	.494	.644
	c	80	.234	.012	.0003	28	.301	.137**
	d	375	.369	.014	.114	217	.439	.234*
	e	80	.234	.012	.0003	28	.301	.137**
	g	371	.223	.480	.517	211	.709	.482
M	a	80	.115	.426	.807	28	.462	.452
N	a	404	.647	.280	.006	242	.489	.356
	b	404	.250	.058	.498	242	.639	.361
	c	390	.132	.439	.431	236	.842	.461
R	a	163	.647	.752	.184	64	.257	.460
Column Means			.453	.354**	.425		.496	.431**

* Significant at the 5% level of probability.
** Significant at the 1% level of probability.

TABLE 9: THE EFFECT OF BLOOD GROUP FACTOR ON CARCASS TRAITS AND RHINITIS SCORE (EXPRESSED AS THE PROBABILITY OF OBTAINING OBSERVED F-VALUE BY CHANCE ALONE)

System	Factor	No. of Pigs	Total Backfat	Length	Area of Eye of Lean	Lean Cut Yield	Row Means	No. of Pigs	Rhinitis Score	Row Means (All Traits)
C	a	142	.260	.432	.237	.301	.308	120	.177	.313*
D	a	198	.235	.969	.024	.498	.432	182	.538	.620
E	a	198	.044	.016	.888	.476	.356	182	.451	.287*
	b	194	.765	.489	.518	.863	.659	179	.561	.514
	e	60	.863	.077	.273	.525	.434	56	.968	.556
	f	195	.752	.259	.324	.104	.360	179	.578	.407
	g	31	.571	.989	.571	.019	.537	29	.474	.453
F	a	198	.172	.001	.296	.407	.219*	182	.792	.296*
G	b	198	.655	.647	.148	.513	.491	182	.455	.419
H	a	185	.222	.222	.277	.888	.402	171	.250	.470
I	b	23	.383	.844	.280	.585	.523	21	.490	.561
K	a	198	.429	.190	.039	.920	.394	182	.920	.470
	b	61	.435	.753	.334	.028	.387	56	.546	.468
	e	198	.316	.339	.109	.792	.389	182	.986	.523
	e_1	187	.094	.312	.039	.634	.271	172	.709	.443
	d	198	.513	.494	.672	.842	.630	182	.355	.554
L	a	177	.261	.350	.105	.007	.181*	154	.508	.423
	c	23	.449	.573	.561	.308	.472	21	.936	.375
	d	226	.663	.920	.036	.008	.407	201	.690	.361
	e	23	.449	.573	.561	.308	.472	21	.936	.375
	g	217	.591	.428	.285	.967	.568	194	.489	.521
M	a	23	.288	.516	.694	.217	.428	21	.342	.426
N	a	245	.001	.336	.729	.680	.437	213	.842	.446
	b	245	.004	.031	.982	.300	.329	213	.937	.411
	c	238	.404	.202	.021	.001	.157**	207	.578	.339*
R	a	57	.289	.626	.178	.191	.321	53	.863	.443
Column Means			.389*	.446	.353**	.438	.406**		.628	.442**

* Significant at the 5% level of probability.
** Significant at the 1% level of probability.

for deviations from an expected uniform distribution with a mean of 0.500 and a variance of 0.0833 (Jensen et al., 1968).

The results showed an excess of F-test probabilities at the low end of the probability distribution. F-values were determined for a total of 237 factor-trait combinations of which 26, or 11.0%, were below the 5% level of probability and 11, or 4.6%, were below the 1% level of probability. The mean probability of the 237 F-value probabilities was 0.442 and was significantly ($P<.01$) different from an expected mean of 0.500.

Ten of 107 factor-growth trait combinations, or 9.3%, and 16 of 104 factor-carcass trait combinations, or 15.4%, were significant at the 5% level of probability. The overall mean probabilities for growth and carcass traits of 0.431 and 0.406 respectively were significantly ($P<.01$) different from an expected mean of 0.500.

An examination of row means revealed that average growth was affected by five factors - E_a ($P<.01$), F_a ($P<.05$), L_c ($P<.01$), L_d ($P<.05$) and L_e ($P<.01$). Factor L_d was used in the double mating program for sire identification. Three factors - F_a ($P<.05$), L_a ($P<.05$) and N_c ($P<.01$) - affected carcass trait averages. Four overall row means, which reflect the average effect of a specific factor on all traits, were significant ($P<.05$). These were for factors C_a, E_a, F_a and N_c. Significant column means, which reflect the average effect of all factors on a specific trait, were observed for 21 day weight ($P<.01$), total backfat ($P<.05$) and area of eye of lean ($P<.01$).

Specific relationships between blood group factors and growth traits, carcass traits and rhinitis score are illustrated in Tables 10 and 11. Least squares estimates, expressed as deviations from the mean, are given for those pigs which were typed positive for each factor. Least

TABLE 10: THE EFFECT OF BLOOD GROUP FACTOR ON GROWTH
(LEAST SQUARES ESTIMATES EXPRESSED AS DEVIATIONS FROM MEAN)

System	Factor	Pigs No. Typed	Pigs No. Pos.	Birth Weight (lbs.)	21 Day Weight (lbs.)	56 Day Weight (lbs.)	Pigs No. Typed	Pigs No. Pos.	154 Day Weight (lbs.)
C	a	239	9	-.096	-.58	-.87	133	0	
D	a	342	94	-.008	.02	.01	202	53	.83
E	a	342	24	.150*	.35	1.49	202	20	-1.96
	b	338	182	-.044	.07	.29	200	95	2.23
	e	169	154	-.005	.46	.59	68	61	-1.66
	f	342	206	.024	.26	.32	200	139	-1.03
	g	96	93	.004	-1.03	-5.86	35	34	-12.01
F	a	342	37	-.019	.42	1.20	202	18	4.15*
G	b	342	328	-.055	-.35	-3.24**	202	188	1.51
H	a	325	66	-.021	-.25	-.14	191	47	.76
	c	17	14	-.002	.93	1.79	7	6	-7.50
I	b	80	43	-.033	-.23	.02	28	15	-3.02
K	a	342	147	.051	.14	.60	202	98	-.08
	b	158	132	-.064	-.78**	-.28	72	62	-.11
	e	342	127	.028	.07	.54	202	88	-.54
	e_1	339	125	.031	.07	.54	192	80	-.35
	d	342	21	.138	.19	.35	202	14	-1.08
L	a	267	86	-.020	-.11	-.07	168	57	-.94
	c	80	73	-.129	-1.26*	-5.85**	28	23	5.73
	d	375	175	-.031	-.41*	-.75	217	93	-.91
	e	80	73	-.129	-1.26*	-5.85**	28	23	5.73
	g	371	351	.081	.23	.60	211	203	1.11
M	a	80	8	.160	.38	.40	28	3	4.36
N	a	404	139	.014	.16	1.15**	242	84	.74
	b	404	397	-.128	-.98	-1.04	242	236	-1.57
	c	390	74	-.062	-.15	-.44	236	51	-.27
R	a	163	17	.034	-.11	-1.37	64	4	-4.50

** Significant at the 1% level of probability.
* Significant at the 5% level of probability.

TABLE 11: THE EFFECT OF BLOOD GROUP FACTOR ON CARCASS TRAITS AND RHINITIS SCORE
(LEAST SQUARES ESTIMATES EXPRESSED AS DEVIATIONS FROM MEAN)

System	Factor	Pigs No. Typed	 No. Pos.	Total Backfat (in.)	Length (in.)	Area of Eye of Lean (sq. in.)	Lean Cut Yield (lbs.)	Pigs No. Typed	 No. Pos.	Rhinitis Score
C	a	142	4	.089	-.15	.137	-.76	120	4	-.472
D	a	198	60	.032	-.002	-.088*	-.18	182	60	.076
E	a	198	15	-.086*	.25*	.010	.31	182	15	.145
	b	194	106	.007	.04	-.022	-.04	179	93	-.065
	e	60	52	-.012	-.28	-.076	-.34	56	49	-.014
	f	195	131	-.009	-.07	.038	.43	179	121	-.068
	g	31	30	-.117	.006	.128	3.83*	29	28	-.594
F	a	198	26	-.050	.35**	-.056	-.30	182	22	.048
G	b	198	179	-.017	.04	-.081	.25	182	165	.205
H	a	185	42	-.037	.09	-.049	-.05	171	43	-.094
I	b	23	14	.106	-.06	-.095	.59	21	12	-.312
K	a	198	107	.020	-.08	.074*	-.03	182	104	-.014
	b	61	54	.060	.06	.092	1.33*	56	49	-.210
	e	198	87	.025	-.06	.059	.07	182	84	-.001
	e_1	187	84	.045	-.07	.079*	.13	172	80	-.048
	d	198	28	-.024	-.06	.023	.08	182	28	-.157
L	a	177	53	.030	.06	-.063	-.77**	154	50	-.082
	c	23	22	.150	.25	-.084	1.77	21	20	.059
	d	226	84	.009	.007	-.068*	-.63**	201	79	.041
	e	23	22	.150	.25	-.084	1.77	21	20	.059
	g	217	214	-.048	.17	.139	.04	194	191	.273
M	a	23	2	-.146	-.20	.041	-1.48	21	2	.518
N	a	245	97	-.064**	.05	.011	-.09	213	86	-.019
	b	245	239	.184**	-.34*	-.002	-.75	213	209	-.028
	c	238	49	.021	.08	-.088*	-.98**	207	43	.070
R	a	57	4	-.099	.11	-.133	-1.01	53	4	-.080

** Significant at the 1% level of probability.
* Significant at the 5% level of probability.

squares estimates for pigs which were typed negative are not listed but are the same in numerical value and opposite in sign to the positive pigs for the respective factors. No factors of five systems - C, H, I, M and R - were associated with any trait studied.

The presence of factor D_a was associated ($P<.05$) with smaller areas of eye of lean but no relationship between D_a and any specific growth trait was observed.

In the E system, pigs which possessed factor E_a were heavier at birth, had less total backfat and had longer carcasses ($P<.05$). E_g, which was associated with greater lean cut yields ($P<.05$), was the only other factor in the E system related to the productive traits studied.

Considering the F system, F_a was associated with heavier weights at 154 days ($P<.05$) and longer carcass lengths ($P<.01$). Pigs with G_b were lighter at 56 days ($P<.01$).

Analysis of the K system revealed that both the K_a and K_{e1} factors were associated with larger areas of eye of lean ($P<.05$). K_b pigs, although lighter at 21 days ($P<.01$), produced greater yields of lean cuts ($P<.05$).

L system factors were frequently associated with traits studied. Pigs possessing factor L_a produced smaller yields of lean cuts ($P<.01$). L_c and L_e pigs were lighter at both 21 days ($P<.05$) and 56 days ($P<.01$) of age. Factor L_d, which was used for sire identification in the double mating program, was detrimentally associated with three traits - weight at 21 days of age ($P<.05$), area of eye of lean ($P<.05$) and lean cut yield ($P<.01$). L_g, which also was used in the double mating program, was not observed to be associated with any trait studied.

Factors of the N system also showed frequent relationships with the productive traits under consideration. Pigs possessing the N_a factor were heavier at 56 days and had less total backfat ($P<.01$). In contrast,

N_b pigs had more backfat ($P<.01$) and shorter carcasses ($P<.05$). Both these factors were used in the double mating program. N_c, the third factor of the N system, was associated with smaller areas of eye of lean ($P<.05$) and reduced lean cut yields ($P<.01$).

Factors L_d, L_g, N_a, and N_b were used for sire identification in the double mating program. The effects of interaction between factors L_d and L_g and factors N_a and N_b on productive traits are illustrated in Table 12. Least squares estimates, expressed as deviations from the mean, are given.

The L and N systems are closed systems in which the respective L_d and L_g factors and N_a and N_b factors are complementary characters. Pigs which, within a system, possessed both factors were classified as 'heterozygous' and those which possessed only one of the factors were regarded as 'homozygous'. In neither system were pigs observed which lacked both factors.

A trend, relative to growth, was observed in each system. In the L system, 'heterozygous' L_{dg} pigs were heavier in weight for all four growth traits than were 'homozygous' L_d and L_g pigs. Differences, however, were significant ($P<.05$) only for 21 day weight. The opposite effect was observed in the N system where 'heterozygous' N_{ab} pigs were lighter than 'homozygous' N_a and N_b pigs for the four growth measures. Differences were significant ($P<.05$) only for 56 day weight.

