MONTANA STATE UNIVERSITY

The Evaluation of paternal half-sib heritabilities and genetic, environmental and phenotypic correlation estimates for randomly selected Hereford cattle

by Dale Allen Veseth

A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science in Animal Science
Montana State University
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Abstract:
Growth and carcass data collected over 10 years at the USDA-ARS, Fort Keogh Livestock and Range Research Laboratory in Miles City, Montana from a Hereford herd selected at random were analyzed with the paternal half-sib intraclass correlation procedure. The objective was to compare the genetic parameter estimates from this random selection study with estimates from selection studies in the literature. All males were maintained intact and only males were included in the data set.

Calves were born in the spring and raised under eastern Montana range conditions. Weaning took place in mid-October, and after an adjustment period calves were started on a 168-d feed trial. Bulls were slaughtered between 14 and 17 months of age. Fixed effects included in the mixed model were calf year of birth, age of dam, and calf age as a covariate. Random effects were sire, replication, and residual. Sires were selected at random and all cow culling was done at random. The data were subdivided into three subgroups. The first group included all male progeny that had recorded birth weights. The second group included bulls with complete records for the growth traits. The third group included progeny with complete carcass and growth records. The heritability estimate for birth weight from 736 progeny from 86 sires was .18±.10. The second group included 616 bull progeny from 85 sires and heritability estimates were as follows: weaning weight, .17±.11; daily gain from birth to weaning, .20±.12; final test weight, .42±.14; and daily gain on test, .47±.14. The third group included 401 records from 75 sires and heritability estimates were as follows: carcass weight, .38±.18; ribeye area, .51 ±.19; marbling, .31 ±.17; slaughter weight, .42±.18; ribeye area/unit of carcass weight, .23±.16; and dressing percentage, .25±.17. Genetic, environmental, and phenotypic correlations were also estimated. Genetic correlations were higher in magnitude compared to the literature estimates for comparisons among the growth traits. Genetic correlations comparing lean meat yielding traits to fat composition traits were lower in magnitude with slight positive relationships. Phenotypic and environmental correlations were in good agreement with the literature reviewed, Thus, estimates of genetic parameters from this nonselected herd were in general agreement with estimates in the literature from selected herds.

THE EVALUATION OF PATERNAL HALF-SIB HERITABILITIES AND GENETIC, ENVIRONMENTAL AND PHENOTYPIC CORRELATION ESTIMATES FROM RANDOMLY SELECTED HEREFORD CATTLE

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Dale Allen Veseth

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APPROVAL

of a thesis submitted by

Dale Allen Veseth

This thesis has been read by each member of the graduate committee and has been found to be satisfactory regarding content, English usage, format, citations, bibliographic style, and consistency, and is ready for submission to the College of Graduate Studies.

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ABSTRACT

Growth and carcass data collected over 10 years at the USDA-ARS, Fort Keogh Livestock and Range Research Laboratory in Miles City, Montana from a Hereford herd selected at random were analyzed with the paternal half-sib intraclass correlation procedure. The objective was to compare the genetic parameter estimates from this random selection study with estimates from selection studies in the literature. All males were maintained intact and only males were included in the data set.

Calves were born in the spring and raised under eastern Montana range conditions. Weaning took place in mid-October, and after an adjustment period calves were started on a 168-d feed trial. Bulls were slaughtered between 14 and 17 months of age. Fixed effects included in the mixed model were calf year of birth, age of dam, and calf age as a covariate. Random effects were sire, replication, and residual. Sires were selected at random and all cow culling was done at random. The data were subdivided into three subgroups. The first group included all male progeny that had recorded birth weights. The second group included bulls with complete records for the growth traits. The third group included progeny with complete carcass and growth records. The heritability estimate for birth weight from 736 progeny from 86 sires was .18±.10. The second group included 616 bull progeny from 85 sires and heritability estimates were as follows: weaning weight, .17±.11; daily gain from birth to weaning, .20±.12; final test weight, .42±.14; and daily gain on test, .47±.14. The third group included 401 records from 75 sires and heritability estimates were as follows: carcass weight, .38±.18; ribeye area, .51±.19; marbling, .31±.17; slaughter weight, .42±.18; ribeye area/unit of carcass weight, .23±.16; and dressing percentage, .25±.17. Genetic, environmental, and phenotypic correlations were also estimated. Genetic correlations were higher in magnitude compared to the literature estimates for comparisons among the growth traits. Genetic correlations comparing lean meat yielding traits to fat composition traits were lower in magnitude with slight positive relationships. Phenotypic and environmental correlations were in good agreement with the literature reviewed. Thus, estimates of genetic parameters from this nonselected herd were in general agreement with estimates in the literature from selected herds.

INTRODUCTION

Cattle have been selected by ranchers primarily with respect to reproduction and growth potential. However, of greater importance to the industry is the carcass. Determining the relationships which exist between cattle growth and carcass traits should improve beef production efficiency.

A shift in consumer preferences for a leaner quality product has demanded selection for carcass traits. A purposed marketing system will dramatically discount producers unable to produce cattle with quality carcasses. This study will determine the relationship between growth and carcass traits and, as a result, will allow the producer to make inferences about the carcass quality of his cattle from past selection for growth traits.

Several studies have evaluated the relationships between growth traits and carcass traits (Shelby et al., 1963; Cundiff et al., 1964; Cundiff et al., 1971; Dinkel and Busch, 1973). However, all previous studies have incorporated some form of selection bias into their respective experimental designs. Brown and Turner (1968) found additive variances were reduced in selected Pepin Merino ewes chosen for clean fleece weight as compared to unselected control lines, in agreement with quantitative genetic theory (Falconer, 1981).

This experiment was conducted with a herd selected at random. Thus, additive variances would not have been expected to be reduced by selection. Though not significantly different from average heritability estimates summarized by Woldehawariat (1977), Urick et al. (1985) noted that heritability estimates generated from previous analysis of earlier portions of these data tended to be higher than average values found within the literature. The estimates of the underlying population genetic parameters will be unbiased. The objectives of this study were to estimate genetic parameters and to compare these estimates to those from selected populations.

LITERATURE REVIEW

Effect of Selection on Genetic Variance

Eklund and Bradford (1977) found that litter size plateaued in mice after 31 generations of selection. The additive genetic variance of the randomly bred control line was 1.60 (mice/litter)^2 compared to .74 (mice/litter)^2 within the selected line over 15 generations. The heritability estimates for the selected line were .16±.06 for generations 1-15, .05±.04 for generations 16-30, and .00±.003 for generations 31-45. In contrast, the nonselected control line heritability estimates were .32±.10 for the first 15 generations, .22±.10 for generations 16-30, and .24±.11 for generations 31-45 (Eklund and Bradford, 1977). The reduction in heritability estimates for the selected line was significant. The decline in heritability estimates in the control line was attributed to an increase in inbreeding. Both lines were initiated at a zero percent inbreeding coefficient and the average inbreeding coefficient of the nonselected line after 45 generations was 45%.

Brown and Turner (1968) evaluated differences in additive genetic variance in Pepin Merino ewes for clean wool weight. Heritability was estimated on three separate lines comprised of a nonselected control line and two selected lines with different degrees of selection intensity. These researchers reported a decrease

in additive genetic variance in the selected lines for clean wool weight. The nonselected control line had an average additive genetic variance of .31, while the two combined selection lines were calculated at .22.

Thrift et al. (1981) estimated heritabilities from three different nonselected and selected herds incorporating four growth traits into the analysis. There was a general trend for the nonselected line heritability estimates to be larger than the selected line heritabilities. However, the only trait that was significantly different between the nonselected and selected herds was postweaning growth. This difference can be attributed to selection pressure reducing sire variance for this trait in the three selected herds. Each selection group was either selected for postweaning gain directly or included postweaning gain as a component of the selected criteria. The first selection line was selected directly for postweaning gain, the second selected for weight at one year of age, and the final selection line selected for weight gain at one year of age. Weight at one year of age and weight gain to one year of age would be highly correlated to postweaning gain.

Son-Sire Regression

The literature is limited in the number of offspring-sire regression analyses documented. Eight studies have been evaluated relative to offspring-sire regression analysis in this review of the literature.

Wilton and McWhir (1985) evaluated sire performance in central test stations relative to their sons' performance in central test stations and within herd tests.

Son-sire regressions were calculated for four growth traits. These traits and their respective average heritability estimates are shown in Table 1. Two subclasses of the data were analyzed in this study. There were significant differences in heritability estimates between two types of central test stations. The authors noted that government central test stations, when compared to private central test stations, tended to have higher heritability estimates (Wilton and McWhir, 1985). The respective heritability estimates for government and private central test stations are also shown in Table 1. Heritability estimates of three of the growth traits -- postweaning average daily gain, yearling weight, and the index -- were significantly different between government and private central test stations. The initial weight for both types of test had the same approximate heritability estimates. This was expected as the two types of test stations were exposed to the same environmental variables for the initial test weight. The authors noted that higher heritability estimates from the four government tests were caused from more uniform environments and management techniques than the 26 privately run central test stations.

Within the study by Wilton and McWhir (1985), 99 sires and 466 sons were incorporated into the analysis. A weighted regression was utilized because there was more than one progeny per sire in most cases. The range of progeny per sire was from 1 to 30, with an average of 4.7 sons per sire. When the data were subdivided between government and private central test stations, the government test included 267 sons and 62 sires; the private test included 199

sons and 37 sires. No age of dam adjustment factors were included in the sire and son central test performance data.

Table 1. Son-sire regression heritability estimates from different types of tests.*

Trait	Government[a]	Private[b]	Combined
BWT	.33 ± .10	.37 ± .06	.35 ± .06
ADG	.50 ± .12	.02 ± .08	.19 ± .07
YW	.84 ± .12	.12 ± .12	.55 ± .09
INDEX	.50 ± .08	.24 ± .08	.36 ± .06

*Source: Wilton and McWhir (1985)
[a]Government owned and managed central performance test center
[b]Privately owned and managed central performance test center
(Refer to Appendix A for a glossary of variables.)

Carter (1971) documented a regression coefficient significantly different from zero when regressing progeny weaning weight on sire's gain from weaning to yearling weight. This regression coefficient was .09, representing 29 sires producing progeny in the analysis. The study included two selection herds and an associated progeny test herd. Carter (1971) also calculated heritability estimates for four growth traits (birth weight, weaning weight, gain from weaning to yearling weight, and yearling weight). These estimates are reproduced in Table 2.

Andersen et al. (1974) calculated heritability estimates using the son-sire regression. Shorthorn bulls were analyzed for growth and carcass parameters over a period of five years, from 1966 through 1970. These heritability estimates for birth weight and the growth traits through yearling weight were comparable

to the Wilton and McWhir (1985) average estimates, but the standard errors tended to be larger for the Andersen et al. (1974) data. These heritability estimates are presented in Table 2. There were two sets of son-sire heritability estimates represented. The first was unadjusted for age of dam and year of dam birth, while the second was adjusted for dam age and dam birth year.

Table 2. Offspring-sire regression heritability estimates.