No consistent effects of blood group factor interaction were observed for the carcass traits. 'Heterozygous' L_{dg} pigs were, however, associated with greater lean cut yields ($P<.01$) and 'homozygous' N_a and N_b pigs had less total backfat ($P<.05$). No relationship between blood group factor interaction and rhinitis score was observed within either system.

TABLE 12: THE EFFECT OF BLOOD GROUP FACTOR INTERACTION WITHIN THE L AND N SYSTEMS (LEAST SQUARES ESTIMATES EXPRESSED AS DEVIATIONS FROM MEAN)

	Growth Traits						Carcass Traits and Rhinitis Score						
Factor	No. Pigs	Birth Weight (lbs.)	21 Day Weight (lbs.)	56 Day Weight (lbs.)	No. Pigs	154 Day Weight (lbs.)	No. Pigs	Total Backfat (in.)	Length (in.)	Area of Eye of Lean (sq. in.)	Lean Cut Yield (lbs.)	No. Pigs	Rhin. Score
L system	371				210		217					194	
L_d or L_g	154	-.012	-.34*	-.62	82	-1.07	77	.004	.02	-.061	-.71**	73	.069
L_{dg}	217	.012	.34	.62	128	1.07	140	-.004	-.02	.061	.71	121	-.069
N system	404				240		245					213	
N_a or N_b	132	.004	.08	1.09*	77	.52	91	-.048*	.02	.011	-.16	82	-.022
N_{ab}	272	-.004	-.08	-1.09	163	-.52	154	.048	-.02	-.011	.16	131	.022

* Significant at the 5% level of probability.
** Significant at the 1% level of probability.

c. Blood Group Factors and Reproductive Traits

The following model was used to investigate the effects of blood group factors on reproductive traits:

$$Y_{ijklm} = \mu + t_i + m_j + q_k + b_l + e_{ijklm}$$

where:

μ = the population mean

t_i = the effect of the i^{th} period of time

m_j = the effect of the j^{th} mating system

q_k = the effect of the k^{th} litter sequence

b_l = the effect of the l^{th} sire-dam blood group factor combination

e_{ijklm} = the random error associated with the m^{th} pig assumed to be N.ID. $(0, \sigma^2_e)$

Equations for the mean and the effects of period of time were absorbed. Mating system, litter sequence and sire-dam blood group factor combination were regarded as fixed effects. Attempts, similar to those undertaken in the productive trait analysis, were made to remove the effects of breed of dam. The number of pigs in each litter that were born dead, born, born alive, alive at 21 days and alive at 56 days were used as criteria of reproductive performance.

The effects of 20 blood group factors, involving nine systems, on reproduction are illustrated in Table 13. The effects are expressed as the probability of obtaining the observed F-value by chance alone.

F-test probabilities were obtained for 100 factor-trait combinations. No excess of low F-values was observed as only five, or 5%, were significant at the 5% level of probability. The overall mean probability of 0.478 was not significantly different from an expected mean of 0.500.

TABLE 13: THE EFFECT OF BLOOD GROUP FACTOR OF REPRODUCTION (EXPRESSED AS THE PROBABILITY OF OBTAINING OBSERVED F-VALUE BY CHANCE ALONE)

System	Factor	No. of Litters	No. Born Dead	No. Born	No. Born Alive	No. Alive 21 Days	No. Alive 56 Days	Row Means
C	a	155	.118	.157	.398	.451	.394	.304
D	a	163	.418	.629	.833	.847	.875	.720
E	a	164	.954	.453	.448	.335	.298	.498
	b	163	.690	.711	.591	.746	.616	.671
	e	80	.659	.563	.400	.500	.536	.532
	f	163	.560	.176	.386	.448	.164	.347
F	a	163	.833	.144	.192	.199	.080	.290
G	b	163	.603	.917	.942	.479	.368	.662
H	a	160	.854	.818	.833	.739	.453	.739
K	a	163	.041	.014	.152	.112	.098	.083**
	b	83	.324	.133	.063	.039	.054	.123**
	d	160	.104	.875	.868	.996	.875	.744
	e	159	.351	.039	.134	.217	.240	.196**
	e_1	163	.355	.029	.107	.199	.231	.184**
L	a	100	.402	.371	.435	.561	.656	.485
	d	235	.622	.596	.739	.917	.804	.736
	g	235	.578	.725	.782	.882	.917	.777
N	a	235	.380	.342	.109	.512	.447	.358
	b	235	.861	.951	.923	.961	.970	.933
	c	194	.169	.110	.311	.251	.052	.179**
Column Means			.494	.438	.482	.520	.456	.478

* Significant at the 5% level of probability.

** Significant at the 1% level of probability.

TABLE 14: THE EFFECT OF BLOOD GROUP FACTOR ON REPRODUCTION (EXPRESSED AS THE MEAN PLUS LEAST SQUARES ESTIMATE OF DEVIATION FROM MEAN)

			Trait				
Factor	Sire/Dam Combination	No. of Litters	No. Born Dead	No. Born	No. Born Alive	No. Alive 21 Days	No. Alive 56 Days
C_a	-/-	150	1.14	11.71	10.58	9.48	9.31
	-/+	5	0.26	9.55	9.30	8.46	8.15
	Total	155					
D_a	-/-	102	0.93	11.02	10.09	9.18	8.95
	+/-	21	0.85	11.45	10.60	9.51	9.18
	-/+	37	0.58	10.55	9.97	8.88	8.60
	+/+	3	0.29	9.21	8.93	8.26	8.14
	Total	163					
E_a	-/-	126	0.68	11.56	10.88	9.78	9.57
	+/-	25	0.54	10.53	9.99	8.52	8.26
	-/+	10	0.62	11.12	10.50	8.74	8.46
	+/+	3	0.89	9.04	8.14	8.56	8.37
	Total	164					
E_b	-/-	41	0.67	10.92	10.25	9.29	9.20
	+/-	37	0.71	10.73	10.02	8.98	8.61
	-/+	48	0.80	10.17	9.38	8.62	8.40
	+/+	37	0.48	10.41	9.94	8.95	8.67
	Total	163					
E_e	+/-	4	0.91	9.32	8.41	7.53	7.44
	-/+	1	0.01	10.55	10.54	10.26	10.21
	+/+	75	0.55	11.04	10.48	9.17	8.93
	Total	80					
E_f	-/-	26	0.63	10.34	9.71	8.96	8.92
	+/-	46	0.62	10.16	9.54	8.61	8.19
	-/+	26	0.53	10.29	9.77	8.77	8.39
	+/+	65	0.87	11.44	10.57	9.49	9.38
	Total	163					
F_a	-/-	133	0.87	10.92	10.05	8.79	8.47
	+/-	9	0.65	11.94	11.29	10.18	10.14
	-/+	20	0.65	9.16	8.52	7.54	6.96
	+/+	1	0.49	10.22	9.73	9.32	9.31
	Total	163					

* Significant at the 5% level of probability

TABLE 14 (CONT'D): THE EFFECT OF BLOOD GROUP FACTOR ON REPRODUCTION (EXPRESSED AS THE MEAN PLUS LEAST SQUARES ESTIMATE OF DEVIATION FROM MEAN)

			Trait				
Factor	Sire/Dam Combination	No. of Litters	No. Born Dead	No. Born	No. Born Alive	No. Alive 21 Days	No. Alive 56 Days
G_b	-/-	1	0.10	9.76	9.65	9.68	9.65
	+/-	10	0.55	10.63	10.08	8.50	8.45
	-/+	18	1.06	10.66	9.60	8.03	7.46
	+/+	134	0.94	11.19	10.25	9.22	8.85
	Total	163					
H_a	-/-	65	0.61	10.66	10.05	9.19	9.09
	+/-	44	0.67	10.19	9.52	8.59	8.19
	-/+	28	0.55	10.55	10.00	8.98	8.84
	+/+	23	0.85	10.91	10.06	9.16	8.84
	Total	160					
K_a	-/-	51	0.80	10.70	9.90	8.90	8.62
	+/-	37	1.00	11.90	10.90	9.94	9.73
	-/+	45	0.27	9.60	9.33	8.56	8.39
	+/+	30	0.58	10.04	9.46	8.43	8.12
	Total	163	*	*			
K_b	-/-	3	1.11	7.94	6.83	5.69	5.81
	+/-	21	0.09	11.00	10.92	10.34	10.00
	-/+	9	0.53	12.03	11.50	10.36	10.26
	+/+	50	0.16	10.53	10.37	9.81	9.50
	Total	83				*	
K_d	-/-	110	0.82	10.63	9.81	9.04	9.04
	+/-	29	1.21	10.66	9.45	8.97	8.64
	-/+	14	0.21	9.92	9.71	8.86	8.97
	+/+	7	0.46	11.06	10.60	8.93	8.18
	Total	160					
K_e	-/-	71	0.79	11.07	10.28	9.22	8.85
	+/-	34	0.84	11.74	10.90	9.83	9.62
	-/+	38	0.36	9.49	9.13	8.63	8.37
	+/+	16	0.73	9.95	9.21	8.10	7.96
	Total	159		*			
K_{e_1}	-/-	74	0.76	11.09	10.34	9.28	8.91
	+/-	34	0.83	11.74	10.91	9.83	9.62
	-/+	39	0.34	9.46	9.12	8.62	8.37
	+/+	16	0.73	9.94	9.22	8.11	7.97
	Total	163		*			

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* Significant at the 5% level of probability.

TABLE 14 (CONT'D): THE EFFECT OF BLOOD GROUP FACTOR ON REPORDUCTION (EXPRESSED AS THE MEAN PLUS LEAST SQUARES ESTIMATE OF DEVIATION FROM MEAN)

			Trait				
Factor	Sire/Dam Combination	No. of Litters	No. Born Dead	No. Born	No. Born Alive	No. Alive 21 Days	No. Alive 56 Days
L_a	-/-	71	0.51	12.32	11.81	10.41	10.08
	+/-	4	1.01	10.57	9.56	8.12	7.98
	-/+	22	0.93	12.59	11.66	10.64	10.29
	+/+	3	0.11	7.72	7.62	7.91	7.78
	Total	100					
L_d	-/-	77	0.73	11.09	10.37	9.37	9.19
	+/-	50	0.45	10.42	9.98	9.08	8.93
	-/+	56	0.60	10.41	9.81	9.04	8.69
	+/+	52	0.65	10.43	9.78	9.03	8.81
	Total	235					
L_g	-/-	1	0.82	8.70	7.88	7.48	7.47
	+/-	8	0.40	11.42	11.02	9.90	9.61
	-/+	26	0.46	10.85	10.39	9.59	9.26
	+/+	200	0.74	11.38	10.65	9.54	9.29
	Total	235					
N_a	-/-	91	0.66	10.58	9.93	9.14	8.83
	+/-	34	0.42	11.16	10.73	9.64	9.46
	-/+	72	0.50	10.84	10.35	9.22	9.04
	+/+	38	0.84	9.77	8.93	8.51	8.30
	Total	235					
N_b	+/-	14	0.48	10.54	10.06	9.16	8.92
	-/+	17	0.72	10.49	9.77	9.00	8.81
	+/+	204	0.62	10.73	10.12	9.22	8.99
	Total	235					
N_c	-/-	156	0.87	12.04	11.16	10.10	9.92
	+/-	4	1.01	10.00	8.99	8.10	8.05
	-/+	31	0.44	10.71	10.27	9.16	8.44
	+/+	3	0.01	9.90	9.88	9.36	9.38
	Total	194					

* Significant at the 5% level of probability.

Examination of the row means revealed that average reproductive performance was affected ($P<.01$) by five factors - K_a, K_b, K_e, K_{e1} and N_c. An examination of the column means, however, failed to detect a significant combined effect of all factors on any reproductive trait considered.

The effects of blood group factors on reproduction, expressed as the mean plus the least squares estimate of deviations from the mean, are illustrated in Table 14. Significant ($P<.05$) effects were observed for the K system only. Number of pigs born was affected by K_a, K_e and K_{e1} while numbers born dead and numbers alive at 21 days were affected by K_a and K_b respectively.

d. The Effect of Double Mating on Litter Size

A total of 190 single and 76 double mated litters were farrowed between 1965-67. The effects of mating technique on litter size are illustrated in Table 15.