Study[a]	BWT	WWT	ADG	FWT
1.	.27 ± .13	.07 ± .18	.13 ± .14	.41 ± .22
2.	.30 ± .13	.34 ± .22	.22 ± .16	.47 ± .23
3.		.20	.04	.46
4.		.28	-.02	.34
5.		.27 ± .13	.93 ± .18	.37 ± .14
6.			.22 ± .18	
7.	.35 ±.08	.25 ± .11		
8.	.42	.00	.46	.69
9.	.34	.30	.97	.94
10.	.50	.01	.34	.53

[a]Studies (refer to Appendix A for a glossary of variables):

1. Andersen et al. (1974): Son-sire regression with unadjusted main effects for age of dam. Yearling weight was the trait measured and depicted under final weight in the table.
2. Andersen et al. (1974): Son-sire regression with adjusted main effects for age of dam. Yearling weight was the trait measured and depicted under final weight in the table.
3. Carter (1971): Son-sire regression heritability estimates from a selection herd.
4. Carter (1971): Son-sire regression heritability estimates from a progeny test herd.
5. Brown and Gacula (1962): Weighted son-sire regression. The weaning weight trait estimate in the table was recorded as initial weight on test from this respective study.
6. Carter and Kincaid (1959a)
7. Koch and Clark (1955)
8. Knapp and Nordskog (1946): Sire-offspring regression with no subclass for sire birth year.
9. Knapp and Nordskog (1946): Sire-offspring regression with subclasses for sire birth year.
10. Henderson (1968)

Andersen et al. (1974) also estimated heritabilities using both paternal half-sib analysis of variance and son-sire regression. These two sets of heritability estimates varied, with the son-sire regression tending to produce the higher heritability estimates. Table 3 compares the findings of Andersen et al. (1974) for both paternal half-sib and son-sire regression. Due to their large standard errors, several of the paternal half-sib estimates are not significantly different from zero. Andersen et al. (1974) theorized that the cause for this was the intensive selection that reduced between-sire variation, while son-sire regression would be less affected by reduced additive variance.

Table 3. Paternal half-sib and son-sire regression heritabilities.

Trait[a]	Paternal Half-Sib		Son-Sire Regression	
	h^2	SE	h^2	SE
BWT	.17	.18	.30	.13
WWT	.47	.20	.34	.22
YWT	.04	.16	.47	.23
WWT/YWT	.19	.18	.38	.21
ADG	.02	.16	.22	.16

[a]Andersen et al. (1974): Both estimates were adjusted for age of dam and year of dam's birth. (Refer to Appendix A for a glossary of variables.)

Brown and Gacula (1962) calculated son-sire regression heritability estimates for eight growth traits in a post-weaning gain test representing 20 sires and 201 progeny. These heritability estimates are reproduced in Table 2. Angus,

Hereford, and Shorthorn breeds were represented in this study and data were collected from 1951 through 1960.

Henderson (1968) analyzed 15 years of growth and carcass data on 339 Hereford steers sired by 78 sires from 1952 through 1966. These cattle were produced at the Northern Montana Branch Experiment Station at Havre, Montana under typical range conditions. Calves were weaned from the beginning- to mid-October. From 1952 through 1959, all the steers were slaughtered on a time constant basis. The slaughter time varied from year to year, but ranged from 196 to 224 d on feed. After that time, steers were slaughtered on a weight constant basis from 1960 through 1966. Under the weight constant slaughter criteria, steers were slaughtered at 1050 pounds or when live visual appraisals estimated a USDA choice quality grade prior to that weight. Ten growth traits and 27 carcass traits were included in the analysis. Simple correlation and regression coefficients were estimated in the son-sire regression. Six identical traits were collected on both the sire and progeny. Heritability estimates were calculated and the results are presented in Table 2.

Koch and Clark (1955) calculated heritability estimates from offspring-sire regression (Table 2). The analysis measured four growth traits: birth weight, weaning weight, weaning gain, and weaning score. The population of sires analyzed in this study had an average inbreeding coefficient of .086. Thus, all regression coefficients were multiplied by 1.92 instead of 2.0 for a random mating population. Eighty-five sires were evaluated within the analysis; subclasses were

assigned according to sire birth date and progeny birth date. The heritability estimates were derived by regressing average progeny performance for a trait on the sire's individual performance for that trait. Koch and Clark (1955) noted that maternal effects were not accounted for within this analysis. This study was the only study reviewed from the literature to estimate genetic correlations by son-sire regression. These offspring-sire regression genetic correlations are presented in Table 4.

Table 4. Offspring-sire regression genetic correlations.[a]

Offspring Traits	Sire Traits		
	BWT	WWT	DGBW
BWT	.18	.11	.08
WWT	.17	.13	.11
DGBW	.12	.11	.09

[a]Koch and Clark (1955)
(Refer to Appendix A for a glossary of variables.)

Knapp and Nordskog (1946) estimated heritabilities with offspring-sire regression. Their data set included 177 steers sired by 20 sires at the U.S. Range Livestock Experiment Station from 1940 to 1944. Sires were randomly mated to 25-30 cows and eight steer progeny were randomly selected from each sire group. These findings are presented in Table 2. The average progeny performance was regressed on the sire's individual performance. The arithmetic average heritability estimates from Tables 1 and 2 are presented in Table 5.

Table 5. Average heritability estimates from Tables 1 and 2.

	Trait			
	BWT	WWT	ADG	FWT
Average Estimate	.36	.19	.35	.52

(Refer to Appendix A for a glossary of variables.)

In summary, there was wide variation among the regression coefficients and regression heritability estimates in the literature. In Table 3, average heritability estimates were calculated from the literature reviewed. Only one estimate of offspring-sire genetic correlation was reported within the literature (by Koch and Clark, 1955). No heritability estimates for carcass traits or estimates for subsequent genetic correlations for carcass traits calculated this way were found.

Paternal Half-Sib Heritabilities and Correlations

The heritability estimates and genetic, environmental, and phenotypic correlation estimates are presented in table form. First, heritability estimates were divided into two tables, one table presenting growth traits and the other presenting carcass traits. The average heritability estimates reviewed in the literature were compared to average estimates summarized by Woldehawariat et al. (1977) and Koch et al. (1982) for growth and carcass traits, respectively. These comparisons are presented in Tables 6 and 7.

Table 6. Heritability estimates for growth traits by paternal half-sib analysis.

Trait	Study[a]									
	1	2	3	4	5	6	7	8	9	10
BWT	.54		.43							
DGBW		.09±.16	.07							
WWT	.24			.40	.58±.21	.08	.31	.08		.48±.25
ITW										
ADG	.48	.36±.09	.57	.55	.60±.22	.32	.32	.38	.88	.92±.25
YWT						.10	.71			.69±.25
FWT	.64			.85	.72±.23	.70				

[a]Studies (refer to Appendix A for a glossary of variables):

1. Shelby et al. (1963)
2. MacNeil et al. (1984)
3. Koch et al. (1982)
4. Dinkel and Busch (1973)
5. Swiger et al. (1965)
6. Blackwell et al. (1962) (steer analysis)
7. Blackwell et al. (1962) (heifer analysis)
8. Carter and Kincaid (1959a) (steer analysis)
9. Christians et al. (1962)
10. Koch (1978)

Table 7. Heritability estimates for carcass traits from paternal half-sib analysis.

Trait	Study[a]											
	1	2	3	4	5	6	7	8	9	10	11	12
SWT												
CWT	.57	.44±.09			.62±.27			.92			.96	.68±.25
CWT/D Age					.39±.24							
DR%	.57			.15				.25			.74	
CUT%				.66		.35±.18						
YG					.36±.24							
BONEWT			.57									.56±.25
BONE%			.53									
KFWT			.77							.72		
KF%			.83									
FTH	.24		.41	.57	.43±.33	.51±.20	.50±.20			.43	.38	.68±.25
FTWT		.50±.09	.47	.39						.50		.94±.25
FT%			.57									
REA	.26		.56	.25	.73±.29	.32±.18				.40	.76	.28±.24
REA/CWT					.29±.22							
CG	.17			.34	.62±.27		.32±.18	.59	.20	.74		
MAR			.40	.31		.30±.17				.73		.34±.25
RPWT		.45±.09	.58	.38			.65±.22					.38±.25
RP%			.63		.40±.24		.24±.17					
W-B			.31									

[a]Studies (refer to Appendix A for a glossary of variables):

1. Shelby et al. (1963)
2. MacNeil et al. (1984)
3. Koch et al. (1982)
4. Dinkel and Busch (1973)
5. Cundiff et al. (1964)
6. Cundiff et al. (1971) (age & weight constant analysis)
7. Swiger et al. (1965)
8. Blackwell et al. (1962)
9. Carter and Kincaid (1959a)
10. Brackelsberg et al. (1971) (slaughtered when visual appraisal evaluation determined choice quality grade)
11. Christians et al. (1962)
12. Koch (1978)

The correlations are tabled under their respective type of correlation. Specific growth traits correlated to the major carcass traits are presented within each of these correlation tables. The growth traits represented are: gain from birth to weaning, weaning weight, average daily gain from weaning weight to yearling weight, and yearling weight.

Shelby et al. (1963) analyzed 616 Hereford steers sired by 87 sires. The data were collected from 1947 through 1956 at the USDA Livestock and Range Research Station at Miles City, Montana. Heritability estimates for growth and carcass traits are presented in Tables 6 and 7, respectively. The genetic correlations between growth and carcass traits are presented in Tables 12, 13, and 14. The phenotypic correlations are presented in Tables 20, 21, and 22.

MacNeil et al. (1984) analyzed data collected in 1970 through 1972. In this study, Hereford and Angus cows were mated to eight different sire breeds. These breeds included Hereford, Angus, Jersey, South Devon, Limousin, Charolais, and Simmental sires. In all, 187 sires were represented in the data set, with an average progeny number of five steers per sire. The heritability estimates calculated on carcass traits from this data set are presented in Table 7.

Dinkel and Busch (1973) analyzed data from 679 head of Hereford steers utilizing the paternal half-sib analysis of variance method. The steers were produced on 18 ranches and sired by 70 sires. At weaning, all the steers were shipped to a centrally located feedlot at Brookings, South Dakota. The experiment began in 1958 and was carried through 1966. The cattle were fed at

one feedlot, but the feeding conditions varied from year to year. After feeding, the cattle were slaughtered on an age constant basis. In the first years of the experiment, slaughter dates were set when an estimated live weight of all the cattle would reach an average of 454 Kg of live weight based on expected gains. In later years, age at slaughter was estimated by historical performance of individual ranch groups (Dinkel and Busch, 1973).

The trait edible portion was calculated by the actual cutout value of retail cuts trimmed to an external fat cover of .95 cm. These data were collected from 1962 to 1964 (Dinkel and Busch, 1973). Prior to 1962, edible portion was estimated with a regression equation formulated by Busch et al. (1968). Another regression derived by Tuma et al. (1967) was used to estimate edible portion of the steers fed in 1965 and 1966.

The regression equation formulated by Busch et al. (1968) accounted for 89% of the variation in edible portion. The regression equation formulated by Tuma et al. (1967) accounted for 94% of the variation in edible portion. The heritability estimates for growth and carcass traits are presented in Tables 6 and 7, respectively; the genetic correlation estimates are reproduced in Tables 12, 13, and 14; and the phenotypic correlation estimates are presented in Tables 20, 21, and 22.

Koch et al. (1982) analyzed 2,453 crossbred steers representing 16 sire breeds and two dam breeds. Angus and Hereford cows were bred to Angus, Hereford, Jersey, South Devon, Simmental, Limousin, Charolais, Red Poll, Brown

Swiss, Gelbvieh, Maine Anjou, Chianina, Sahiwal, Brahman, Pinzgauer, and Tarentaise sires in the germ plasm evaluation program at the Roman L. Hruska U.S. Meat Animal Research Center in Clay Center, Nebraska. The project was subdivided into three phases. The first phase, cycle I, began in 1970 and continued until 1972. The sire groups represented in this phase included: Angus, Hereford, Charolais, Jersey, Limousin, Simmental, and South Devon sires. The second phase, cycle II, was carried out from 1973 through 1974 calf crops. This sire group included: Angus, Hereford, Brown Swiss, Chianina, Gelbvieh, Maine Anjou, and Red Poll sires mated to the Angus and Hereford dams. The third and final phase, cycle III, was implemented to produce the calf crops in 1975 and 1976. This sire group contained six different sire breeds: Angus, Hereford, Brahman, Pinzgauer, and Tarentaise. Calves were conditioned for 25 to 30 days after weaning and then entered the feedlot for the finishing phase. Cattle were randomly selected for slaughter in three or four groups at the end of the finishing phase. This was an effort to standardize age and weight consistency among breed types at slaughter. Carcass data collection followed industry standards for yield and quality grading. Carcass cutout data were obtained from the right side of the carcass for evaluation at Kansas State University. Retail cuts were trimmed to 8mm of external fat. Retail product was defined as the sum of roast and steak meat plus the adjusted lean trim (Koch et al., 1982). Fat trim was defined as the external fat trimmed from carcass plus the kidney with kidney fat and the pelvic fat (Koch et al., 1982). The paternal analysis of variance method

was used to estimate heritabilities and genetic, environmental, and phenotypic correlations. Heritability estimates for growth and carcass traits are presented in Tables 6 and 7 and genetic correlations are presented in Tables 11, 13, and 14; phenotypic correlations are presented in Tables 19, 21, and 22; and environmental correlations are reproduced in Tables 15, 17, and 18.

Tables 8 and 9 are average estimates presented from Tables 6 and 7, respectively. These values are compared to estimates summarized in the literature by Woldehawariat et al. (1977).

Table 8. Average heritability estimates for the growth traits.

Trait	Study[a]		
	1	2	3
BWT	.40	.49 ± .17	.49
DGBW	.28	.34 ± .16	.08
WWT	.32	.32 ± .16	.31
DGOT	.44	.65 ± .19	.54
FWT	.47	.52 ± .18	.73

[a]Studies (refer to Appendix A for a glossary of variables):

1. Woldehawariat et al. (1977): An average heritability estimate reviewed from the literature incorporating unweighted paternal half-sib heritability estimates.
2. Urick et al. (1985): Heritability estimates from 431 bulls produced within the randomly selected herd. These data were collected between the years of 1977 and 1983.
3. The average heritability estimate reviewed within this respective literature review.

Table 9. Average heritability estimates for the carcass traits.

Trait	Study[a]			
	1	2	3	4
Carcass Wt	.55	5	.70	6
Retail Pro Wt	.52	4	.49	5
Retail Pro %	.41	4	.42	3
Fat Trim Wt	.57	4	.56	5
Bone Wt	.47	2	.57	2
Kidney Fat Wt	.72	1	.75	2
Fat Thickness	.48	7	.46	9
REA	.40	7	.45	8
Marbling	.42	7	.42	5

[a]Studies (refer to Appendix A for a glossary of variables):

1. Koch et al. (1982): Summarized heritability estimates for carcass traits from the literature.
2. The number of studies included in the review by Koch et al. (1982).
3. Average heritability estimates reviewed for this thesis analyzed with paternal half-sib analysis of variance.
4. The number of studies included in the review for this thesis.

Growth and carcass data were collected on 265 steers sired by 47 sires (Cundiff et al., 1964). The experiment was carried out from 1961 through 1963 involving two calf crops at the Fort Reno Livestock Station, El Reno, Oklahoma. Carcass weight per day of age was calculated by dividing chilled carcass weight by age at slaughter (Cundiff et al., 1971). Yield and quality grades were evaluated by the U.S. Meat Grading Service. Percentage of retail cuts was the percentage of boneless retail cuts from the round, loin, rib, and chuck derived from the regression equation by Murphy et al. (1960). In this analysis, carcass

weight per day of age was characterized as the measure of relative growth for comparison of carcass traits. The heritability estimates are presented in Tables 6 and 7.

Cundiff et al. (1971) analyzed carcass information on 503 steers sired by 75 sires. This data set originated from a heterosis experiment involving Hereford, Angus, and Shorthorn cattle and included data collected from 1961 through 1965 at the Fort Robinson Beef Cattle Research Station. Carcass weight adjusted for age was the measure of growth. Percent of closely trimmed boneless retail cuts from the round, loin, rib, and chuck was derived from the regression equation formulated by Murphy et al. (1960). Heritability estimates were calculated with the paternal half-sib analysis of variance. Age and weight were both used as covariates in the mixed model. Table 10 is reproduced directly from Cundiff et al. (1971) to demonstrate the difference in heritability estimates utilizing the different types of covariates. However, the heritability estimates calculated with the different models were not significantly different from each other. The genetic correlations between carcass weight and the carcass traits are presented in Table 14. Phenotypic and environmental correlations between carcass weight and carcass traits are reproduced in Tables 22 and 18, respectively.

Table 10. Age and weight constant heritability estimates.[a]

Trait	Age Constant[b]	Weight Constant[c]	Age & Weight Constant[d]
CWT	.56 ± .21		
MAR	.31 ± .17	.33 ± .18	.30 ± .17
FTH	.50 ± .19	.53 ± .20	.51 ± .20
REA	.41 ± .19	.32 ± .17	.32 ± .18
CUT%	.28 ± .17	.35 ± .18	.35 ± .18

[a]From Cundiff et al. (1971)
[b]Age covariate in the mixed linear model
[c]Weight covariate in the mixed linear model
[d]Age and weight as covariates in the mixed linear model (Cundiff et al., 1971)

(Refer to Appendix A for a glossary of variables.)

Table 11. Genetic correlations between gain from birth to weaning and respective carcass traits.

Trait	Study[a] 1	Trait	Study[a] 1
SWT	.73	FT%	.08
CWT		BONEWT	.38
CWT/D Age		BONE%	-.31
DR%		KFWT	.66
CUT%		KF%	.55
RPWT	.62	FTH	.04
RP%	-.03	REA	.49
FTWT	.32	MAR	.31

[a]Study (refer to Appendix A for a glossary of variables):

1. Koch et al. (1982) noted that standard errors for genetic correlations ranged from .24 to .34 for daily gain from birth to weaning.

Table 12. Genetic correlations between weaning weight and carcass traits.

Trait	Study[a]					
	1	2	3	4	5	6
SWT						
CWT	.90			1.10		.48±.25
CG	-.04	-.75	-.43	.92	.84	
DR%	.30			1.56		
CUT%		1.08				
RPWT		1.11	.91			.37±.36
RP%			.09			
FTWT		-1.20	-.29			.40±.26
FT%						
BONEWT						.55±.24
BONE%						
KFWT						
KF%						
FTH	.91					.59±.34
REA	.40					.16±.50
MAR		-.40				-.02±.47

[a]Studies (refer to Appendix A for a glossary of variables):

1. Shelby et al. (1963)
2. Dinkel and Busch (1973)
3. Swiger et al. (1965)
4. Blackwell et al. (1962)
5. Carter and Kincaid (1959b)
6. Koch (1978)

Table 13. Genetic correlations between average daily gain on test and carcass traits.

Trait	Study[a]						
	1	2	3	4	5	6	7
SWT		.89					
CWT	.90				-.02		.78±.11
CG	.25		-.12	.08	-.07	.85	
DR%	.01		-.08		.09		
CUT%			.50				
RPWT		.73	.48	.82			.73±.20
RP%		-.13		-.45			
FTWT		.40	-.81	.49			.64±.14
FT%		.12					
BONEWT		.79					.49±.22
BONE%		.02					
KFWT		.40					
KF%		.16					
FTH	.14	.05	-.25				.62±.21
REA	-.10	.34	.49				-.07±.38
MAR		.15	.15				-.62±.35

[a]Studies (refer to Appendix A for a glossary of variables):

1. Shelby et al. (1963)
2. Koch et al. (1982)
3. Dinkel and Busch (1973): Edible portion is defined as retail product weight in this table.
4. Swiger et al. (1965)
5. Blackwell et al. (1962)
6. Carter and Kincaid (1959b)
7. Koch (1978)

Table 14. Genetic correlations between final weight and carcass traits.

Trait	Study[a]						
	1	2	3	4	5	6	7
SWT							
CWT		.95				.60	.96±.03
CG		.12			-.14	-.23	
DR%		.04	-.23			1.07	
CUT%			.74	.33±.29			
RPWT	.81		.80	.95±.03	.96		.85±.11
RP%	-.11				-.25		
FTWT	.45		-1.02	.78±.13			.78±.11
FT%	.13						
BONEWT	.71			.86±.09			.72±.15
BONE%	-.20						
KFWT	.48						
KF%	.22						
FTH	.08	.29	-.56	.34±.24	.18		.86±.24
REA	.44	.03	.54	.66±.19			.01±.46
MAR	.25		.02	.23±.31			-.57±.41

[a]Studies (refer to Appendix A for a glossary of variables):

1. Koch et al. (1982): Carcass weight rather than final weight was correlated to the respective carcass traits.
2. Shelby et al. (1963)
3. Dinkel and Busch (1973)
4. Cundiff et al. (1971): All traits were correlated to carcass weight rather than final weight.
5. Swiger et al. (1965)
6. Blackwell et al. (1962): Yearling weight rather than final weight was correlated to the respective carcass traits.
7. Koch (1978): Yearling weight rather than final weight was correlated to the respective carcass traits.

Table 15. Environmental correlations between gain from birth to weaning and carcass traits.

Trait	Study[a] 1	Trait	Study[a] 1
SWT	.67	FT%	.46
CWT		BONEWT	.51
CG		BONE%	-.32
DR%		KFWT	.49
CUT%		KF%	.11
RPWT	.55	FTH	.41
RP%	-.47	REA	.24
FTWT	.57	MAR	.07

[a]Study (refer to Appendix A for a glossary of variables):

1. Koch et al. (1982)

Table 16. Environmental correlations between weaning weight and carcass traits.

Traits	Study[a]	
	1	2
SWT		
CWT		.95
CG	.47	-.13
DR%		-.10
CUT%		
RPWT	.27	
RP%	-.37	
FTWT	.74	
FT%		
BONEWT		
BONE%		
KFWT		
KF%		
FTH		
REA		
MAR		

[a]Studies (refer to Appendix A for a glossary of variables):

1. Swiger et al. (1965)
2. Blackwell et al. (1962)

Table 17. Environmental correlations between average daily gain on test and carcass traits.

Trait	Study[a]		
	1	2	3
SWT	.57		
CWT			.31
CG		.27	.04
DR%			.14
CUT%			
RPWT	.57	.50	
RP%	-.17	.01	
FTWT	.35	-.03	
FT%	.21		
BONEWT	.39		
BONE%	-.29		
KFWT	.14		
KF%	-.22		
FTH	.28		
REA	.30		
MAR	.00		

[a]Studies (refer to Appendix A for a glossary of variables):

1. Koch et al. (1982)
2. Swiger et al. (1965)
3. Blackwell et al. (1962)

Table 18. Environmental correlations between final weight and carcass traits.

Trait	Study[a]			
	1	2	3	4
SWT				
CWT				.17
CG			.53	.23
DR%				.04
CUT%		-.55		
RPWT	.89	.85	.62	
RP%	-.55		-.23	
FTWT	.76	.72		
FT%	.56			
BONEWT	.74	.74		
BONE%	-.47			
KFWT	.64			
KF%	.10			
FTH	.56	.43	.45	
REA	.42	.39		
MAR	.04	.14		

[a]Studies (refer to Appendix A for a glossary of variables):

1. Koch et al. (1982): All carcass traits were correlated to cold side weight rather than final weight.
2. Cundiff et al. (1971): All carcass traits were correlated to cold side weight rather than final weight.
3. Swiger et al. (1965)
4. Blackwell et al. (1962): All carcass traits were correlated to yearling weight rather than final weight.