TABLE 15: THE EFFECT OF MATING TECHNIQUE ON LITTER SIZE

Mating Technique	Number of Litters	Average Litter Size	t-value
Single Mating	190	9.6	1.98*
Double Mating	76	10.5	

* Significant at the 5% level of probability.

Examination by t-test revealed that litter size, when measured as the number of pigs born alive, was significantly ($P<.05$) affected by mating technique. Double mated litters averaged almost one pig more per litter than did single mated litters farrowed during the same period.

e. The Effect of Double Mating on Sex Ratio

It was observed that the sex ratio of double mated litters tended to differ from that of single mated litters. The effects of mating technique on the sex ratios of 303 single and 100 double mated litters, farrowed between 1965-68, were tested for randomness by adjusted chi-square. The results are illustrated in Table 16.

TABLE 16: THE EFFECT OF MATING TECHNIQUE ON SEX RATIO

Mating Technique	No. of Litters	Males Obs.	Males Exp.	Females Obs.	Females Exp.	Total	χ^2
Single Mating	303	1512	1530	1447	1429	2959	
Double Mating	100	567	549	495	513	1062	
Total	403	2079		1942		4021	1.55$^{ns.}$

$^{ns.}$ Non-significant at the 5% level of probability.

In 303 single mated litters, male pigs comprised 51.1% of the live births compared to 53.4% males observed in 100 double mated litters. The difference was not significant (P<.05).

However, a closer examination of the effects of preferential fertilization within double mated litters on sex ratio was made. If in any double mated litter a boar sired at least two-thirds of the pigs he was considered dominant while the boar that sired the remaining one-third or fewer pigs was regarded as dominated. This criterion of preferential fertilization was observed in 64 double mated litters. The effects of preferential fertilization on the sex ratio of double mated litters are illustrated in Table 17.

TABLE 17: THE EFFECT OF PREFERENTIAL FERTILIZATION ON SEX RATIO IN DOUBLE MATED LITTERS

Boar	Males Obs.	Males Exp.	Females Obs.	Females Exp.	Total	χ^2
Dominant	270	283	255	242	525	
Dominated	86	73	49	62	135	
Total	356		304		660	6.05*

* Significant at the 5% level of probability.

In 64 preferentially fertilized litters dominant boars sired 51.4% male pigs while pigs sired by dominated boars were 63.7% males. The difference was significant ($P < .05$).

2. Components of Variance

Components of variance were estimated for the field, random, sequential and double mating data. The following models were used:

Field and Random:

$$Y_{ijklmno} = \mu + a_i + b_{ij} + c_{ijk} + d_{ijkl} + f_{ijklm} + g_n + e_{ijklmno}$$

where: μ = the population mean

a_i = the effect of the i^{th} breed of sire

b_{ij} = the effect of the j^{th} sire within the i^{th} breed of sire

c_{ijk} = the effect of the k^{th} breed of dam within the ij^{th} sire

d_{ijkl} = the effect of the l^{th} dam within the ijk^{th} breed of dam

f_{ijklm} = the effect of the m^{th} litter within the $ijkl^{th}$ dam

g_n = the effect of the n^{th} sex

$e_{ijklmno}$ = the random error associated with the o^{th} pig assumed to be N.I.D. $(0,\sigma^2_e)$

Sequential:

$$Y_{ijklm} = \mu + a_i + b_{ij} + c_{ijk} + d_l + e_{ijklm}$$

where: μ = the population mean

a_i = the effect of the i^{th} breed of dam

b_{ij} = the effect of the j^{th} dam within the i^{th} breed of dam

c_{ijk} = the effect of the k^{th} litter within the ij^{th} dam

d_l = the effect of the l^{th} sex

e_{ijklm} = the random error associated with the m^{th} pig assumed to be N.I.D. $(0,\sigma^2_e)$

Double:

$$Y_{ijklm} = \mu + a_i + b_{ij} + c_{ijk} + d_l + e_{ijklm}$$

where: μ = the population mean

a_i = the effect of the i^{th} breed of dam

b_{ij} = the effect of the j^{th} litter within the i^{th} breed of dam

c_{ijk} = the effect of the k^{th} sire within the ij^{th} litter

d_l = the effect of the l^{th} sex

e_{ijklm} = the random error associated with the m^{th} pig assumed to be N.I.D. $(0,\sigma_e^2)$

In all three models, sex effects were regarded as fixed and the remaining effects formed random nested classifications. The regression of carcass weight was included also in the analysis of carcass traits in the random, sequential and double mating data and for all traits in the field data analysis.

The components of variance for the five traits considered in the field study are illustrated in Table 18. A total of 2304 pigs from 734 litters were involved in the analysis.

The error components were relatively high for the two measures of backfat depth, intermediate for the two growth traits and low for trimmed loin weight. The litter components were low for the two measures of growth, absent for the two backfat traits but high for weight of trimmed loin. Appreciable dam components were observed for age at market and daily gain but dam components were lower for trimmed loin weight and loin backfat and absent for shoulder backfat. The sire components were small for all traits. Also the breed of dam and breed of sire components were small or absent for all traits considered.

TABLE 18: NEWFOUNDLAND FIELD DATA COMPONENTS OF VARIANCE

Trait	Breed of Sire	Sire	Breed of Dam	Dam	Litter	Error	Total
Age at Market (days)	0. (0.%)	4.81 (1.2%)	15.79 (3.7%)	107.05 (25.3%)	64.08 (15.2%)	230.91 (54.6%)	422.64
Daily Gain (lbs./day)	0. (0.%)	.00007 (0.9%)	.00027 (3.5%)	.00206 (26.5%)	.00121 (15.5%)	.00417 (53.6%)	.00778
Shoulder Backfat (in.)	0. (0.%)	.00045 (1.7%)	0. (0.%)	0. (0.%)	0. (0.%)	.02669 (98.3%)	.02714
Loin Backfat (in.)	0. (0.%)	.00024 (.7%)	0. (0.%)	.00283 (8.5%)	0. (0.%)	.03031 (90.8%)	.03338
Trimmed Loin (lbs.)	.0470 (2.5%)	.0050 (0.3%)	.0647 (3.4%)	.3594 (18.9%)	.8000 (42.1%)	.6232 (32.8%)	1.8993

The random mating components of variance are illustrated in Tables 19 and 20. A total of 5303 pigs from 718 litters were involved in the analysis.

The error components for growth traits in the random mating analysis were somewhat lower than those observed in the field data but litter components were substantial for all growth traits. Dam components were high, particularly among the early growth traits, in contrast to the relatively small size of the sire components. The dam component for birth weight was approximately seven times that of the sire component and was from two to 2-1/2 times greater for the other growth traits. The breed of dam and breed of sire components were small or absent for all traits.

The error components for carcass traits generally were lower in the random mating analysis than those observed in the field study. In contrast with the results of the growth trait analysis, error components generally were higher and litter components were lower for the carcass traits considered. Dam components also were lower for the carcass traits. The sire components were approximately equal to the dam components for all traits except loin backfat where the dam component was zero. The breed of dam and breed of sire components were small or negligible for all traits except length, where the breed of sire component was high, and loin backfat, where the breed of dam component was substantial.

The sequential mating components of variance are illustrated in Table 21. A total of 2315 pigs from 312 litters were involved in the analysis.

As was observed in the field and random mating studies, the error components were lower for the growth traits than for the carcass traits. Similarly, litter components were relatively higher for growth traits than

TABLE 19: RANDOM MATING COMPONENTS OF VARIANCE (GROWTH TRAITS)

Trait	Breed of Sire	Sire	Breed of Dam	Dam	Litter	Error	Total
Birth Weight (lbs.)	0. (0. %)	.02185 (5.1%)	.01978 (4.6%)	.14870 (34.3%)	.08456 (19.5%)	.15821 (36.5%)	.43310
21 Day Weight (lbs.)	0. (0. %)	.9506 (8.4%)	.0885 (.8%)	2.3903 (21.0%)	3.2376 (28.5%)	4.6939 (41.3%)	11.3609
56 Day Weight (lbs.)	0. (0. %)	13.053 (11.2%)	2.783 (2.4%)	23.663 (20.3%)	39.600 (33.9%)	37.670 (32.2%)	116.769
154 Day Weight (lbs.)	14.41 (2.0%)	64.14 (8.7%)	0. (0. %)	124.03 (16.9%)	193.89 (26.4%)	337.32 (46.0%)	733.79
Age at Market (days)	2.73 (.6%)	38.74 (8.9%)	0. (0. %)	76.51 (17.6%)	121.48 (27.9%)	196.36 (45.0%)	435.82
Daily Gain (lbs./day)	.00023 (1.3%)	.00133 (7.5%)	.00003 (.2%)	.00346 (19.6%)	.00410 (23.2%)	.00851 (48.2%)	.01766

TABLE 20: RANDOM MATING COMPONENTS OF VARIANCE (CARCASS TRAITS)

Trait	Breed of Sire	Sire	Breed of Dam	Dam	Litter	Error	Total
Length (in.)	.11695 (16.6%)	.13304 (18.8%)	0. (0. %)	.09864 (14.0%)	.05294 (7.5%)	.30398 (43.1%)	.70555
Shoulder Backfat (in.)	0. (0. %)	.01115 (18.4%)	.00111 (1.8%)	.00689 (11.3%)	.00284 (4.7%)	.03876 (63.8%)	.06075
Loin Backfat (in.)	0. (0. %)	.00939 (22.1%)	.00366 (8.6%)	0. (0. %)	.00296 (7.0%)	.02639 (62.3%)	.04240
Area of Eye of Lean (sq.in.)	.00728 (2.5%)	.04127 (14.4%)	0. (0. %)	.04446 (15.5%)	.03433 (12.0%)	.15912 (55.6%)	.28646
Trimmed Ham (lbs.)	.02041 (2.1%)	.07062 (7.3%)	.03493 (3.6%)	.08915 (9.2%)	.11832 (12.3%)	.63220 (65.5%)	.96563
Trimmed Shoulder (lbs.)	0. (0. %)	.25575 (15.1%)	0. (0. %)	.18038 (10.7%)	.33220 (19.6%)	.92485 (54.6%)	1.69318
Trimmed Loin (lbs.)	0. (0. %)	.07942 (8.0%)	0. (0. %)	.09384 (9.5%)	.01926 (1.9%)	.79748 (80.6%)	.99000
Lean Cut Yield (lbs.)	0. (0. %)	3.5267 (15.4%)	0. (0. %)	2.0206 (8.8%)	2.3760 (10.3%)	15.0593 (65.5%)	22.9826

TABLE 21: SEQUENTIAL MATING COMPONENTS OF VARIANCE

Trait	Breed of Dam	Dam	Litter	Error	Total
Birth Weight (lbs.)	.04108 (10.4%)	.11856 (29.9%)	.09615 (24.2%)	.14102 (35.5%)	.39681
21 Day Weight (lbs.)	.1129 (1.3%)	1.8166 (20.0%)	2.8116 (31.0%)	4.3198 (47.7%)	9.0609
56 Day Weight (lbs.)	0. (0. %)	19.968 (21.1%)	39.202 (41.3%)	35.626 (37.6%)	94.796
154 Day Weight (lbs.)	51.07 (7.5%)	73.78 (10.8%)	197.76 (29.1%)	358.32 (52.6%)	680.93
Age at Market (days)	21.97 (6.1%)	49.33 (13.6%)	100.39 (27.8%)	189.55 (52.5%)	361.24
Daily Gain (lbs./day)	.00114 (6.9%)	.00189 (11.5%)	.00515 (31.2%)	.00830 (50.4%)	.01648
Length (in.)	0. (0. %)	.13711 (19.8%)	.09462 (13.7%)	.45944 (66.5%)	.69117
Shoulder Backfat (in.)	0. (0. %)	.01150 (20.6%)	.01160 (20.7%)	.03283 (58.7%)	.05593
Loin Backfat (in.)	.00066 (1.5%)	.00773 (17.6%)	.00865 (19.7%)	.02686 (61.2%)	.04390
Area of Eye of Lean (sq.in.)	0. (0. %)	.04994 (19.2%)	.05743 (22.0%)	.15330 (58.8%)	.26067
Trimmed Ham (lbs.)	.00838 (.9%)	.13663 (14.0%)	.16187 (16.7%)	.66471 (68.4%)	.97159
Trimmed Shoulder (lbs.)	0. (0. %)	.26516 (17.5%)	.28366 (18.7%)	.96776 (63.8%)	1.51658
Trimmed Loin (lbs.)	0. (0. %)	.10364 (12.1%)	.07384 (8.6%)	.67996 (79.3%)	.85744
Lean Cut Yield (lbs.)	0. (0. %)	3.540 (20.9%)	2.857 (16.9%)	10.528 (62.2%)	16.925

for carcass traits. The dam components ranged from a low of 10.8% for 154 day weight to a high of 29.9% for weight at birth and were comparatively higher for the early growth traits than for the late growth traits. The breed of dam components were substantial for four growth traits - birth weight, 154 day weight, age at market and daily gain - but were insignificant for all carcass traits.