Table 19. Phenotypic correlations between gain from birth to weaning and carcass traits.

Trait	Study[a] 1	Trait	Study[a] 1
SWT	.61	FT%	.31
CWT		BONEWT	.40
CG		BONE%	-.27
DR%		KFWT	.38
CUT%		KF%	.17
RPWT	.47	FTH	.31
RP%	-.29	REA	.25
FTWT	.46	MAR	.10

[a]Study (refer to Appendix A for a glossary of variables):

1. Koch et al. (1982)

Table 20. Phenotypic correlations between weaning weight and carcass traits.

Trait	Study[a]					
	1	2	3	4	5	6
SWT						
CWT	.57	.08		.54		.59
CG	.09	-.17	.06	.11	.23	
DR%	.18	-.09		.14		
CUT%		.12				
RPWT		.08	.66			.59
RP%			-.18			
FTWT		-.11	.18			.35
FT%						
BONEWT						.64
BONE%						
KFWT						
KF%						
FTH	.14	-.13				.12
REA	.24	.04				.23
MAR		-.12				-.05

[a]Studies (refer to Appendix A for a glossary of variables):

1. Shelby et al. (1963)
2. Dinkel and Busch (1973): Edible portion is categorized with retail product weight in the table.
3. Swiger et al. (1965)
4. Blackwell et al. (1962)
5. Carter and Kincaid (1959b)
6. Koch (1978)

Table 21. Phenotypic correlations between average daily gain on test and carcass traits.

Trait	Study[a]						
	1	2	3	4	5	6	7
SWT		.72					
CWT	.81				.31		.74
CG	.37		.08	.17	.04	.31	
DR%	.10		-.18		.14		
CUT%			.09				
RPWT		.66	.11	.70			.62
RP%		-.15		-.16			
FTWT		.37	-.09	.25			.62
FT%		.15					
BONEWT		.61					.44
BONE%		-.12					
KFWT	.31						
KF%		.05					
FTH	.30	.17					.32
REA	.36	.32	.03				.27
MAR		.07	.10				.20

[a]Studies (refer to Appendix A for a glossary of variables):

1. Shelby et al. (1963)
2. Koch et al. (1982)
3. Dinkel and Busch (1973)
4. Swiger et al. (1965)
5. Blackwell et al. (1962)
6. Carter and Kincaid (1959b)
7. Koch (1978)

Table 22. Phenotypic correlations between final weight and carcass traits.

Trait	Study[a]						
	1	2	3	4	5	6	7
SWT							
CWT	.96					.67	.94
CG	.35		-.14		.16	.09	
DR%	.19		-.18			.20	
CUT%			.16	-.44			
RPWT		.84	.15	.91	.85		.84
RP%		-.31			-.21		
FTWT		.62	-.16	.73			.70
FT%		.34					
BONEWT		.72		.78			.73
BONE%		-.34					
KFWT		.51					
KF%		.16					
FTH	.31	.36	-.12	.38	.27		.33
REA	.41	.43	.05	.52			.35
MAR		.13	.01	.17			.13

[a]Studies (refer to Appendix A for a glossary of variables):

1. Shelby et al. (1963)
2. Koch et al. (1982): All carcass traits were correlated to cold side weight rather than final weight.
3. Dinkel and Busch (1973)
4. Cundiff et al. (1971)
5. Swiger et al. (1965)
6. Blackwell et al. (1962): Yearling weight was correlated to the carcass traits rather than final weight.
7. Koch (1978): Yearling weight was correlated to the carcass traits rather than final weight

Swiger et al. (1965) analyzed 480 steer and heifer calves for growth traits from three different sources. The first group was produced in a heterosis experiment containing all crossbred steers of one- and two-way cross combinations of Hereford, Angus, and Shorthorn. The second group of cattle was Hereford heifers from three selection lines. The selection criteria had recently been implemented. Consequently, the heifers were treated as one group. The third group was comprised of Angus steers. An Angus herd produced all the male Angus progeny for slaughter. The only exceptions to this group were a few herd sire prospects retained for breeding purposes. This study also collected feed efficiency data. Thus, all animals were separately tied to individual feeders at night. The source of animals in this study was treated as a fixed effect in the mixed model. Calves were also grouped and analyzed in groups determined by management or environmental variation. An example of grouping was date of castration. The estimates of heritability are reproduced in Tables 6 and 7. Genetic correlation estimates are presented in Tables 12, 13, and 14; environmental correlations are presented in Tables 16, 17, and 18; and phenotypic correlations are presented in Tables 20, 21, and 22.

Blackwell et al. (1962) analyzed growth and carcass traits from 420 Hereford heifers and 499 Hereford steers using the paternal half-sib intraclass correlations. The data were collected from 1936 to 1952 at the New Mexico Agricultural Experiment Station. Animals excluded from the analysis were heifers selected for in-herd use or the small, young steers used in nutrition studies. As percentages

of the calf crop, 60% of the heifers and 50% of the steers were incorporated into this data set. The management practices included weaning spring calves in the fall and grazing the calves until 18 months of age. They were then placed on a finishing ration on a 168 day test. The cattle were slaughtered when they were approximately two years old. Ration was included in the mixed model as a fixed effect. Steers were fed three or four different rations per test period. Heritability estimates are reproduced in Tables 6 and 7. Genetic correlations are presented in Tables 12, 13, and 14; environmental correlations are reproduced in Tables 16, 17, and 18; and phenotypic correlations are shown in Tables 20, 21, and 22.

Carter and Kincaid (1959a) used paternal half-sib analysis of variance to calculate heritability estimates. This data set included 212 steers and 212 heifers in the weaning analysis. The carcass analysis incorporated 192 steers and 202 heifers in the yearling analysis. The study spanned six years and utilized 38 sires. The objective of the study was to compare different levels of individual sire performance to the average performance of their respective progeny. The paternal half-sib correlation, the offspring-dam regression, and offspring-sire were all utilized to estimate heritabilities. The paternal half-sib heritability estimates are presented in Tables 6 and 7; the son-sire heritability is presented in Table 2.

In a second paper, Carter and Kincaid (1959b) estimated genetic and phenotypic correlations among various growth and carcass traits. This data set was described previously within this literature review (Carter and Kincaid, 1959a). The 38 sires incorporated within this study were comprised of 22 Hereford, 12

Angus, and 4 Shorthorn sires bred to Hereford cows. Genetic correlations are presented in Tables 12 and 13, and phenotypic correlations are presented in Tables 20 and 21.

Two hundred fifty-seven steers sired by 46 sires were analyzed for carcass traits (Brackelsberg et al., 1971). The data set was comprised of straightbred Hereford and Angus represented by 35 Hereford sires and 11 Angus sires. The data were collected over four years. Calves were weaned at an approximate average age of 205 days. These calves were randomly selected within sire groups allocated to three different feeding regimens. The first group of calves was placed in a feedlot and moved to the finishing ration as soon as possible. The second group was fed to gain .34 to .45 kg per day over the winter and then was placed on the finishing ration. The third group was fed over winter to gain approximately .34 to .45 kg per day over winter and then placed on summer pasture before returning to the feedlot that fall. Cattle were slaughtered when live visual evaluation estimated the carcass at a USDA low choice quality grade estimate. The same technician cut the right side of the carcass into trimmed retail cuts including fat, bone, and lean trim. Retail trimmed cuts were measured from each wholesale cut, quarter, and side (Brackelsberg et al., 1971). The heritability estimates are presented in Table 7.

Christians et al. (1962) analyzed 176 Angus calves sired by 24 sires for postweaning growth and carcass traits. The calves were weaned at approximately seven months of age. They were placed on feed for six months and

slaughtered at approximately 385 days of age. Paternal half-sib heritabilities were estimated from this data set. The growth and carcass heritability estimates are presented in Tables 6 and 7, respectively.

Koch (1978) analyzed 377 Hereford heifers for growth and carcass traits from 1963 through 1970. Three heifers were randomly sampled from six different sire groups. All heifers sampled were produced from four- to seven-year-old dams. This sampling criteria was an effort to reduce maternal effects for age of dam. This data set was comprised of three separate selection lines which included: a selection line for weaning weight, a yearling weight selection line, and an index of yearling weight and muscling score as a selection line. There were 20, 21, and 23 sires represented within each of the lines, respectively. In the weaning weight line, selection was based on weaning performance relative to contemporaries. In the yearling weight line males were selected at 452 days of age and females at 550 days of age. At approximately 200 days, heifers were placed on finishing rations for 254 days. At that time, the heifers were slaughtered. Boneless wholesale cuts were trimmed to an 8mm external fat cover. Retail product, fat, and bone weights were determined and incorporated into the analysis. Heritability estimates for both growth and carcass traits are presented in Tables 6 and 7, respectively. Genetic correlation estimates are presented in Tables 12, 13, and 14; phenotypic correlation estimates are presented in Tables 20, 21, and 22.

MATERIALS AND METHODS

Data

The Selection Criteria Study (SCS) herd was a randomly selected herd of Hereford cattle (Nelsen et al., 1984) at the USDA-ARS, Fort Keogh Livestock and Range Research Laboratory (LARRL) at Miles City, Montana. The data in this study were collected from 1977 through 1987.

Cows were allocated from a completed linecross study. These cattle included lines 1, 4, 6 and 10. There were 114 pregnant cows and 36 yearling heifers originally allocated to one of two replications. The two respective replications were maintained throughout the data collection period. Each replication included five single sire mating herds. However, due to drought conditions in 1980, one sire group was dropped from each replication.

Sire selection was totally randomized. All yearling heifers were recruited as replacement females. Older cow age groups were culled at random. The nonrandomized culling included injury, disease, or diagnosed reproductive abnormalities. Bulls were pasture exposed to approximately 240 females per year (Nelsen et al., 1984).

Cattle were raised under eastern Montana range conditions. A detailed discussion of this environment was given by Houston and Woodward (1966).

Winter supplementation was fed as needed, depending on the severity of winter conditions. The winter supplementation consisted of two feedstuffs: 22% crude protein barley pellets and a grass-alfalfa mixture of hay (IFN 1-00-890) (Urick et al., 1985).

Bulls were maintained intact to meet the random selection criteria. Only bulls were utilized in the analysis. Calves were born in the spring. Calf day born (CADB) was a julian date that was recorded for each calf at birth. The average julian date for calf birthdate was 105 d with a standard deviation of 15 d. The minimum and maximum julian date for calf birthdate on 736 bull calves born was 64 d and 150 d, respectively, with a range of 86 d.

Weaning usually took place in mid-October, with weaning date (WND) being the julian date designated to each weaning group each year and the overall mean was 290. The minimum weaning date was 286 and the maximum weaning date was 295.

There was an adjustment period between weaning and the initial test date (ITD) for the 168-day gain test. The adjustment period varied from 6 to 14 d. However, after the second year, the minimum adjustment period was 10 d and in 5 of the 10 years, bulls were placed in the postweaning daily gain test at exactly 14 d postweaning.

Final test date (FTD) also corresponded directly with ITD. Bulls were fed a ration of 48% corn silage, 48.7% barley grain, 1.8% soybean meal, .5% urea, salt, calcium, phosphate, trace minerals, and vitamins A and D on a dry

matter basis which contained approximately 2.62 Mcal energy/kg of dry matter (Reynolds et al., 1990).