The components of variance for the double mating data are illustrated in Table 22. A total of 697 pigs from 80 litters were involved in the analysis.

The error components were generally higher for carcass traits than for growth traits. The sire components were moderate, ranging from a low of zero for trimmed shoulder weight to a high of 24.8% for length. Litter variances were appreciable and reasonably consistent but were generally higher for growth traits than for carcass traits. In contrast, moderate breed of dam components were observed for most carcass traits but breed of dam components were insignificant for all growth traits except weight at birth.

TABLE 22: DOUBLE MATING COMPONENTS OF VARIANCE

Trait	Breed of Dam	Litter	Sire	Error	Total
Birth Weight (lbs.)	.01569 (4.6%)	.12182 (35.8%)	.01765 (5.2%)	.18539 (54.4%)	.34055
21 Day Weight (lbs.)	.0161 (0.2%)	2.1896 (25.4%)	.3530 (4.1%)	6.0625 (70.3%)	8.6212
56 Day Weight (lbs.)	0. (0. %)	31.196 (38.8%)	11.169 (13.9%)	38.087 (47.3%)	80.452
154 Day Weight (lbs.)	0. (0. %)	110.99 (25.8%)	66.51 (15.4%)	253.33 (58.8%)	430.83
Age at Market (days)	0. (0. %)	91.83 (28.3%)	60.38 (18.7%)	171.51 (53.0%)	323.72
Daily Gain (lbs./day)	.00001 (0.1%)	.00284 (20.5%)	.00241 (17.4%)	.00859 (62.0%)	.01385
Length (in.)	.0529 (5.8%)	.2825 (31.1%)	.2248 (24.8%)	.3475 (38.3%)	.9077
Shoulder Backfat (in.)	.00226 (4.4%)	.00994 (19.2%)	.00549 (10.6%)	.03398 (65.8%)	.05167
Loin Backfat (in.)	.00452 (8.9%)	.00820 (16.2%)	.00643 (12.7%)	.03154 (62.2%)	.05069
Area of Eye of Lean (sq.in.)	.01006 (4.2%)	.06230 (25.9%)	.02826 (11.8%)	.13949 (58.1%)	.24011
Trimmed Ham (lbs.)	.07062 (8.8%)	.09946 (12.5%)	.02783 (3.5%)	.60046 (75.2%)	.79837
Trimmed Shoulder (lbs.)	.03336 (3.0%)	.29829 (26.5%)	0. (0. %)	.79283 (70.5%)	1.12448
Trimmed Loin (lbs.)	0. (0. %)	.06167 (7.9%)	.07328 (9.4%)	.64240 (82.7%)	.77735
Lean Cut Yield (lbs.)	.919 (6.5%)	1.374 (9.6%)	.876 (6.2%)	11.063 (77.7%)	14.232

3. Heritability Estimates

Data from the field, random and double mating variance component analyses were used to obtain heritability estimates for the growth and carcass traits studied. The formulae used to compute the estimates are illustrated as follows:

COMPUTATION OF HERITABILITY ESTIMATES FROM FIELD, RANDOM AND DOUBLE MATING DATA

Analysis	Trait	h^2
Field and Random	Growth	$\frac{4\sigma_s^2}{\sigma_1^2+\sigma_e^2+\sigma_s^2+\sigma_d^2}$
	Carcass	$\frac{2(\sigma_s^2+\sigma_d^2)}{\sigma_1^2+\sigma_e^2+\sigma_s^2+\sigma_d^2}$
Double	All	$\frac{4\sigma_s^2}{\sigma_1^2+\sigma_e^2+\sigma_s^2}$

where: σ_s^2 = sire component of variance

σ_d^2 = dam component of variance

σ_1^2 = litter component of variance

σ_e^2 = error component of variance

Estimates of genetic variance for all traits in the double mating analysis and for growth traits in the field and random mating analyses were based on the sire components only. However, for carcass traits in the field and random mating analyses, estimates of genetic variance were based on combined sire and dam components.

Heritabilities of growth and carcass traits, as estimated from field, random and double mating data, are illustrated in Table 23.

Heritabilities estimated from field data were low for all traits considered, ranging from .01 for weight of trimmed loin to .18 for loin backfat. Estimates obtained from the random mating data were markedly higher and reasonably consistent heritabilities were observed for all growth traits, both pre- and post-weaning. Carcass trait heritabilities tended to be higher, but more variable, than those observed for growth traits.

Estimates based on the double mating data were similar to the random mating estimates for the early growth traits but were higher for the three late growth traits. Carcass trait heritabilities were highly variable but were, on the whole, lower than those observed in the random mating study.

TABLE 23: HERITABILITIES OF GROWTH AND CARCASS TRAITS AS ESTIMATED FROM FIELD, RANDOM AND DOUBLE MATING DATA

	Analysis		
Trait	Field	Random	Double
Growth Traits[a]			
Birth Weight		.21	.22
21 Day Weight		.34	.16
56 Day Weight		.46	.56
154 Day Weight		.36	.62
Age at Market	.05	.36	.75
Daily Gain	.04	.31	.70
Carcass Traits[b]			
Length		.79	1.05
Shoulder Backfat	.03	.60	.44
Loin Backfat	.18	.48	.56
Area of Eye of Lean		.61	.49
Trimmed Ham		.35	.15
Trimmed Shoulder		.52	0.
Trimmed Loin	.01	.35	.38
Lean Cut Yield		.48	.26

[a] Growth trait heritabilities are based on the sire component of variance only.

[b] Carcass trait heritabilities are based on combined sire and dam components of variance except for the double mating estimates which are based on the sire component only.

4. The Evaluation of Sires and Mating Systems

Litter averages, adjusted for sex differences, were obtained from the field, random and sequential mating data. Also all traits in the field study and carcass traits in the random and sequential mating studies were adjusted for carcass weight differences. The following models were used for the respective analyses:

Field: $Y_{ijkn} = \mu + t_i + s_j + m_k + e_{ijkn}$

Random: $Y_{ijkln} = \mu + t_i + s_j + m_k + q_l + e_{ijkln}$

Sequential: $Y_{ijklmn} = \mu + t_i + s_j + m_k + q_l + d_m + e_{ijklmn}$

where: μ = the population mean
t_i = the effect of the i^{th} period of time
s_j = the effect of the j^{th} sire
m_k = the effect of the k^{th} mating system
q_l = the effect of the l^{th} litter sequence
d_m = the effect of the m^{th} dam
$e_{i,\ldots,n}$ = the random error associated with the n^{th} litter assumed to be N.I.D. $(0,\sigma_e^2)$

The field and random mating analyses were similar, differing only by the inclusion of the effects of litter sequence in the latter model. Time, which was based on consecutive six month periods, was considered as a random effect in both studies. The remaining effects, except the mean, were regarded as fixed.

The sequential mating analysis differed somewhat. Dam effects were included in the model and considered as random and time, which in this model comprised only spring and fall seasons rather than consecutive six month periods, was treated as a fixed effect.

The double mating data were analyzed on a within litter basis through the following model:

Double: $Y_{ijklm} = \mu + l_i + s_j + m_k + x_l + e_{ijklm}$

where: μ = the population mean

l_i = the effect of the i^{th} litter

s_j = the effect of the j^{th} sire

m_k = the effect of the k^{th} mating system

x_l = the effect of the l^{th} sex

e_{ijklm} = the random error associated with the m^{th} pig assumed to be N.I.D. $(0,\sigma_e^2)$

In the double mating model the effects of litter were regarded as random while sire, mating system and sex effects were considered as fixed. Carcass traits were adjusted for carcass weight differences.

The four mating systems were considered simultaneously in the field and random mating analyses. The sequential and double mating studies were, however, divided into two separate analyses which compared purebreds to single crosses and backcrosses to three-breed crosses.

a. Sire Evaluation

The effects of sire on growth, expressed as the probability of obtaining the observed F-value by chance alone, are illustrated in Table 24 for field, random, sequential and double mating data.

Neither the random nor sequential mating studies detected a significant ($P<.05$) sire effect for weight at birth or 21 days of age. The double mating study observed significant ($P<.05$) sire differences for birth weight among purebred and single cross pigs (analysis 'a') and for 21 day weight among backcross and three-breed cross pigs (analysis 'b').

TABLE 24: THE EFFECT OF SIRE ON GROWTH AS EVALUATED FROM FIELD, RANDOM, SEQUENTIAL AND DOUBLE MATING DATA (EXPRESSED AS THE PROBABILITY OF OBTAINING OBSERVED F-VALUE BY CHANCE ALONE)

Analysis		No. of Litters	Birth Weight	21 Day Weight	56 Day Weight	No. of Litters	154 Day Weight	Age at Market	Daily Gain
Field						622		<.001**	.003**
Random		718	.097	.152	<.001**	680	<.001**	<.001**	<.001**
Sequential	a	184	.304	.387	.102	162	.214	.120	.341
	b	128	.839	.532	.023*	124	.308	.315	.380
Double	a	57	.020*	.469	.011*	40	.098	.145	.087
	b	33	.483	.037*	.353	29	.015*	<.001**	.037*

a Purebred and single cross litters.

b Backcross and three-breed cross litters.

* P<.05

** P<.01

Results for 56 day weight were more consistent as significant sire effects were observed in the random mating analysis ($P<.01$), sequential mating analysis 'b' ($P<.05$) and double mating analysis 'a' ($P<.05$).

Significant sire effects on post-weaning growth were observed in the field, random and double mating studies but were not detected in either of the two sequential mating analyses. The field data analysis revealed significant ($P<.01$) sire differences for both traits studied - age at market and daily gain. Significant sire effects were observed in both the random mating study ($P<.01$) and double mating analysis 'b' ($P<.05$) for 154 day weight, age at market and daily gain. Although probabilities obtained in double mating analysis 'a' were low, none was significant.

The effects of sire on carcass traits, as evaluated from field, random, sequential and double mating data, are illustrated in Table 25. Effects are expressed as the probability of obtaining the observed F-value by chance alone.

Significant ($P<.01$) sire differences were observed with the field data for shoulder backfat only. However, sire effects were significant ($P<.01$) for all carcass traits considered in the random mating study. In the sequential mating analyses, significant ($P<.05$) sire effects were observed only for length 'a', shoulder backfat 'b', loin backfat 'a' and trimmed ham weight 'b'. Significant sire differences for length 'a' and 'b' ($P<.01$), shoulder backfat 'b' ($P<.05$), loin backfat 'a' ($P<.05$) and 'b' ($P<.01$), area of eye of lean 'b' ($P<.05$), trimmed loin weight 'a' ($P<.05$) and lean cut yield 'a' ($P<.01$) were observed in the double mating analyses.

An attempt was made to rank sires on the basis of relative merit for both growth and carcass traits. Eight sires were common to the three experimental studies based on random, sequential and double matings. The

TABLE 25: THE EFFECT OF SIRE ON CARCASS TRAITS AS EVALUATED FROM FIELD, RANDOM, SEQUENTIAL AND DOUBLE MATING DATA
(EXPRESSED AS THE PROBABILITY OF OBTAINING OBSERVED F-VALUE BY CHANCE ALONE)

Analysis		No. of Litters	Length	Shoulder Backfat	Loin Backfat	Area of Eye of Lean	Trimmed Ham	Trimmed Shoulder	Trimmed Loin	Lean Cut Yield
Field		622		<.001**	.166				.790	
Random		692	<.001**	<.001**	<.001**	<.001**	<.001**	<.001**	<.001**	<.001**
Sequential	a	166	.017*	.081	.021*	.144	.062	.669	.190	.203
	b	116	.597	.036*	.151	.174	.020*	.174	.303	.225
Double	a	33	<.001**	.064	.031*	.134	.057	.350	.035*	.005**
	b	25	<.001**	.040*	.004**	.033*	.337	.827	.216	.346

a Purebred and single cross litters.

b Backcross and three-breed cross litters.