Slaughter date (SLD) was recorded on bulls the day prior to slaughter in most years. There was variation as to when progeny bulls were slaughtered. One year, 1979, did not include slaughter weights on any of the carcasses and was excluded from the carcass analysis. In the years from 1978 through 1983, bulls were fed to gain .9 kg/d and were slaughtered at approximately 490 days of age. However, bulls born in 1982 were fed an *ad libitum* ration until slaughter instead of the target gain at .9 kg/d. Bulls born in 1983 and 1984 were sent to slaughter 48 d after the 168-d trial had concluded. Bulls born in 1986 and 1987 were fed increased concentrate levels and marketed after a longer feeding period. Bulls that were used as sires were excluded from this carcass data set because slaughter dates for bulls used as sires were 12 mo to 14 mo longer than for the progeny bulls. The minimum slaughter date was 154 d and the maximum slaughter date was 244 d. Bulls were slaughtered on the same day within each year. The mean slaughter date was 206 in julian d in the year following the birth year. The approximate age at slaughter for the progeny bulls was 13.8 mo to 16.8 mo of age.

Traits reported were as follows. Birth weight (CBWT) was recorded soon after birth. Only single-birth bull calves raised on their own dams were included. Calves were weaned at approximately 185 d in mid-October (Reynolds et al., 1990). The weaning weight (WWT) record is an actual

weight uncorrected for age of dam or maternal effects. Daily gain from birth to weaning (DGBW) was calculated by equation 1.

$$DGBW = (WWT\text{-}CBWT)/(WND\text{-}CADB) \quad [Eq\ 1]$$

The initial test weight (ITW) was the weight taken when placed on the 168-day postweaning feed trial. The final test weight (FTW) was an actual weight recorded on the completion of the 168-day postweaning gain test. The FTW weight is an average of three weights recorded on consecutive days at the conclusion of the postweaning gain trial. Daily gain on test (DGOT) was calculated by equation 2.

$$DGOT = (FTW\text{-}ITW)/[(FTD+365) - ITD] \quad [Eq\ 2]$$

Leap years, 1980 and 1984, were accounted for by adding FTD + 366 d.

A detailed description of the carcass data collected at the Livestock and Range Research Laboratory was given by Reynolds et al. (1990). Slaughter weights (SLWT) were recorded and bulls were transported 150 or 230 miles to slaughter facilities. Hot carcass weights (HCWT) were recorded at slaughter. Ribeye area (REA) from the 11th-12th ribs was measured in square inches to two decimal points. REA was measured with acetate (003 matte) paper. Planimeter measurements were used to calculate the REA. Pelvic, heart and kidney fat (KF) was estimated by USDA officials as a percentage of carcass weight. All progeny bulls were slaughtered within the A maturity specifications for degree of bone ossification. Marbling (MAR) scores were recorded by USDA officials using the guidelines established in *USDA Official United States Standards for Grades of Carcass Beef* (USDA,

1975). The MAR number score was represented by: 1 = devoid, 2 = partially devoid minus, 3 = partially devoid, 4 = partially devoid plus, 5 = traces minus, 6 = traces, 7 = traces plus, 8 = slight minus, 9 = slight, 10 = slight plus, 11 = small minus, 12 = small, 13 = small plus, 14 = moderate minus, 15 = moderate, 16 = moderate plus, 17 = medium minus, 18 = medium, 19 = medium plus, 20 = slightly abundant minus, 21 = slightly abundant, 22 = slightly abundant plus, 23 = moderately abundant minus, 24 = moderately abundant, 25 = moderately abundant plus, 26 = abundant minus, 27 = abundant, and 28 = abundant plus. Ribeye area per hundred kilograms of carcass weight (REACWT) was obtained by dividing REA by HCWT and multiplying by 100. Dressing percentage (DR) was calculated by dividing HCWT by SLWT and multiplying by 100.

The SCS herd produced 1,451 births from 1978 through 1987, and 736 of these were males sired by 86 sires. Birth weight heritabilities were estimated from a data set that included both surviving and nonsurviving male calves. Thus, no selection bias was incorporated into the estimate due to natural selection from calving dystocia or calf viability.

Analyses of other traits included individuals with complete records throughout the growth phase of the study. This group included 616 bull progeny sired by 85 sires.

The third group consisted of bulls which had no missing records throughout both the growth and carcass phases of the study. This group did not include bulls from 1979 due to lack of carcass information collected in that

year. Also, bulls that were retained for use as sires were not included in this group due to differences in slaughter age. The carcass group consisted of 401 individuals with complete records for all traits analyzed. The carcass group was represented by 76 sires. This is a reduction of 335 and 212 records from groups 1 and 2, respectively. One animal was dropped from the third group for inconsistencies within the carcass record between fat composition traits. The number of observations within each year that were analyzed are presented in Table 23.

Table 23. Number of animals represented in the analysis groups by year.

Year[a]	Analysis Groups		
	1[b]	2[c]	3[d]
1978	69	59	39
1979	74	64	--
1980	87	66	48
1981	73	61	47
1982	71	61	43
1983	84	68	51
1984	90	65	50
1985	69	51	35
1986	56	56	40
1987	63	62	48

[a]Year of birth

[b]Birth weight group, which included all bull calves born with the SCS herd from 1978-1987

[c]Growth group, which included all complete individual records throughout the growth phase

[d]Carcass group, which included all individuals with complete records throughout the data collection period

Statistical Analyses

Data were analyzed by least-squares analysis of variance procedures for unequal subclasses (Harvey, 1975). Fixed effects included in the model were year of birth, age of dam, and the linear partial regression on age. Random effects were replication, sire, and residual. The mixed model included the following main effects.

$$Y_{ijklm} = \mu + YB_i + AD_j + R_k + S/R/YB_{ikl} + b_m + e_{ijklm}$$

where

Y_{ijklm} = individual observation in the j^{th} age of dam, l^{th} sire within k^{th} replication within i^{th} year

μ = the population mean

$S/R/YB_{ikl}$ = the random effect of sire nested within replication and calf year born

YB_i = the fixed effect of calf year born

R_k = the random effect of replication

AD_j = the fixed effect of age of dam

b_m = the linear regression on age

e_{ijklm} = random error associated with the trait

All two-way interactions among main effects were tested in preliminary analyses and none were significant.

Calf day born (CADB) was used as the age covariate for all three analyses evaluating growth traits. Slaughter weight was utilized as a covariate

for all carcass traits evaluating composition traits. Cundiff et al. (1969, 1971) evaluated the differences between age and weight as covariates in an ANOVA model. Age was used to account for variation for rate of growth. Weight was used as a covariate to account for differences in carcass composition and quality.

Paternal half-sib correlations were used to estimate heritabilities for growth and carcass traits. The intraclass correlation formula (Becker, 1984) used in this analysis was:

$$h^2_s = \frac{4\hat{\sigma}_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_w^2}$$

The standard error estimate for the paternal half-sib heritability estimates used in this analysis was:

$$SE\ (h^2_s) \simeq 4\sqrt{\frac{2(1-t)^2\ [1+(k-1)t]^2}{k(k-1)(s-1)}}$$

where

k = the average number of progeny per sire

t = the intraclass correlation =

$$\frac{\hat{\sigma}_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_w^2}$$

An analysis of covariance was used to estimate genetic, environmental, and phenotypic correlations. The following formulas for genetic, environmental, and phenotypic correlations were used and reproduced from Becker (1984).

(1) Paternal half-sib genetic correlation formula:

$$r_G = \frac{4\,\widehat{COV}_s}{\sqrt{4\hat{\sigma}_{s(X)}^2\ 4\hat{\sigma}_{s(Y)}^2}}$$

(2) Paternal half-sib environmental correlation formula:

$$r_E = \frac{\widehat{COV}_w - 3\,\widehat{COV}_s}{\sqrt{(\hat{\sigma}_{w(X)}^2 - 3\hat{\sigma}_{s(X)}^2)\,(\hat{\sigma}_{w(Y)}^2 - 3\hat{\sigma}_{s(Y)}^2)}}$$

(3) Paternal half-sib phenotypic correlation formula:

$$r_P = \frac{\widehat{COV}_w + \widehat{COV}_s}{\sqrt{(\hat{\sigma}_{w(X)}^2 + \hat{\sigma}_{s(X)}^2)\,(\hat{\sigma}_{w(Y)}^2 + \hat{\sigma}_{s(Y)}^2)}}$$

Heritability estimates were also calculated by son-sire regression for growth and carcass traits based on the following formula reproduced from Becker (1984). Regression coefficients were weighted to account for the differences in progeny numbers between sires.

$$h^2 = 2\,\widehat{COV}_{XZ}/\hat{\sigma}_X^2 = 2b$$

where x denotes sire trait and z denotes progeny trait

Standard errors of the son-sire regression heritability estimates were calculated from the following formula (Becker, 1984):

$$S_b^2 = \frac{\Sigma z^2 - \frac{(\Sigma xz)^2}{\Sigma x^2}}{N-2}$$

$$SE(b) = \sqrt{\frac{S_b^2}{\Sigma x^2}}$$

Covariances were used to estimate the genetic correlations from the son-sire regressions. The arithmetic method was used, which included all covariances of the two respective traits within the formula to estimate the genetic correlation. The arithmetic formula is shown below (Becker, 1984):

$$r_G = \frac{\widehat{COV}_{x_1z_2} + \widehat{COV}_{x_2z_1}}{2\sqrt{\widehat{COV}_{x_1z_1} + \widehat{COV}_{x_2z_2}}}$$

The standard error estimate for the son-sire genetic correlation is presented below (Becker, 1984):

$$SE(r_G) \simeq \frac{1 - r_G^2}{\sqrt{2}} \sqrt{\frac{SE(h_1^2)\ SE(h_2^2)}{h_1^2\ h_2^2}}$$

RESULTS

General

The results section will be presented in two separate parts. First, the results will be presented in table form and defined. This will be followed by the discussion, where comparisons are made between findings of this study and the literature reviewed.

The number of cows for cow age subclasses are presented for each year in Table 33. Due to unequal representation of cows in the older age groups in the herd, all cows 5 years and older were consolidated into one group (Table 34). Tables 33 and 34 are presented in Appendix B.

The means, minimum, maximum, range, standard deviation, and coefficient of variation were calculated for all 15 traits analyzed and are presented in Tables 24, 25, and 26.

Table 24. Statistics from the birth weight group (N=736).

Trait	Min	Max	Range	Mean	Std	CV
CADB	64.0	150.0	86.0	104.97	15.08	14.37
BWT[a]	17.7	54.5	36.8	34.30	4.76	13.89

[a]Weights recorded in kilograms (kg)

(Refer to Appendix A for a glossary of variables.)

Table 25. Statistics from the growth subgroup (N=616).

Trait	Min	Max	Range	Mean	Std	CV
WWT[a]	82.60	258.00	175.40	172.00	30.00	17.38
FTW	192.00	526.00	334.00	366.00	47.00	12.81
DGBW	0.29	1.11	0.82	0.74	0.14	18.88
DGOT	0.52	1.99	1.48	1.16	0.16	13.91

[a]Weights recorded in kilograms (kg)

(Refer to Appendix A for a glossary of variables.)

Table 26. Statistics from the carcass subgroup (N=401).

Trait	Min	Max	Range	Mean	Std	CV
CWT[a]	154.00	390.00	236.00	275.00	40.00	14.48
REA[b]	54.50	115.20	60.70	82.00	9.87	12.04
KF	0.00	3.50	3.50	1.00	0.61	60.37
MAR	1.00	12.00	11.00	7.56	1.86	24.53
SLWT	291.00	652.00	361.00	468.00	59.00	12.67
REACWT	9.55	20.71	11.16	13.68	1.48	10.71
DR	51.00	67.00	16.00	58.73	1.93	3.29

[a]Weights recorded in kilograms (kg)
[b]Area recorded in square centimeters (cm)

(Refer to Appendix A for a glossary of variables.)

The ranges from all three record groups were large. Both viable and nonviable progeny were included in the birth weight group, which may have contributed to the large range. Large ranges also occurred in the growth and carcass traits. Environmental year effects had not been accounted for and the

range conditions under which these bulls were raised were subject to considerable yearly variation (Houston and Woodward, 1966). The lack of selection pressure placed on performance traits could have allowed large variation to persist for growth and carcass traits (Brown and Turner, 1968).

The coefficient of variation statistics varied in magnitude. Generally, lower values were observed on the growth traits and higher values were observed for the fat composition carcass traits. One reason for large coefficients of variation for these traits could have been the use of subjective measures in assigning specific trait scores. KF and MAR scores were assigned by a subjective system of measures.

Heritability Estimates

The paternal half-sib heritability estimates for the growth traits are presented in Table 27. Age was the covariate in the ANOVA model (Appendix C).

Table 27. Paternal half-sib heritability estimates and standard errors for the growth traits (N=616).

Trait	$h^2 \pm SE$	Trait	$h^2 \pm SE$
BWT[a]	.18 ± .10	FTW	.42 ± .14
WWT	.17 ± .11	DGOT	.47 ± .14
DGBW	.20 ± .12		

[a]BWT heritability was estimated from the BWT group (N=736).

(Refer to Appendix A for a glossary of variables.)

Heritability estimates for carcass traits are presented in Tables 28 and 29. Table 28 presents growth and lean meat yielding traits analyzed with age as a covariate in the ANOVA model. Table 29 presents fat composition traits analyzed with CADB, an age covariate, and SLWT, a weight covariate. There was no significant difference between heritabilities based on age and weight covariates. These findings were in agreement with Cundiff et al. (1971) and Cundiff et al. (1969). CADB was utilized as the covariate in the mixed model for all traits in the three subgroups for the remainder of the analyses. The ANOVA tables for the carcass traits are presented in Appendix C.

Table 28. Paternal half-sib heritability estimates for the lean meat yielding carcass traits (N=401).

Trait	$h^2 \pm SE$	Trait	$h^2 \pm SE$
CWT	.38 ± .18	SLWT	.42 ± .18
REA	.51 ± .19	REACWT	.23 ± .16

(Refer to Appendix A for a glossary of variables.)

Table 29. Paternal half-sib heritability estimates for the fat composition carcass traits (N=401).

Trait	Age[a]	Weight[b]
	$h^2 \pm SE$	$h^2 \pm SE$
FTH	.08 ± .15	.05 ± .15
KF	.37 ± .18	.38 ± .18
MAR	.31 ± .17	.28 ± .17
DR	.25 ± .17	.26 ± .17

[a]Age covariate in ANOVA model
[b]Weight covariate in ANOVA model
(Refer to Appendix A for a glossary of variables.)

Discussion

The birth weight heritability of .18±.10 estimated from the LARRL data set was lower than most values found in the literature. The average heritability estimate from Woldehawariat et al. (1977) was .40 for the paternal half-sib intraclass correlation procedure, with 68 studies included in this average estimate. The growth-carcass relationship literature not included in the average summary by Woldehawariat et al. (1977) was an estimate of .37±.17 from MacNeil et al. (1984).

The weaning weight heritability estimate for the LARRL data set was .17±.11. This estimate was also below the average of the literature. Woldehawariat et al. (1977) documented an average unweighted paternal half-sib estimate of .32 averaged over 72 studies. Koch (1978) presented an estimate of .48 for weaning weight.

The DGBW estimate of .20±.12 is in general agreement with the average estimates summarized by Woldehawariat et al. (1977). The average estimate was .28, which included 54 unweighted paternal half-sib studies. Two more recent estimates from the literature were reviewed for this study. The first, from Koch et al. (1982), estimated a heritability of .07. The second, from Urick et al. (1985), documented an estimate of .34±.16 from a subgroup of the LARRL data set represented in this analysis. Both estimates from the literature were within two standard errors of the LARRL estimate.

The FTW estimate of .42±.13 was in agreement with the average literature estimates summarized by Woldehawariat et al. (1977) for unweighted paternal half-sib intraclass correlation, which was .47 averaged from 28 studies.

Heritability for DGOT was in good general agreement at .47±.14 with the average paternal half-sib values found in the literature and reviewed in this thesis literature review. The Woldehawariat et al. (1977) average estimate, including 36 studies, was .42. The estimates from the literature reviewed after the Woldehawariat et al. (1977) average summary included: .92±.25 (Koch, 1978), .57 (Koch et al., 1982), and .36±.09 (MacNeil et al., 1984). The heritability plus or minus the standard error of the Koch (1978) estimate does not overlap the heritability plus or minus the standard error of the LARRL estimate. Other estimates were within two standard errors of the estimate for this present research.

The heritability estimate for carcass weight was .38±.18. This was lower than estimates in the literature. Paternal half-sib estimates from the literature were: .92 (Blackwell et al., 1962), .96 (Christians et al., 1962), .57 (Shelby et al., 1963), .62±.27 (Cundiff et al., 1964), .68±.25 (Koch, 1978), and .44±.09 (MacNeil et al., 1984). Koch et al. (1982) documented an estimate for cold side weight of .43. The average heritability estimate for carcass weight from the literature reviewed for this thesis was .66, while the MacNeil et al. (1984) and Koch et al. (1982) findings were in good agreement with the LARRL estimate.

The heritability estimate for REA was .51±.19 and agreed with the literature. There was a wide range of estimates for this trait, including: .76 (Christians et al., 1962), .26 (Shelby et al., 1963), .73±.29 (Cundiff et al., 1964), .40 (Brackelsberg et al., 1971), .32±.18 (Cundiff et al., 1971), .25 (Dinkel and Busch, 1973), .28±.24 (Koch, 1978), and .56 (Koch et al., 1982).

The heritability estimate for KF was .37±.18. The literature reports two kidney, heart, and pelvic fat measures. The first is kidney, heart, and pelvic fat weight with estimates from the following studies: .72 (Brackelsberg et al., 1971) and .77 (Koch et al., 1982). The second is percentage of heart, kidney, and pelvic fat from Koch et al. (1982) of .83. Thus, it appears that the LARRL estimate was low in magnitude.

The paternal half-sib estimate of heritability for MAR was .31±.17. This estimate was in general agreement with the literature which included: .30±.17 (Cundiff et al., 1971), .73 (Brackelsberg et al., 1971), .31 (Dinkel and Busch, 1973), .34±.25 (Koch et al., 1978), and .40 (Koch et al., 1982). The Brackelsberg et al. (1971) estimate was higher in magnitude than the LARRL estimate, but all other estimates were approximately the same.

The heritability estimate for SLWT was .42±.18 and was lower in magnitude compared to other estimates from the literature. Shelby et al. (1963) estimated a heritability of .70 for slaughter weight. Christians et al. (1962) estimated a slaughter weight heritability of 1.00. The final weight from the Blackwell et al. (1962) study was collected at the end of the fattening period; this estimate was .70.

The LARRL heritability estimate for REACWT was .23±.16. There was only one estimate of this measure in the literature, provided by Cundiff et al. (1964), which was an estimate of .29±.22.

The heritability estimate for DR was .25±.17 and the literature estimates ranged from .74 to .15. The estimates from the literature reviewed were: .25 (Blackwell et al., 1962), .74 (Christians et al., 1962), .57 (Shelby et al., 1963), and .15 (Dinkel and Busch, 1973).

Genetic Correlations

The paternal half-sib genetic correlation estimates are presented in Table 30 and are in general agreement with the literature. Lean meat yielding traits were depicted as CWT, REA, and REACWT. Additional lean meat yielding traits found in the literature included RPWT, RP%, and Round Weight. The traits REA and REACWT were moderate indicators of lean meat yield in comparison to RPWT, RP%, and Round Weight. CWT must be considered an intermediate between lean meat yielding traits and fat composition traits because a combination of lean, fat, and bone make up CWT. The fat composition traits were: MAR and KF. DR was considered an intermediate measure of lean and fat because both contribute to the CWT/SLWT. High DR percentages are usually characterized by increased fat levels in the carcass. Measures of fat composition found in the literature also include fat thickness over the 13th rib, carcass fat trim weight, and carcass fat trim percentage. The contributions of MAR and KF as indicators of fat composition traits were also moderate in comparison to FTWT and FT%.

Table 30. LARRL genetic correlation estimates and standard errors for growth and carcass traits (N=401).

	WWT		DGBW		FTW		DGOT		CWT		REA		KF		MAR		SLWT		REACWT		DR	
Trait	r_G	SE	r_G	SE	r_G	SE	r_G	SE	r_G	SE	r_G	SE	r_G	SE	r_G	SE	r_G	SE	r_G	SE	r_G	SE
BWT	.54	.60	.20	.68	.28	.41	.32	.39	.11	.50	.57	.45	-.59	.54	-.18	.56	.25	.46	.74	.74	-.57	.64
WWT			.95	.06	1.17	.23	1.39	.49	1.11	.25	.72	.38	.33	.50	.81	.55	1.13	.26	-.20	.73	.01	.62
DGBW					1.14	.23	1.34	.49	1.11	.27	.68	.39	.49	.50	.89	.56	1.10	.27	-.26	.75	.16	.60
FWT							1.04	.05	.98	.04	.71	.19	.25	.32	.47	.32	.98	.04	-.10	.45	.18	.38
DGOT									1.11	.09	.82	.17	.15	.31	.19	.33	1.08	.08	-.12	.41	.36	.34
CWT											.80	.18	.21	.38	.38	.38	.97	.03	-.05	.51	.32	.40
REA													.36	.33	.51	.35	.84	.18	.57	.31	-.11	.41
KF															.59	.35	.24	.36	.20	.51	-.06	.46
MAR																	.41	.36	.38	.56	.00	.50
SLWT																			.09	.51	.06	.44
REA-CWT																					-.70	.66
DR																						

(Refer to Appendix A for a glossary of variables.)

Genetic relationships among growth traits were highly positive with the exception of BWT. Correlations between BWT and the other growth traits ranged from .20 to .54 and were slightly smaller than most estimates in the literature. Other estimates were in good agreement with the average estimates from the literature summarized by Woldehawariat et al. (1977). Average genetic correlations from Woldehawariat et al. (1977) between BWT and other traits were: DGBW, .33; WWT, .55; DGOT, .48; and FTW, .62. The number of studies included in the literature average for BWT and DGBW, WWT, DGOT, and FTW were 19, 25, 9, and 13, respectively. The largest difference between LARRL estimates and the literature average was for BWT and FTW (.28 versus .62), but this difference was smaller than the standard error. A possible cause might be the random experimental design. No selection pressure on growth traits, such as FTW, might have caused less pleiotropic gene action with BWT.