* $P<.05$

** $P<.01$

rankings of these sires for growth and carcass merit are illustrated in Tables 26 and 27. The mean plus the least squares estimate of the deviation from the mean is given also.

The three analyses showed some agreement relative to sire rank for the individual growth traits studied. Sire ranking was reasonably consistent between all three studies for age at market. The random and double mating studies showed close agreement for 154 day weight as did the random and sequential mating studies for daily gain. Little consistency was observed between the three studies for 56 day weight.

An overall rank for growth was assigned based on the average rank for all four growth traits. General agreement was observed between the three studies for overall growth. Sire 93 was ranked first by all three analyses. Sire 38 was ranked eighth by the random and double mating studies and seventh by the sequential mating analysis. The rankings of the remaining six sires were consistent except for sires 41 and 80 which were ranked differently by the double mating study.

There was considerably more variation between the random, sequential and double mating analyses in the ranking of sires for carcass traits. Relatively close agreement was, however, observed for the two backfat measurements.

As with the growth traits, an overall rank for carcass merit was assigned based on the average of the eight carcass traits. Sire 93 was ranked last by all three studies. Sire 38 was ranked first by both the random and sequential mating analyses but was ranked fourth by the double mating study which ranked sire 26 first. The sequential and double mating studies showed close agreement for the overall ranking of the remaining sires but the random mating ranks differed.

TABLE 26: THE RANKING OF 8 SIRES FOR GROWTH AS EVALUATED FROM RANDOM, SEQUENTIAL AND DOUBLE MATING DATA

(EXPRESSED AS THE MEAN PLUS LEAST SQUARES ESTIMATE OF DEVIATION FROM THE MEAN)

			Sire No.							
Trait	Analysis	No. of Litters	26	29	38	41	53	73	80	93
56 Day Weight (lbs.)	Random	173	1 (34.91)	4 (31.87)	5 (31.20)	8 (28.20)	7 (28.66)	2 (33.20)	6 (29.22)	3 (32.69)
	Sequential	56	6 (30.54)	4 (34.99)	3 (35.04)	5 (30.81)	8 (15.32)	1 (40.87)	7 (26.60)	2 (36.58)
	Double	54	6 (24.26)	2 (39.84)	8 (17.82)	4 (38.64)	3 (38.72)	7 (20.63)	5 (37.66)	1 (38.92)
154 Day Weight (lbs.)	Random	158	7 (165.5)	5 (168.2)	8 (165.0)	4 (171.3)	1 (173.8)	6 (168.1)	3 (172.2)	2 (173.7)
	Sequential	55	1 (154.7)	5 (170.1)	4 (167.6)	6 (171.4)	3 (161.6)	8 (175.7)	2 (158.9)	7 (173.3)
	Double	39	7 (165.0)	5 (169.1)	8 (152.6)	1 (200.6)	4 (180.8)	6 (167.9)	2 (192.5)	3 (182.5)
Age at Market (days)	Random	158	6 (174.8)	4 (167.1)	7 (174.9)	2 (164.3)	5 (170.0)	8 (175.1)	3 (165.0)	1 (160.2)
	Sequential	55	8 (208.5)	3 (158.6)	6 (194.0)	2 (158.2)	5 (190.5)	7 (195.4)	4 (168.6)	1 (150.7)
	Double	39	8 (173.4)	2 (153.2)	7 (168.6)	4 (163.4)	5 (165.5)	6 (167.8)	1 (142.5)	3 (162.7)
Daily Gain (lbs./day)	Random	158	8 (1.086)	4 (1.133)	6 (1.121)	7 (1.115)	1 (1.194)	5 (1.222)	2 (1.187)	3 (1.174)
	Sequential	55	4 (1.160)	5 (1.163)	7 (1.219)	6 (1.186)	1 (1.048)	8 (1.241)	3 (1.128)	2 (1.122)
	Double	39	1 (1.162)	6 (1.232)	8 (1.257)	5 (1.206)	2 (1.166)	3 (1.182)	7 (1.275)	4 (1.199)
Overall Rank	Random	158	7 (21)[a]	4 (24)	8 (33)	5-6 (23)	2-3 (10)	5-6 (19)	2-3 (16)	1 (12)
	Sequential	55	5-6 (4)	3-4 (6)	7 (13)	5-6 (11)	3-4 (4)	8 (9)	2 (6)	1 (2)
	Double	39	6-7 (8)	4-5 (5)	8 (5)	2-3 (11)	2-3 (10)	6-7 (9)	4-5 (5)	1 (6)

[a] Number of litters observed.

TABLE 27: THE RANKING OF 8 SIRES FOR CARCASS TRAITS AS EVALUATED FROM RANDOM, SEQUENTIAL AND DOUBLE MATING DATA (EXPRESSED AS THE MEAN PLUS LEAST SQUARES ESTIMATE OF DEVIATION FROM THE MEAN)

Trait	Analysis	No. of Litters	Sire No.							
			26	29	38	41	53	73	80	93
Length (in.)	Random	162	6 (29.85)	3 (30.48)	1 (30.55)	4 (30.28)	2 (30.49)	5 (30.13)	8 (29.47)	7 (29.80)
	Sequential	50	3 (30.64)	6 (30.18)	1 (31.26)	5 (30.19)	4 (30.26)	2 (30.71)	7 (29.83)	8 (29.75)
	Double	34	2 (30.53)	5 (30.03)	4 (30.20)	6 (29.76)	3 (30.42)	1 (30.59)	8 (29.01)	7 (29.05)
Shoulder Backfat (in.)	Random	162	3 (1.563)	6 (1.590)	1 (1.437)	7 (1.610)	5 (1.588)	2 (1.511)	4 (1.578)	8 (1.706)
	Sequential	50	1 (1.242)	7 (1.500)	2 (1.279)	5 (1.346)	3 (1.291)	4 (1.302)	6 (1.428)	8 (1.830)
	Double	34	4 (1.548)	7 (1.706)	1 (1.434)	6 (1.619)	3 (1.503)	2 (1.460)	5 (1.617)	8 (1.757)
Loin Backfat (in.)	Random	162	5 (1.238)	4 (1.230)	3 (1.229)	6 (1.287)	7 (1.399)	1 (1.175)	2 (1.202)	8 (1.502)
	Sequential	50	2 (0.979)	6 (1.370)	3 (1.112)	5 (1.304)	4 (1.252)	1 (0.881)	7 (1.438)	8 (1.645)
	Double	34	3 (1.229)	5 (1.280)	2 (1.216)	7 (1.342)	4 (1.257)	1 (1.174)	6 (1.306)	8 (1.521)
Area of Eye of Lean (sq. in.)	Random	162	2 (4.614)	5 (4.153)	3 (4.499)	4 (4.217)	7 (4.112)	6 (4.125)	1 (4.948)	8 (3.577)
	Sequential	50	3 (4.673)	5 (4.308)	2 (4.726)	7 (3.869)	6 (3.972)	1 (5.066)	4 (4.383)	8 (2.988)
	Double	34	3 (4.430)	7 (3.995)	2 (4.487)	6 (4.047)	5 (4.216)	4 (4.229)	1 (4.998)	8 (3.446)
Trimmed Ham (lbs.)	Random	162	5 (15.22)	4 (15.34)	2 (15.75)	3 (15.35)	7 (15.02)	6 (15.14)	1 (16.26)	8 (14.27)
	Sequential	50	7 (14.50)	5 (14.78)	1 (15.51)	6 (14.51)	2 (15.28)	4 (14.82)	3 (15.10)	8 (14.48)
	Double	34	5 (15.78)	3 (16.08)	6 (15.29)	2 (16.56)	1 (16.76)	7 (15.12)	4 (15.99)	8 (14.90)
Trimmed Shoulder (lbs.)	Random	162	3 (12.72)	7 (12.53)	1 (12.83)	5 (12.55)	6 (12.54)	2 (12.77)	4 (12.66)	8 (11.37)
	Sequential	50	6 (12.80)	1 (13.44)	4 (13.13)	5 (13.00)	2 (13.25)	3 (13.16)	8 (12.24)	7 (12.28)
	Double	34	1 (14.01)	5 (12.59)	2 (13.74)	7 (12.30)	6 (12.33)	3 (13.12)	4 (13.01)	8 (12.04)
Trimmed Loin (lbs.)	Random	162	7 (11.37)	6 (11.41)	3 (11.67)	2 (11.72)	5 (11.45)	8 (11.11)	1 (12.10)	4 (11.58)
	Sequential	50	3 (12.14)	7 (11.11)	1 (12.87)	6 (11.40)	4 (11.90)	2 (12.83)	5 (11.47)	8 (9.24)
	Double	34	2 (11.67)	8 (10.78)	6 (11.10)	4 (11.61)	3 (11.66)	5 (11.17)	1 (12.18)	7 (10.83)
Lean Cut Yield (lbs.)	Random	162	4 (78.64)	5 (78.52)	2 (80.50)	3 (79.22)	7 (78.00)	6 (78.04)	1 (82.04)	8 (74.42)
	Sequential	50	5 (78.87)	6 (78.66)	1 (82.99)	4 (79.02)	3 (80.86)	2 (81.99)	7 (77.57)	8 (71.99)
	Double	34	1 (82.48)	7 (78.90)	6 (80.26)	5 (80.94)	2 (81.48)	4 (81.03)	3 (81.22)	8 (74.11)
Overall Rank	Random	162	4 (22)[a]	6 (26)	1 (33)	3 (19)	7 (12)	5 (19)	2 (17)	8 (14)
	Sequential	50	4 (4)	5-6 (6)	1 (11)	5-6 (9)	3 (4)	2 (8)	7 (6)	8 (2)
	Double	34	1 (7)	7 (4)	4 (4)	6 (10)	2-3 (7)	2-3 (10)	5 (4)	8 (5)

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[a] Number of litters observed.

b. Mating System Evaluation

The effects of mating system on growth, as evaluated from field, random, sequential and double mating data, are illustrated in Table 28. Mating system effects are expressed as the mean plus the least squares estimate of the deviation from the mean.

No significant mating system differences were observed for the early growth traits of birth, 21 day and 56 day weight. Significant ($P<.01$) differences for the late growth traits were observed in the field study for age at market and daily gain and in the random mating analysis for 154 day weight, age at market and daily gain. The sequential mating study also observed significant ($P<.01$) differences between purebred and single cross litters for all three late growth traits. Similar effects were observed in the double mating study where single cross pigs were superior ($P<.05$) to purebreds for weight at 154 days and age at market although differences for daily gain were not significant. In both the sequential and double mating analyses, no significant differences between backcrosses and three-breed crosses were observed for any growth trait.

The effects of mating system on growth, expressed as the probability of obtaining the observed F-value by chance alone, are illustrated in Table 29.

Intermediate probabilities were observed for the early growth traits in the random, sequential and double mating analyses. The pattern was altered for the late growth traits where extremely low probabilities were found in the field and random mating studies. Low probabilities were observed also for the comparisons between purebreds and single crosses in both the sequential and double mating studies while probabilities were intermediate or high for the backcross and three-breed cross comparisons.