Relationships among other growth traits were strong and positive, and this was in direct agreement with the literature. Most of the LARRL estimates were greater than 1.0, with standard errors ranging from .23 to .49. Average genetic correlation estimates for the growth traits from Woldehawariat et al. (1977) were moderate to high, with a large range among the estimates. The average estimate for genetic correlation between DGBW and WWT was .95; for DGBW and DGOT, .18; and for DGBW and FTW, .65. The number of studies were: 20, 8, and 8, respectively. Thus, the only genetic correlation which did not correspond from the LARRL data and average literature summary was between

DGBW and DGOT. The average literature estimate was .18, and the LARRL estimate was 1.34±.49. Differences between the two estimates could possibly be attributed to the genetic maternal environment with no selection bias present. The Hereford genetic base was not selected for milk production or increased WWT. Absolute weaning weights were relatively low, presenting a situation where larger calves at weaning went on feed and possibly gained faster throughout the postweaning feed period than the small calves. Thus, SCS calves that were genetically predisposed to high rates of gain from birth to weaning were also predisposed to high rates of gain on test after weaning.

Average genetic correlations in the literature summarized by Woldehawariat et al. (1977) were .42 for WWT and DGOT and .73 for WWT and FTW. The number of studies included in those averages of the literature were 16 and 18, respectively. Dinkel and Busch (1973) estimated genetic relationships of .77 for WWT and DGOT, .83 for WWT and FTW, and .99 for DGOT and FTW. Shelby et al. (1963) estimated a genetic correlation between FTW and SLWT of .98; that estimate was in direct agreement with the comparative LARRL estimate of .98. The LARRL estimates for growth trait relationships with other growth traits tended to be higher in magnitude than most of the literature reviewed.

The relationships between the growth traits and lean meat yielding traits were moderately to strongly positive (Table 30). These relationships were documented throughout the literature. Lean meat yielding traits represented in this study were REA, REACWT, and CWT. Ribeye area had moderate to strong

positive relationships with the other lean meat yielding traits such as cutability, retail product weight, and retail product percentage (Dinkel and Busch, 1973; Koch, 1978; Koch et al., 1982). Koch (1978) did document a genetic correlation of .02±.46 in comparison to the LARRL estimate of .80±.18 for a genetic correlation between ribeye area and carcass weight. There was only one comparable estimate in the literature for REACWT, where Cundiff et al. (1964) determined a genetic correlation between ribeye area and ribeye area/cwt carcass of .75 compared to the LARRL estimate of .57. Genetic correlations of CWT with retail product weight and ribeye area had moderate to high positive correlations. Genetic correlation estimates between carcass weight and relative lean meat yielding traits such as retail product percentage were slightly negative in the literature (Koch et al., 1982). This was in direct agreement with the present correlation between CWT and REACWT.

The fat composition traits represented from the LARRL study were KF, MAR, and DR. Positive relationships between the fat composition traits were documented in the literature (Blackwell et al., 1962, Shelby et al., 1963; Cundiff et al., 1964; Brackelsberg et al., 1971; Dinkel and Busch, 1973; Koch, 1978; Koch et al., 1982). The LARRL genetic correlations were not of the magnitude of the estimates for MAR, KF, and DR documented by Cundiff et al. (1964), Brackelsberg et al. (1971), and Koch (1978).

Genetic correlations between the fat composition traits (KF, MAR, and DR) and the growth traits (BWT, WWT, DGBW, FTW, DGOT, and SLWT) are

presented in Table 30. The genetic correlations for the LARRL study between MAR and BWT, WWT, DGBW, FTW, DGOT, and SLWT were -.18, .81, .89, .47, .19, and .41, respectively, with standard errors ranging from .56 to .32. These findings are in direct contrast with Koch (1978) and the marbling and weaning weight correlation from Dinkel and Busch (1973). The LARRL estimates are higher in magnitude; however, standard errors overlapped for the rest of the estimates by Dinkel and Busch (1973) and Koch et al. (1982).

Only one study examined correlations of kidney fat percentage with birth weight and the respective growth traits. Koch et al. (1982) found positive relationships between kidney fat and growth traits, and this was in good agreement with the LARRL estimates.

The genetic correlations of DR with birth weight and the growth traits were slightly to moderately positive, with the exception of the DR and BWT correlation in the LARRL data set. The findings of Dinkel and Busch (1973) were in contrast to the LARRL estimates. Their estimates for dressing percentage and weaning weight, daily gain, and final weight were -.81, -.08, and -.23, respectively. Correlations documented by Shelby et al. (1963) were in agreement with the LARRL estimates, including the negative relationship between DR and BWT. Blackwell et al. (1962) found positive relationships between dressing percent and the respective growth traits that were higher in magnitude than the relationships from LARRL.

The characteristics defined as lean meat yielding traits for the LARRL data were REA, REACWT, and CWT, and the characteristics defined as fat composition traits were MAR, KF, and DR. Other lean meat yielding traits, such as retail product weight and retail product percentage, will be included in this discussion. Other fat composition traits to be discussed are fat thickness, fat trim weight, and fat trim percentage. The LARRL estimates were generally slightly positive, while most of the literature reported slight negative relationships between lean meat and fat composition traits. The traits represented in the LARRL data were moderate indicators of both lean meat yielding traits and fat composition traits. Cundiff et al. (1964) reported a slight to moderate positive relationship between ribeye area and fat composition traits. Shelby et al. (1963) estimated a moderate positive relationship between ribeye area and dressing percentage. Dinkel and Busch (1973) found that DR had a moderate positive relationship with ribeye area, and marbling had a slight negative relationship. Brackelsberg et al. (1971) determined slight negative relationships between ribeye area and fat thickness and marbling. That author also found moderate negative relationships between ribeye area and fat trim and kidney fat. Koch et al. (1982) found essentially no relationship between ribeye area and kidney fat, and slight negative relationships between ribeye area and marbling and fat trim weight. Koch (1978) found slight positive relationships between ribeye area and fat thickness and fat trim (.03 and .10, respectively), but a strong negative relationship between ribeye area and marbling (-1.34). This estimate was much higher in magnitude than any

others referenced from the literature. All the marbling genetic correlations in the Koch (1978) literature had strong negative relationships with lean meat yielding and growth traits. There was a large range of estimates correlating ribeye area to other fat composition traits. Generally, the LARRL correlations for REA and MAR and KF are of opposite sign and higher in magnitude than the rest of the documentation. The REA and DR correlation is of opposite sign but low in magnitude with a large standard error.

There was only one study that provided genetic correlations for ribeye area/cwt carcass (Cundiff et al., 1964). Ribeye area/cwt carcass was negatively correlated with backfat thickness and was in agreement with the LARRL estimates for REACWT.

The LARRL estimates are in good agreement with those found in the literature for CWT and the fat composition traits. Koch et al. (1982) and Shelby et al. (1963) reported that genetic correlations of carcass weight with fat composition traits were positive. Koch (1978) found very strong positive relationships among ribeye area and fat thickness and fat trim. However, a moderate negative relationship was shown between carcass weight and marbling (Koch, 1978). The Koch (1978) study had larger negative relationships between marbling and other lean meat yielding and growth traits than any of the other studies reviewed. The LARRL estimates are in agreement with those found in the literature for CWT and the respective fat composition traits.

In summary, the LARRL genetic correlations based on data from an unselected herd were in general agreement with those found in the literature based on selected herds. The genetic correlations for the growth traits tended to be of higher magnitude than estimates in the literature. The fat composition traits had higher positive correlations with the growth traits and REA than the average of the literature. However, there was a tremendous amount of variation between ribeye area and the fat composition traits documented in the literature. A possible explanation for the differences between the literature and the LARRL study would include the difference between bull carcasses from the LARRL study and steer and heifer carcasses in the other analyses. In particular, this could be reflected in some of the fat composition traits. Also, the bulls were slaughtered from approximately 13.8 to 16.8 months of age, which was relatively young compared to some of the other studies cited (Blackwell et al., 1962). The literature indicated negative relationships between the lean meat yielding traits and the fat composition traits. These relationships existed in strong indicator type traits such as retail product weight and retail product percentage for the lean meat yielding traits and fat thickness over the 12th rib and fat trim for fat composition traits. The LARRL data set included only moderate indicator traits for both lean meat yielding traits and fat composition traits, which could reduce the magnitude and even the direction of these relationships. There was a tremendous amount of variation in the literature for genetic correlations between the fat composition traits and the lean meat yielding traits.

Phenotypic Correlations

The phenotypic correlations are presented in Table 31. The literature was in good general agreement with these findings (Carter and Kincaid, 1959b; Blackwell et al., 1962; Shelby et al., 1963; Swiger et al., 1965; Koch, 1978; Koch et al., 1982; Urick et al., 1985).

The growth traits phenotypically correlated to the lean meat yielding traits for the LARRL study were positive and moderate in magnitude, with the exception of the negative correlations with REACWT. The phenotypic correlations found in the literature for growth traits correlated to ribeye area and carcass weight were in good agreement with the LARRL estimates (Blackwell et al., 1962; Shelby et al., 1963; Koch, 1978; Koch et al., 1982). The REACWT phenotypic correlations with growth traits were in agreement with the literature for relative ratio traits correlated to growth traits as well (Cundiff et al., 1964; Swiger et al., 1965; Koch et al., 1982).

The LARRL estimates for comparing growth traits to fat composition traits were generally low in magnitude and positive. The correlations with negative relationships were DR correlated with BWT and WWT, with relationships of -.01 and -.34, respectively. The LARRL phenotypic correlation between BWT and MAR (-.02) was in direct agreement with Koch et al. (1982). Shelby et al. (1963) also found a slight negative relationship between birth weight correlated to carcass grade and dressing percentage (-.05 and -.02, respectively).

Table 31. LARRL phenotypic correlation estimates and standard errors for growth and carcass traits (N=401).

Trait	r_P										
	WWT	DGBW	FTW	DGOT	CWT	REA	KF	MAR	SLWT	REACWT	DR
BWT	.25	.05	.24	.16	.21	.11	.03	-.02	.23	-.09	-.01
WWT		.97	.82	.37	.68	.35	.19	.16	.68	-.31	-.34
DGBW			.79	.35	.67	.34	.19	.17	.65	-.30	.23
FTW				.80	.90	.49	.24	.24	.91	-.39	.27
DGOT					.79	.44	.19	.24	.79	-.32	.23
CWT						.58	.31	.28	.96	-.38	.44
REA							.19	.16	.53	.51	.35
KF								.31	.28	-.12	.18
MAR									.28	-.11	.08
SLWT										-.40	.18
REACWT											-.09
DR											

(Refer to Appendix A for a glossary of variables.)

The fat composition traits correlated with the other fat composition traits for the LARRL data set were positive and slight to moderate in magnitude. The studies reviewed maintained this same trend, but were moderate to high in magnitude (Blackwell et al., 1962; Shelby et al., 1963; Cundiff et al., 1964; Swiger et al., 1965; Brackelsberg et al., 1971; Koch, 1978; Koch et al., 1982).

Correlations of lean meat yielding traits with the other lean meat yielding traits in the LARRL study were positive and of moderate to high magnitude, with the exception of REACWT correlated with CWT. However, this was a relative ratio trait correlated with a size trait, and increases in carcass weight do not necessarily mean increases in ribeye area per unit of carcass weight. The relative ratio traits in the literature, such as retail product percentage correlated with cold side weight, were in good agreement with the LARRL estimate (Koch et al., 1982). The rest of the literature was in good agreement with the LARRL estimates (Shelby et al., 1963; Cundiff et al., 1971; Brackelsberg et al., 1971; Koch, 1978; and Koch et al., 1982).