TABLE 28: THE EFFECT OF MATING SYSTEM ON GROWTH AS EVALUATED FROM FIELD, RANDOM, SEQUENTIAL AND DOUBLE MATING DATA (EXPRESSED AS THE MEAN PLUS LEAST SQUARES ESTIMATE OF DEVIATION FROM MEAN)

			Mating System			
Trait	Analysis	Litters	Purebred	Single Cross	Backcross	3-breed Cross
Birth Weight (lbs.)	Random	718	(2.84	2.89	2.93	2.91)
	Sequential	312	(2.82	2.80)[a]	(2.95	2.92)[b]
	Double	80	(2.87	2.80)	(2.96	3.01)
21 Day Weight (lbs.)	Random	718	(12.16	11.74	12.30	12.12)
	Sequential	312	(12.00	12.40)	(13.29	12.16)
	Double	80	(11.62	11.32)	(11.42	11.39)
56 Day Weight (lbs.)	Random	718	(31.35	31.48	32.36	32.13)
	Sequential	312	(29.20	31.81)	(33.48	30.49)
	Double	80	(34.49	34.66)	(35.00	34.65)
154 Day Weight (lbs.)	Random	680	(158.18	167.58	167.10	170.46)**
	Sequential	286	(154.10	167.56)**	(163.58	169.64)
	Double	69	(170.22	185.02)*	(179.45	179.35)
Age at Market (days)	Field	622	(200.18	190.55	195.25	194.33)**
	Random	680	(178.75	172.30	173.12	169.63)**
	Sequential	286	(181.53	170.95)**	(172.55	171.08)
	Double	69	(170.49	159.66)*	(164.12	165.41)
Daily Gain (lbs./day)	Field[c]	622	(0.791	0.832	0.814	0.816)**
	Random	680	(1.084	1.133	1.127	1.144)**
	Sequential	286	(1.072	1.139)**	(1.121	1.140)
	Double	69	(1.151	1.214)	(1.182	1.188)

[a] Purebred vs. single cross.

[b] Backcross vs. three-breed cross.

[c] Daily gain is expressed as pounds carcass weight per day of age in the Newfoundland field data.

* Significant at the 5% level of probability.

** Significant at the 1% level of probability.

TABLE 29: THE EFFECT OF MATING SYSTEM ON GROWTH AS EVALUATED FROM FIELD, RANDOM, SEQUENTIAL AND DOUBLE MATING DATA
(EXPRESSED AS THE PROBABILITY OF OBTAINING OBSERVED F-VALUE BY CHANCE ALONE)

Analysis		No. of Litters	Birth Weight	21 Day Weight	56 Day Weight	No. of Litters	154 Day Weight	Age at Market	Daily Gain
Field		622				622		.003**	.002**
Random		718	.374	.133	.388	680	<.001**	<.001**	<.001**
Sequential	a	184	.771	.345	.060	162	<.001**	<.001**	<.001**
	b	128	.853	.380	.358	124	.429	.787	.684
Double	a	47	.503	.663	.916	40	.013*	.031*	.075
	b	33	.611	.950	.807	29	.979	.681	.840

a Purebred vs. single cross.

b Backcross vs. three-breed cross.

* P<.05

** P<.01

The effects of mating system on carcass traits, expressed as the mean plus the least squares estimate of the deviation from the mean and as the probability of obtaining the observed F-value by chance alone, are illustrated in Tables 30 and 31 respectively.

No consistent effects of mating system on carcass traits were observed. The field study failed to detect significant mating system differences for any of the three carcass traits considered. Mating system had a significant ($P<.05$) effect on area of eye of lean and trimmed ham weight in the random mating analysis. The sequential mating analysis found purebred litters superior ($P<.05$) to single cross litters for area of eye of lean, trimmed ham weight and lean cut yield. No differences between backcross and three-breed cross litters were observed for any of the carcass traits. In the double mating analyses, the only significant ($P<.05$) mating system effect observed was a backcross advantage over three-breed cross pigs for trimmed loin weight.

Examination of the probabilities illustrated in Table 31 failed to indicate any clear or consistent mating system effect on any carcass trait.

TABLE 30: THE EFFECT OF MATING SYSTEM ON CARCASS TRAITS AS EVALUATED FROM FIELD, RANDOM, SEQUENTIAL AND DOUBLE MATING DATA (EXPRESSED AS THE MEAN PLUS LEAST SQUARES ESTIMATE OF DEVIATION FROM MEAN)

Trait	Analysis	No. of Litters	Mating System Purebred	Single Cross	Backcross	3-breed Cross
Length (in.)	Random	692	(30.52	30.56	30.46	30.43)
	Sequential	282	(30.60	30.60)[a]	(30.48	30.61)[b]
	Double	58	(30.31	30.37)	(30.30	30.12)
Shoulder Backfat (in.)	Field	622	(1.556	1.569	1.562	1.567)
	Random	692	(1.537	1.525	1.522	1.537)
	Sequential	282	(1.526	1.531)	(1.539	1.508)
	Double	58	(1.604	1.526)	(1.563	1.525)
Loin Backfat (in.)	Field	622	(1.329	1.327	1.318	1.334)
	Random	692	(1.259	1.283	1.270	1.291)
	Sequential	282	(1.272	1.289)	(1.321	1.255)
	Double	58	(1.309	1.317)	(1.234	1.210)
Area of Eye of Lean (sq. in.)	Random	692	(4.150	4.108	4.163	4.029)*
	Sequential	282	(4.157	3.983)*	(4.011	4.137)
	Double	58	(4.263	4.270)	(4.221	4.184)
Trimmed Ham (lbs.)	Random	692	(15.58	15.43	15.62	15.58)*
	Sequential	282	(15.71	15.38)*	(15.63	15.55)
	Double	58	(15.29	15.65)	(15.79	15.83)
Trimmed Shoulder (lbs.)	Random	692	(12.84	12.75	12.83	12.71)
	Sequential	282	(12.94	12.67)	(12.91	12.69)
	Double	58	(12.40	13.00)	(12.87	12.73)
Trimmed Loin (lbs.)	Field	622	(15.16	15.31	15.22	15.23)
	Random	692	(11.49	11.54	11.57	11.33)
	Sequential	282	(11.59	11.49)	(11.24	11.66)
	Double	58	(11.56	11.50)	(11.80	11.26)*
Lean Cut Yield (lbs.)	Random	692	(79.82	79.43	80.03	79.24)
	Sequential	282	(80.51	79.09)*	(79.21	80.09)
	Double	58	(78.51	80.29)	(80.90	79.60)

[a] Purebred vs. single cross.

[b] Backcross vs. three-breed cross.

* Significant at the 5% level of probability.

TABLE 31: THE EFFECT OF MATING SYSTEM ON CARCASS TRAITS AS EVALUATED FROM FIELD, RANDOM, SEQUENTIAL AND DOUBLE MATING DATA
(EXPRESSED AS THE PROBABILITY OF OBTAINING OBSERVED F-VALUE BY CHANCE ALONE)

Analysis		No. of Litters	Length	Shoulder Backfat	Loin Backfat	Area of Eye of Lean	Trimmed Ham	Trimmed Shoulder	Trimmed Loin	Lean Cut Yield
Field		622		.825	.811				.818	
Random		692	.188	.710	.353	.049*	.027*	.523	.058	.084
Sequential	a	166	.937	.880	.520	.011*	.013*	.151	.343	.015*
	b	116	.644	.660	.327	.545	.792	.609	.693	.824
Double	a	33	.812	.245	.909	.962	.227	.058	.836	.143
	b	25	.264	.518	.632	.752	.888	.618	.024*	.201

a Purebred vs. single cross.

b Backcross vs. three-breed cross.

* $P < .05$

VII. DISCUSSION

1. Blood Group Factors

The use of blood group factors as genetic markers for sire identification provided an opportunity to consider both the practical value of blood group markers to a double mating program as well as possible relationships between blood group factors and economic traits in swine.

a. Blood Group Factors and Double Mating

The feasibility of using blood group markers for sire identification in double mated litters has been demonstrated by Widdowson and Newton (1964), Buschmann (1964) and Saison and Moxley (1966). The importance of the relative frequency of factors selected as markers, however, has received little past consideration. The range of choice, in the pairing of boars for use in a double mating, is severely restricted when factors with relatively high or low frequencies are used as markers. It is desirable, therefore, to use factors of intermediate frequency.

In this study, one-half of 32 factors considered were categorized as rare or common; that is, had respective frequencies of less than 0.100 or greater than 0.900. It must be noted also that the population was not inbred as replacement boars were usually obtained from diverse sources outside the herd.

Unfortunately, two of the factors used for sire identification in this study, L_g and N_b, were considered as common and this resulted in considerable difficulty in obtaining suitable boar pairs for double matings. However, when this project was initiated in 1964, few reagents were available which restricted the selection of blood group factors for use in the program. Nonetheless, the limited occurrence of factors with intermediate frequencies may hinder the practical use of blood group markers in double mating programs.

This problem aside, with the aid of an efficient blood typing laboratory, blood group markers proved to be a convenient and accurate method for sire identification when boars of like breed or color were paired to produce mixed litters.

b. Blood Group Factors and Economic Traits

The second aspect of the blood group study investigated the possible relationship of blood group factors to economic traits in swine. The results of this study would indicate that some general association between blood group factors and economic traits does exist.

Examination of the effects of up to 27 blood group factors on 14 productive and reproductive traits showed that 9.2% of the F-values were significant at the 5% level of probability. This is almost twice the number that would be expected by chance.

These findings are similar to those noted in two other reports - a German study by Baltzer (1964) and an Iowa report by Jensen _et al._ (1968). Baltzer (1964) considered the relationship of 17 factors to ten growth and carcass traits and observed significance ($P<.05$) in 9.3% of the cases. Jensen _et al._ (1968) investigated the effects of 12 blood and four serum systems on ten productive and reproductive traits and found that 12.7% of the F-values were significant ($P<.05$).

However, when productive and reproductive traits are considered separately, inconsistencies become apparent. Although the frequency of significant F-values for productive traits was similar for this study and the Iowa report, that is 11.0% and 11.3% respectively, marked dissimilarities were observed with reproductive traits. In the Iowa study, 14.0% of the reproductive trait F-values, or almost three times the number expected, were significant ($P<.05$). In contrast, only 5.0% of the reproductive F-values obtained in this study, that is no more than would be expected by chance, were significant ($P<.05$).

Also when specific effects are considered, few consistencies can be found between this report and either of the two previous studies. Baltzer (1964) observed that the most consistent effects were associated with the M_a factor. This study failed to associate the M_a factor with any trait considered. It should be noted, however, that the number of pigs typed for the M_a factor in this study was relatively small.

Specific comparisons with the Iowa report are more difficult as it considered the effects of phenotype rather than individual factors. In any event, the findings of this study and those of the Iowa workers show little accord.

Although Jensen et al. (1968) noted a consistent effect of the H system on reproductive performance, this study failed to find any significant effect of the H_a factor on any reproductive trait considered. This study did observe a frequent association of the K system with reproductive performance but the Iowa study failed to detect any significant effect of the K system on reproduction.

One area of agreement was found between the two studies. Both observed a significant effect of the C system on productive trait averages.

One last item worthy of note is that five of 12 F-tests conducted to consider the effects of the N system on carcass merit were significant. Unfortunately, the Iowa study did not include data on the N system and thus a comparison is impossible.

2. Some Effects of Double Mating

a. Litter Size

In this study, double mated litters significantly ($P<.05$) averaged one pig more per litter than did single mated litters. This is in agreement with the findings of Roberts and Carroll (1939) and several U.S.S.R. workers (Sokolovskaja *et al.*, 1964; Hlebov, 1965; Sokolovskaja *et al.*, 1966). The Yugoslav workers, Cerne and Salehar (1964), however, observed smaller litter sizes with double matings.

Overall, most of the evidence indicates that double mating, or mixed insemination, has a beneficial effect on litter size.

b. Sex Ratio

Although the effects of double mating on sex ratio were not significant, double mated litters tended to have more male pigs than female. This difference was probably due to some phenomenon associated with preferential fertilization.

When preferential fertilization occurred, that is when one boar dominated another in a double mating, the sex ratio of the dominated boar was drastically altered while the sex ratio of the dominant boar remained normal. This study found the sex ratio of dominant boars to be 51.4% males which compares closely to the average sex ratio of 51.2% reported by Belanger (1964). However, dominated boars had a significantly ($P<.05$) higher sex ratio of 63.7% male pigs. This may reflect some disadvantage of female bearing sperm from dominated boars.

3. Comparison of Evaluation Techniques

The primary purpose of this investigation was to compare several sire and mating system evaluation techniques which differ in their respective abilities to control variation due to dam and litter differences. The comparative merits of the techniques - field, random, sequential and double mating - depend on the relative importance of dam and litter effects as sources of 'uncontrollable' variation.