The LARRL estimates for phenotypic correlations between lean meat yielding traits and fat composition traits were in general agreement with estimates from the literature. Carcass weight and ribeye area were positively correlated with the fat composition traits (Shelby et al., 1963; Cundiff et al., 1964; Koch, 1978). Koch et al. (1982) found both slight negative and slight positive relationships between the lean meat yielding and the fat composition traits. In contrast, Brackelsberg et al. (1971) determined negative relationships slight to moderate in magnitude.

In summary, the LARRL estimates of phenotypic correlations were in good agreement with the literature for almost every combination of traits. The possible exceptions were that the correlations among fat composition traits were lower in magnitude than most of the other values found in the literature. The relationships between the lean meat yielding traits and fat composition traits varied throughout the literature. The LARRL estimates were in agreement with the majority of the literature and the correlations were low in magnitude. Thus, these results in the LARRL study from bull carcasses were in good agreement with other studies that included data from steer and heifer progeny.

Environmental Correlations

The LARRL environmental correlations are presented in Table 32. The literature reporting environmental relationships among growth and carcass traits was limited to four separate studies.

The LARRL environmental relationships among the growth traits were generally positive and from slight to moderate in magnitude, with the exception of DGBW and WWT correlated at .98. The only negative relationship determined was between DGOT and WWT and DGBW, respectively. Swiger et al. (1965) documented a negative relationship between weaning weight and postweaning daily gain at -.17. Koch et al. (1982) reported a relationship of .03 between daily gain from birth to weaning and daily gain in the feedlot. The other environmental relationships were in good agreement with the literature reviewed (Blackwell et al., 1962; Swiger et al., 1965; Koch et al., 1982).

Table 32. LARRL environmental correlation estimates and standard errors for growth and carcass traits (N=401).

Trait	r_E										
	WWT	DGBW	FTW	DGOT	CWT	REA	KF	MAR	SLWT	REACWT	DR
BWT	.18	.01	.26	.07	.25	-.11	.27	.03	.23	-.31	.15
WWT		.98	.75	-.32	.54	.21	.14	-.05	.53	-.34	.27
DGBW			.72	-.32	.51	.21	.09	-.06	.50	-.32	.25
FTW				.34	.87	.22	.25	.07	.87	-.63	.37
DGOT					.49	-.19	.27	.34	.50	-.61	.16
CWT						.42	.37	.23	.96	-.53	.50
REA							.06	-.07	.27	.52	.64
KF								.17	.30	-.25	.29
MAR									.21	-.29	.11
SLWT										-.63	.25
REACWT											.10
DR											

(Refer to Appendix A for a glossary of variables.)

The relationships between BWT and the respective growth traits and the lean meat yielding traits were generally positive and of a moderate to moderately high magnitude. Koch et al. (1982) reported relationships that were in close agreement with the LARRL data. The only negative relationships consistently documented between growth and the lean meat yielding traits were between relative ratio traits, such as retail product percent (Swiger et al., 1965; Koch et al., 1982). These findings were in agreement with the LARRL data for the relationship between REACWT and BWT, WWT, DGBW, FTW, DGOT, and SLWT. Cundiff et al. (1964) also found a strong negative relationship between ribeye area/cwt carcass and carcass weight/day of age.

The LARRL environmental correlations among fat composition traits were positive and slight to moderate in magnitude. These findings were in good agreement with the literature between fat composition traits (Swiger et al., 1965; Koch et al., 1982). Blackwell et al. (1962) found a negative environmental correlation between dressing percent and carcass grade of -.05, and Cundiff et al. (1964) determined a negative relationship between backfat thickness and carcass grade of -.40.

There was a wide range of correlations found in the literature between fat composition traits and growth traits. Most of the estimates were positive and slight in magnitude for the LARRL data. Koch et al. (1982) found a negative relationship between birth weight and marbling of -.25. Koch et al. (1982) documented slight positive relationships for the rest of the growth traits correlated

to the fat composition traits. Cundiff et al. (1964) found a moderate positive environmental relationship between carcass weight/day of age and backfat thickness. Swiger et al. (1965) documented positive relationships between weaning weight, postweaning daily gain, and final weight correlated to fat and quality grade, with the exception of postweaning daily gain and fat at .03. In contrast, Blackwell et al. (1962) reported slight negative environmental relationships between weaning weight and daily gain and dressing percent and carcass grade. There were similar to slight negative relationships between WWT and DGBW with MAR in the LARRL data. The yearling weight and yearling gain were slightly positive for Blackwell et al. (1962). Some of the Blackwell et al. (1962) and Cundiff et al. (1964) findings were in contrast to the LARRL data, but Koch et al. (1982) and Swiger et al. (1965) were in good agreement.

The relationships between lean meat yielding traits and fat composition traits for the LARRL data set was generally slight to moderately positive, with the exception of REACWT, which was generally negatively related to the fat composition traits. Koch et al. (1982) determined that the relationship between ribeye area and cold side weight was positive and slight to moderate in magnitude for the environmental correlations with fat trim weight, fat trim percentage, kidney fat weight, fat thickness, and marbling. In contrast, Cundiff et al. (1964) documented negative relationships between ribeye area and backfat thickness and carcass grade. Blackwell et al. (1962) also found a negative relationship between carcass weight and carcass grade.

REACWT, the relative ratio trait, compares favorably with findings for environmental correlations for this type of trait in other studies. Swiger et al. (1965) documented estimates between percent retail product and fat and quality grade of -.42 and -.29, respectively.

In summary, the environmental correlations generally agreed with the literature estimates. The LARRL data were in good agreement with the studies of Koch et al. (1982) and Swiger et al. (1965). There was some variation between the above studies and LARRL data estimates in contrast to the findings of Blackwell et al. (1962) and Cundiff et al. (1964).

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LITERATURE CITED

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APPENDICES

APPENDIX A

GLOSSARY OF VARIABLES

GLOSSARY OF VARIABLES

ADG	--	average daily gain
BWT	--	actual calf birth weight
BONE%	--	bone percentage of carcass
BONEWT	--	bone weight of carcass
CADB	--	julian date of calf birth
CG	--	carcass quality grade
CUT%	--	cutability percentage
CV	--	coefficient of variation
CWT	--	carcass weight
CWT/D AGE	--	carcass weight per day of age
DAGE	--	dam age
DF	--	degrees of freedom
DGBW	--	daily gain from birth to weaning
DGOT	--	daily gain on postweaning gain test
DR%	--	carcass dressing percentage
FTD	--	julian final test date
FT%	--	fat trim percentage
FTW	--	average final test weight
FTWT	--	fat trim weight
FTH	--	fat thickness over the 12th rib
INDEX	--	average daily gain relative to test group average
ITD	--	julian initial test date
ITW	--	actual initial test weight
KF	--	kidney, heart, and pelvic fat percentage
KFWT	--	kidney, heart, and pelvic fat weight

MAR	--	marbling in the ribeye
Max	--	maximum
Min	--	minimum
MS	--	mean square
P	--	one-sided P-value
REA	--	ribeye area
REA/CWT	--	ribeye area per hundred weight of carcass
REP	--	replication
RP%	--	retail product percentage
RPWT	--	retail product weight
SWT	--	carcass side weight
SID	--	sire identification
SLWT	--	actual slaughter weight
SLD	--	slaughter date
Std	--	standard deviation
W-B	--	Warner-Bratzler Shear
WND	--	julian weaning date
WWT	--	actual weaning weight
YRB	--	calf year born

APPENDIX B

COW AGE SUBCLASS

Table 33. Unadjusted cow age subclasses within year.

Age of Dam[b]	Year[a]									
	78	79	80	81	82	83	84	85	86	87
2	20	15	23	25	16	27	29	23	16	26
3	12	16	22	19	23	15	14	19	22	18
4	4	20	15	16	18	19	22	12	10	9
5	9	3	13	13	14	13	14	13	7	7
6	9	5	7			10	10	2	1	2
7	8	5	1				1			1
8	3	8	3							
9	1	1	2							
10	3		1							
11		1								
Total[c]	69	74	87	73	71	84	90	69	56	63

[a]The number of records within each year

[b]The age of dam represented within year

[c]The total number of progeny included in the birth weight group

Table 34. Adjusted cow age subclasses within year.

Age of Dam[b]	Year[a]									
	78	79	80	81	82	83	84	85	86	87
2	20	15	23	25	16	27	29	23	16	26
3	12	16	22	19	23	15	14	19	22	18
4	4	20	15	16	18	19	22	12	10	9
5	33	23	27	13	14	23	25	15	8	10
Total[c]	69	74	87	73	71	84	90	69	56	63

[a]The number of records within each year

[b]The adjusted age of dam represented within year

[c]The total number of progeny included in the birth weight group

APPENDIX C

ANOVA TABLES

Table 35. ANOVA: BWT (N=736).

Source	DF	MS	P
YRB	9	509.6	.00
REP:YRB	10	72.5	.82
SID:YRB	66	123.4	.02
DAGE	3	2572.8	.00
CADB Regression	1	926.9	.00
Remainder	646	87.9	

(Refer to Appendix A for a glossary of variables.)

Table 36. ANOVA: DGBW and WWT (N=616).

Source	DF	DGBW		WWT	
		MS	P	MS	P
YRB	9	9306	.00	33055	.00
REP:YRB	10	1088	.18	3873	.18
SID:YRB	65	751	.03	2664	.05
DAGE	3	46551	.00	193149	.00
CADB Regression	1	801342	.00	445937	.00
Remainder	527	5109		2011	

(Refer to Appendix A for a glossary of variables.)

Table 37. ANOVA: DGOT and FTW (N=616).

Source	DF	DGOT		FTW	
		MS	P	MS	P
YRB	9	29583	.00	33055	.00
REP:YRB	10	1037	.64	3873	.39
SID:YRB	65	1316	.00	9365	.00
DAGE	3	4843	.00	264267	.00
CADB Regression	1	17962	.00	801342	.00
Remainder	527	675		5108	

(Refer to Appendix A for a glossary of variables.)

Table 38. ANOVA: HCWT, REA, and KF (N=401).

Source	DF	HCWT		REA		KF	
		MS	P	MS	P	MS	P
YRB	8	184361	.00	266146	.00	793.17	.00
REP:YRB	9	10335	.01	38404	.15	6.70	.98
SID:YRB	57	3896	.00	24641	.00	24.44	.01
DAGE	3	93225	.00	194616	.00	43.37	.05
CADB Regression	1	195782	.00	132976	.00	30.43	.17
Remainder	322	2428		13853		16.11	

(Refer to Appendix A for a glossary of variables.)

Table 39. ANOVA: MAR, FTH, and CG (N=401).

Source	DF	MAR		FTH		CG	
		MS	P	MS	P	MS	P
YRB	8	46.94	.00	16705	.00	756.99	.00
REP:YRB	9	4.03	.30	1049	.27	3.25	.72
SID:YRB	57	3.33	.03	822	.29	4.71	.05
DAGE	3	4.98	.09	3382	.00	4.39	.28
CADB Regression	1	4.09	.19	4323	.02	5.41	.21
Remainder	322	2.32		744		3.54	

(Refer to Appendix A for a glossary of variables.)

Table 40. ANOVA: SLWT, REACWT, and DR (N=401).

Source	DF	SLWT		REACWT		DR	
		MS	P	MS	P	MS	P
YRB	8	389303	.00	7368	.00	51.21	.00
REP:YRB	9	27080	.01	461	.43	2.94	.50
SID:YRB	57	9554	.00	446	.08	3.12	.06
DAGE	3	213690	.00	1486	.01	15.57	.00
CADB Regression	1	369907	.00	9119	.00	67.82	.00
Remainder	322	5696		340		2.31	

(Refer to Appendix A for a glossary of variables.)

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