An impartial assessment of each technique requires that the statistical model used for sire or mating system evaluation be suitable within the biological framework of the technique. The linear models used for evaluation in this study generally were adequate. However, the model used in the analysis of the field data failed to include the effects of farm origin which is a probable source of variation. Also in the sequential mating analysis, computational difficulties restricted the separation of time effects into spring and fall seasons only in contrast to the consecutive six month intervals used in the field and random mating models.

Although interactions were considered absent in all models, there was considerable _a priori_ justification for this assumption. Roache (1964), using data from the same herd as was used in this study, reported that sire by mating system interaction was unimportant for growth and carcass traits.

One consideration, intrinsic to the design of the three techniques, is that a simultaneous comparison of all four mating systems is possible only with the random mating technique. Mating system evaluation, with the sequential and double mating techniques, is restricted to separate comparisons of purebreds to single crosses and backcrosses to three-breed crosses. A comparison, for example, between purebreds and three-breed crosses is not possible with the latter two techniques. The random mating technique, therefore, possesses a degree of flexibility that is not shared by either sequential or double mating.

a. Variance Components

The intent of the variance component analysis was to investigate the relative importance of dam and litter effects as sources of variation in the expression of growth and carcass traits. The analysis also produced estimates of sire variance components which, in conjunction with the dam components, were used to provide heritability estimates.

The variance component analysis for the field data was generally characterized by high error components particularly for the two measures of backfat depth. This was probably due, in part, to variation attributable to the effects of farm origin. In the random mating analysis, where the effects of farm origin were not a factor, error components generally were lower.

Variation due to litter effects appears to be more important to the expression of growth traits than carcass traits as demonstrated in the random mating analysis where relatively high litter components were obtained for all growth traits considered. Also litter components were relatively consistent for all growth traits which suggests that, as a source of variation, litter effects are of uniform importance to the expression of growth through all ages.

Dam components for growth, however, were higher for the early growth traits than for the late growth traits which suggests that dam effects contribute substantially to variation in the expression of growth in the early stages but diminish in importance with age. In contrast, sire components tended to be uniform throughout all growth periods. Also they were substantially lower than the dam components with the differences being attributable to maternal effects. Maternal effects were not a factor in the expression of carcass merit as sire and dam components were approximately equal for most carcass traits.

Unlike the variance component analysis of the random mating data, the sequential mating model did not include the effects of sire and breed of sire. The effects were confounded with the litter effects. As a result, for most traits, higher litter components were observed in the sequential mating analysis than in the random mating analysis. Dam components for growth traits, in the sequential mating analysis, were similar to those observed in the random mating analysis. However, slightly higher dam components for carcass traits were found in the sequential mating study.

In the double mating variance component analysis, dam effects were not included in the model but were confounded with litter effects. Litter components, therefore, generally were higher than those observed in the random mating analysis. Of course, no dam components of variance were available for comparison with either the random or sequential mating studies.

b. Heritability Estimates

Heritability estimates, from field, random and double mating data, were derived using the variance component estimates obtained from the respective analyses. The field and random mating heritability estimates of growth traits were based on sire components of variance only, as maternal effects were regarded as important to the expression of growth at all ages. Heritability estimates of carcass traits, for which no evidence of maternal effects was observed, were based on both sire and dam components. All double mating heritability estimates were based on sire components only, as dam components were not available from the variance component analysis.

Double mating heritabilities may be slightly biased as the effects of breed of sire were confounded with the sire variance component. However, in the random mating analysis, only one trait, length, had an appreciable breed of sire component which suggests that the bias probably is very minor for all traits other than length. No heritability estimates were obtained from the sequential mating data as sire variance components were not available.

The heritability estimates from the random and double mating analyses were generally consistent with reported values (Craft, 1953; Fredeen, 1953; Craft, 1958; Hazel, 1963). Estimates obtained from the field data, however, were much lower than those obtained from experimental data where more control over environmental variation is exercised.

The random mating heritability estimates were within generally accepted ranges. The high variability observed among double mating carcass trait heritability estimates was probably due to sampling errors as only 80 litters were used to provide the variance component estimates. However, the bias due to the effects of breed of sire is the most likely reason for the extremely high estimate obtained for length in the double mating analysis.

c. Sire Evaluation

The results of the random mating analysis lend support to the contention that sire effects are most important for those traits expressed later in life, that is post-weaning growth and carcass merit, and are of lesser importance for those traits that are expressed early in life.

In the random mating study, significant sire effects were observed on 56 day weight, 154 day weight, age at market and daily gain. The detection of sire differences for post-weaning growth and the failure to detect sire differences for pre-weaning growth, that is for birth weight and 21 day weight, is consistent with most other reports.

Baker et al. (1943) also failed to detect sire effects on birth weight and 21 day weight but observed significant sire differences for all subsequent stages of growth. Duckworth et al. (1961) found sire differences for age at market and daily gain but failed to detect sire effects for age at 60 pounds, a trait similar to 56 day weight. Similarly, Roache (1964) observed significant sire effects on 154 day weight and age at market but not on 56 day weight.

The practice of early weaning, that is weaning at 21 days of age, as was done in this study, may have contributed to the success in detecting sire differences at 56 days of age although it must be noted that early weaning was practiced also in the study by Roache (1964).

The random mating study also observed significant sire differences for all carcass traits considered. Again this is consistent with the literature.

Duckworth et al. (1961) reported significant sire differences for length, three measures of backfat depth and belly thickness. Significant sire effects on loin eye area and percent ham, shoulder, loin and belly were noted by Roache (1964). Also Bereskin et al. (1968) found significant differences among boars for length, loin eye area, backfat thickness, percent ham and percent loin.

The field study, however, failed to detect significant sire differences for two of the three carcass traits considered - depth of loin backfat and trimmed loin weight - although significant sire effects on shoulder backfat depth were observed. Also significant sire differences were observed for the two growth traits considered - age at market and daily gain. Approximately the same number of litters were used in the field and random mating studies.

The sequential mating analysis failed to detect sire effects on most growth and carcass traits considered. Less than one-half the number of litters employed in the random mating study were used in the sequential mating analysis. Also these litters were split into two separate analyses, one comprising purebreds and single crosses and another comprising backcrosses and three-breed crosses. Therefore, approximately one-fourth the number of litters employed in the random mating study were used in each of the two sequential mating analyses. Apparently the removal of variation due to dam differences by the sequential mating technique was not sufficient to compensate for the smaller number of litters used in the study.

The double mating analysis, which involved less than one-eighth the number of litters used in the random mating study, was more successful. Significant sire differences were observed for all growth traits in at least one of the two analyses performed. Noteworthy is the fact that the double mating analysis detected sire differences for the pre-weaning growth traits, birth weight and 21 day weight, which the random mating technique failed to do. The double mating technique was not quite as successful in detecting sire effects on carcass merit as significant sire differences were observed only for six of the eight carcass traits.

The success of the double mating technique in detecting sire effects on growth, in particular pre-weaning growth, reflects the ability of the technique to control variation due to dam and litter effects, both pre- and post-natal. The removal of the dam and litter variation, afforded by within litter comparisons, compensated for the very small number of litters used in the analysis.

The lack of universal success in detecting sire effects on carcass merit can be attributed to the fact that dam and litter effects are of lesser importance in the expression of carcass traits as was illustrated in the variance component analysis.

The ranking of boars for specific growth and carcass traits was not highly successful. Discrepancies in rankings on the basis of random, sequential and double mating data were frequent. However, consistent rankings were made for overall growth and carcass performance particularly in the cases of highly superior and inferior boars.

No consideration, in the rankings, was given to the relative importance of each trait, correlations between traits, the degree of variability exhibited by the traits and no adjustments were made for the number of observations on each boar. Perhaps, had these criteria been considered, more successful rankings could have been achieved.

d. Mating System Evaluation

In the random mating analysis it was observed that mating system had no effect on birth weight, 21 day weight or 56 day weight but did have a significant effect on 154 day weight, age at market and daily gain. The failure to detect mating system effects on early growth is at variance with several previous reports.

Fredeen (1957) stated that the effects of heterosis appear greatest for traits expressed early in life and are less important as the individual develops. The effects of mating system on weaning weight were demonstrated by Winters *et al.* (1935) and Lush *et al.* (1939). However, Lush (1939) reported that, although single and three-breed crosses were superior to purebreds, backcrosses were inferior. Also Hazel (1963) estimated an 8-10% crossbred advantage for 56 day weight. The failure, by this study, to detect mating system effects on birth weight, however, is not as surprising as differences are often small and inconsistent (Winters et al., 1935; Lush et al., 1939).

Roache (1964), using a portion of the Yorkshire and Landrace data obtained in this study, reported that mating system was not an important source of variation prior to 154 days of age. Also the Newfoundland field data study, using largely Landrace and Yorkshire data, found significant mating system effects on both age at market and daily gain. It is possible, as Fredeen (1957) suggested, that the effects of heterosis may be specific to the breeds or breed strains used in the crosses.

The sequential mating analysis, in the comparisons between purebreds and single crosses, also observed significant mating system effects on 154 day weight, age at market and daily gain. Similar results were observed in the double mating study except that a significant effect on daily gain was not detected. In neither study were significant differences observed between backcrosses and three-breed crosses for any growth trait considered.

If variation due to dam and litter differences were masking the effects of mating system on early growth traits, significant results should probably have been observed in either the sequential or double mating analyses. The failure to detect significant effects suggests that, at least for these data, mating system is not important for early growth but the effects of heterosis on growth become important later in life.

Also examination of the least squares estimates in the field and random mating data and the results of the sequential and double mating studies indicate a simple superiority of crossbreds over purebreds for growth to market weight. Additional heterotic effects were not observed with either the backcrosses or three-breed crosses.

Significant effects of mating system on carcass merit were few and inconsistent. Mating system effects were significant on area of eye of lean and trimmed ham weight in the random and sequential mating studies, lean cut yield in the sequential mating study and trimmed loin weight in the double mating study.

Carcass traits tend to exhibit little heterosis and crossbreds are usually intermediate to parental breed averages (Fredeen, 1957; Hazel, 1963). In other reports, Roache (1964) failed to detect mating system effects on any carcass traits considered but Bereskin et al. (1968) indicated some possible heterotic effects on backfat thickness and percent ham. The results of this study indicate that mating system has little effect on carcass merit.

e. Comparison of Techniques

As each of the sire and mating system evaluation techniques - field, random, sequential and double mating - included different numbers of litters, it is difficult to conclude definitively which technique is most efficient. The criterion of the number of litters required to detect given differences between sires or mating systems, however, is a good measure of the relative efficiency of an evaluation technique.

Tukey's method, as presented by Steel and Torrie (1960), provides a procedure for estimating the number of observations required to detect specified differences between two or more treatments. Through Tukey's method, estimates of the number of litters required to detect given differences, for growth and carcass traits, between sires or mating systems can be obtained for each technique. Tukey's formula is expressed as follows:

$$r = s^2 q^2_{\alpha}(t, df_2)\, F_{\gamma}(df_2, df_1) \;/\; d^2$$

where: r = the number of observations required on each sire or mating system

s^2 = an estimate of the error variance for the technique as obtained from the sire and mating system analysis

df_1 = degrees of freedom associated with s^2

df_2 = degrees of freedom associated with estimate of r

t = the number of sires or mating systems to be compared

d = the desired half length confidence interval for the trait in question (given difference)

q = Tukey's studentized range statistic associated with significance level α

F = F-value associated with assurance γ of detecting given difference

The number of litters required to detect differences between two sires for growth and carcass traits, as estimated from field, random, sequential and double mating data, are presented in Tables 32 and 33 respectively. The estimates for the field, sequential and double mating techniques are expressed also as a percentage of the number of litters required by the random mating technique.

The given difference for each trait was selected more or less arbitrarily but consideration was given to both the relative importance of the trait and to the amount of variation exhibited in its expression. The estimates were based on a 90% assurance of detecting the given difference at the 5% level of significance.

As the double mating technique provides within litter comparisons, the number of observations required to detect differences were calculated

TABLE 32: THE NUMBER OF LITTERS REQUIRED TO DETECT SIRE DIFFERENCES FOR GROWTH AS ESTIMATED FROM FIELD, RANDOM, SEQUENTIAL AND DOUBLE MATING DATA[a]

	Trait					
Analysis	Birth Weight (lbs.)	21 Day Weight (lbs.)	56 Day Weight (lbs.)	154 Day Weight (lbs.)	Age at Market (days)	Daily Gain (lbs./day)
Difference	.25	1.0	3.0	4.0	4.0	.025
Field					282 (186)[b]	134 (78)
Random	74 (100)	86 (100)	78 (100)	242 (100)	152 (100)	172 (100)
Sequential	52 (70)	107 (124)	97 (124)	318 (131)	165 (109)	246 (143)
Double[c]	11 (15)	20 (23)	16 (21)	79 (33)	53 (35)	69 (40)

[a] 90% assurance of detecting the given difference at the 5% significance level.

[b] The number of litters expressed as a percentage of the random mating litters.

[c] Double mating estimates of litters required are based on six and four pigs per litter for the early and late growth traits respectively.

TABLE 33: THE NUMBER OF LITTERS REQUIRED TO DETECT SIRE DIFFERENCES FOR CARCASS TRAITS AS ESTIMATED FROM FIELD, RANDOM, SEQUENTIAL AND DOUBLE MATING DATA[a]

	Trait							
Analysis	Length (in.)	Shoulder Backfat (in.)	Loin Backfat (in.)	Area of Eye of Lean (sq.in.)	Trimmed Ham (lbs.)	Trimmed Shoulder (lbs.)	Trimmed Loin (lbs.)	Lean Cut Yield (lbs.)
Difference	.25	.075	.075	.10	.25	.25	.25	.75
Field		42 (62)[b]	60 (94)				224 (220)	
Random	80 (100)	68 (100)	64 (100)	172 (100)	148 (100)	100 (100)	102 (100)	172 (100)
Sequential	78 (98)	73 (107)	58 (91)	222 (129)	109 (74)	207 (207)	110 (108)	227 (132)
Double[c]	29 (36)	32 (47)	28 (44)	72 (42)	47 (32)	63 (63)	51 (50)	96 (56)

[a] 90% assurance of detecting the given difference at the 5% significance level.

[b] The number of litters expressed as a percentage of the random mating litters.

[c] Double mating estimates of litters required are based on four pigs per litter.

in units of pigs rather than litters as was the case with the field, random and sequential mating techniques which use between litter comparisons. Estimates of the number of litters required with the double mating technique were based on six pigs per litter for the early growth traits and four pigs per litter for the late growth and carcass traits being available for comparison purposes. At first consideration these estimates may appear conservative; however, as only two-thirds of the double matings performed are successful in producing mixed litters (Howard, 1968), the estimates provided are probably realistic.

An examination of Tables 32 and 33 indicates that sire evaluation for age at market by field data requires almost twice the number of litters that are required with random mating experimental data. Although the estimates for daily gain suggest that fewer litters are required with field data, the criterion used to measure daily gain in the field study was not the same as that used in the experimental studies. Daily gain was expressed as pounds liveweight per day of age in the experimental data in contrast to pounds carcass weight per day of age which was used in the field study. The latter measurement is subject to considerably less variation, thus the relatively low field estimate for daily gain is not surprising.

While there appears to be little difference between the two techniques for efficiency of sire evaluation for depth of loin backfat, the field data estimate for shoulder backfat depth is less than two-thirds that of the random mating technique. The number of field litters required to detect sire differences for weight of trimmed loin, however, is over twice the random mating number.

The sequential mating litter estimate for weight at birth is approximately two-thirds that of the random mating estimate. However, the sequential mating technique appears to be less efficient than random mating for all post-natal growth traits. Also sequential mating has no apparent advantage for sire evaluation of carcass traits.

Estimates, based on the double mating technique, are much lower than both the random and sequential mating estimates for all traits considered. The double mating estimates for growth, when expressed as a percentage of the random mating estimates, range from a low of 15% for birth weight and increase with age to a high of 40% for daily gain. The carcass trait estimates tend to be higher than the growth trait estimates.

The number of litters required to detect mating system differences for growth and carcass traits, as estimated from field, random, sequential and double mating data, are illustrated in Tables 34 and 35 respectively. Again the estimates for the field, sequential and double mating techniques are expressed also as a percentage of the random mating litters.

The field and random mating techniques compare all four mating systems simultaneously while the sequential and double mating techniques are limited to two separate analyses - one comparing purebreds to single crosses and the other comparing backcrosses to three-breed crosses. The sum of the estimates of the two analyses is used to compare both the sequential and double mating techniques to the random mating technique for relative efficiency in mating system evaluation.

The estimates of the number of litters required with the field data, expressed as a percentage of the random mating estimates, are very similar to those observed for sire evaluation.

Similarly, the sequential mating estimate for weight at birth is substantially lower than the random mating estimate. However, unlike the sire evaluation estimates, the sequential mating estimates are slightly lower than the random mating estimates for the remaining growth traits and all car-

TABLE 34: THE NUMBER OF LITTERS REQUIRED TO DETECT MATING SYSTEM DIFFERENCES FOR GROWTH AS ESTIMATED FROM FIELD, RANDOM, SEQUENTIAL AND DOUBLE MATING DATA[c]

Analysis		Trait					
		Birth Weight (lbs.)	21 Day Weight (lbs.)	56 Day Weight (lbs.)	154 Day Weight (lbs.)	Age at Market (days)	Daily Gain (lbs./day)
Difference		.25	1.0	3.0	4.0	4.0	.025
Field						920 (181)[d]	452 (78)
Random		236 (100)	284 (100)	256 (100)	800 (100)	508 (100)	576 (100)
Sequential	a	56	88	102	280	144	188
	b	48	126	92	356	186	304
	Total	104 (44)	214 (75)	194 (76)	636 (80)	330 (65)	492 (85)
Double[e]	a	10	23	16	78	56	70
	b	12	17	16	80	50	69
	Total	22 (9)	40 (14)	32 (13)	158 (20)	106 (21)	139 (24)

[a] Purebred vs. single cross.

[b] Backcross vs. three-breed cross.

[c] 90% assurance of detecting the given difference at the 5% significance level.

[d] The number of litters expressed as a percentage of the random mating litters.

[e] Double mating estimates of litters required are based on six and four pigs per litter for the early and late growth traits respectively.

TABLE 35: THE NUMBER OF LITTERS REQUIRED TO DETECT MATING SYSTEM DIFFERENCES FOR CARCASS TRAITS AS ESTIMATED FROM FIELD, RANDOM, SEQUENTIAL AND DOUBLE MATING DATA[c]

		Trait							
Analysis		Length (in.)	Shoulder Backfat (in.)	Loin Backfat (in.)	Area of Eye of Lean (sq. in.)	Trimmed Ham (lbs.)	Trimmed Shoulder (lbs.)	Trimmed Loin (lbs.)	Lean Cut Yield (lbs.)
Difference		.25	.075	.075	.10	.25	.25	.25	.75
Field			122 (57)[d]	192 (96)				744 (224)	
Random		260 (100)	214 (100)	200 (100)	572 (100)	496 (100)	324 (100)	332 (100)	576 (100)
Sequential	a	76	90	62	200	124	250	100	252
	b	80	56	54	244	94	164	120	202
	Total	156 (60)	146 (68)	116 (58)	444 (78)	218 (44)	414 (128)	220 (66)	454 (79)
Double[e]	a	32	28	29	72	43	53	50	86
	b	26	36	28	71	51	73	52	106
	Total	58 (22)	64 (30)	57 (29)	143 (25)	94 (19)	126 (39)	102 (31)	192 (33)

[a] Purebred vs. single cross.

[b] Backcross vs. three-breed cross.

[c] 90% assurance of detecting the given difference at the 5% significance level.

[d] The number of litters expressed as a percentage of the random mating litters.

[e] Double mating estimates of litters required are based on four pigs per litter.

cass traits except weight of trimmed loin. It is difficult to assess, however, if this slight advantage compensates for the inability of the sequential mating technique to make comparisons between all four mating systems.

Again, the estimates of the number of litters required with double mating are much lower than both the sequential and random mating estimates for all traits considered.

In summary, little difference in efficiency, when measured as the number of litters required to detect sire or mating system differences, exists between the field and random mating techniques although distinct advantages and disadvantages were observed for some traits. It must be noted, however, that the cost of obtaining data from the field is generally less than using experimental data.

The sequential mating technique, which provides within dam comparisons, offers little advantage, if any, over the random mating technique except for detecting differences for birth weight, a trait which is greatly influenced by dam effects.

The double mating technique is very efficient. Comparisons on a within litter basis result in effective control over variation due to both dam and litter effects and substantially reduce the number of litters required to detect sire or mating system differences for all traits considered. The advantage is most distinct for the early growth traits when maternal influences are greatest. However, the control over litter variation also makes double mating a highly efficient evaluation technique for traits expressed later in life.

The double mating technique is efficient also when time, rather than numbers of litters, is used as a measure of efficiency as the technique requires only one breeding season in contrast to the two seasons required by the sequential mating technique. Two difficulties, however, which are inherent with the double mating technique, but not with the random mating technique, are the identification of sires in mixed litters and the inability of the double mating technique to make comparisons between all four mating systems. However, the substantial saving in time and resources by double mating should compensate for these biological difficulties which are intrinsic to double mating.

VIII. SUMMARY AND CONCLUSIONS

The primary purpose of this investigation was to compare several techniques - field, random, sequential (within dam) and double (within litter) mating - for their relative effectiveness in the evaluation of sires and mating systems for growth and carcass merit. The techniques differed in ability to control variation due to dam and litter effects.

Blood group factors were used as genetic markers for paternity identification within double mated litters and, as an auxiliary study, the practical use of blood group markers to a double mating program and the relationship of blood group factors to economic traits were considered. Some biological peculiarities of mixed insemination were investigated also.

The use of blood group markers was determined to be an efficient method of establishing paternity in mixed litters when boars of like breed or color were double mated. However, factors selected as markers should be intermediate in frequency.

A general relationship, as demonstrated by an excess of significant F-values, was established between blood group factors and economic traits. This relationship was limited to growth and carcass traits as no excess of significant F-values was observed for the reproductive traits. Also no relationship was established between any blood group factor and rhinitis score, the sole health trait considered. Regarding specific effects, the K and N systems were frequently associated with reproductive and carcass traits respectively.

Double mating was found to significantly increase litter size by almost one pig per litter. In double mated litters, when preferential fertilization occurred, the sex ratio of dominated boars was significantly altered to produce an excess of male pigs.

Components of variance were estimated to assess the relative importance of dam and litter effects to the expression of growth and carcass traits. Dam components were very high for birth weight but diminished with age. Maternal effects, although evident for all stages of growth, were not noticeable for carcass traits. Litter components were substantial for all growth traits but generally were lower for carcass traits. Heritability estimates were obtained from the variance component analyses.

The effects of sire and mating system on growth and carcass traits were evaluated by the four techniques. Sire effects were most important for traits expressed late in life, that is post-weaning growth and carcass traits. Significant sire effects on all these traits were observed in the random mating analysis. The field study found significant sire effects on both measures of post-weaning growth but failed to detect significant sire differences for two of the three carcass traits considered. The sequential mating technique generally was unsuccessful in detecting sire differences but did find significant sire effects on 56 day weight and several carcass traits. However, the double mating technique, using a small number of litters, found significant sire effects on all growth traits, including the pre-weaning growth traits, and most carcass traits considered.

Similar effects of mating system on growth and carcass traits were observed by all four techniques. Mating system had a significant effect on late growth traits although no effect of mating system was observed on early growth. This is contrary to most published reports but may reflect an effect of heterosis that is specific to the breeds or strains used in the crosses. Also single crosses had a marked advantage over purebreds for growth to market weight but little, if any, additional heterosis was observed with backcrosses or three-breed crosses. No consistent effects of mating system on carcass merit were found.

Estimates of the number of litters required to detect sire and mating system differences for growth and carcass traits were made to compare the relative efficiencies of the four evaluation techniques. Comparisons between the field and random mating experimental studies were inconsistent. The sequential mating technique, which was designed to remove dam effects through within dam comparisons, offered little advantage over the random mating technique for the evaluation of most traits except for birth weight where dam effects are extremely important. The double mating technique, which removes both dam and litter effects through within litter comparisons, had a distinct advantage over both the random and sequential mating techniques for all traits considered. This advantage was particularly evident with the early growth traits which are greatly influenced by dam effects.

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