



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 $.18 \pm .10$. The second group included 616 bull progeny from 85 sires and heritability estimates were as follows: weaning weight, $.17 \pm .11$; daily gain from birth to weaning, $.20 \pm .12$; final test weight, $.42 \pm .14$; and daily gain on test, $.47 \pm .14$. The third group included 401 records from 75 sires and heritability estimates were as follows: carcass weight, $.38 \pm .18$; ribeye area, $.51 \pm .19$; marbling, $.31 \pm .17$; slaughter weight, $.42 \pm .18$; ribeye area/unit of carcass weight, $.23 \pm .16$; and dressing percentage, $.25 \pm .17$. 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**

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
Bozeman, Montana**

March 1990

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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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ACKNOWLEDGEMENTS

I would especially like to thank my parents, Fred and Jackie Veseth. Without their support and encouragement, this achievement would not have been possible. I would also like to thank my brother, Don, for his help and insight. We have come a long way over the years.

Special acknowledgement is given to my grade school teacher, Mrs. Vera Black, for her spark, encouragement, and drive that allowed me to take advantage of higher education possibilities in later years.

I would like to express gratitude and appreciation to my adviser and committee chairman, Dr. Don Kress, for his foresight and reassurance during my graduate program. I would also like to extend my appreciation and sincere thanks to Dr. Lamar Reynolds and the LARRS staff for their cooperation and hard work, which allowed me to bring this project to fruition. Finally, I would like to thank Joe Urick, Brad Knapp, and my graduate committee members for their help, interaction, and cooperation. I would also like to thank the USDA-ARS Livestock and Range Research Laboratory for allowing me to use the data from the Selection Criteria Study as my thesis project.

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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 $.18 \pm .10$. The second group included 616 bull progeny from 85 sires and heritability estimates were as follows: weaning weight, $.17 \pm .11$; daily gain from birth to weaning, $.20 \pm .12$; final test weight, $.42 \pm .14$; and daily gain on test, $.47 \pm .14$. The third group included 401 records from 75 sires and heritability estimates were as follows: carcass weight, $.38 \pm .18$; ribeye area, $.51 \pm .19$; marbling, $.31 \pm .17$; slaughter weight, $.42 \pm .18$; ribeye area/unit of carcass weight, $.23 \pm .16$; and dressing percentage, $.25 \pm .17$. 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 proposed 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 $.16 \pm .06$ for generations 1-15, $.05 \pm .04$ for generations 16-30, and $.00 \pm .003$ for generations 31-45. In contrast, the nonselected control line heritability estimates were $.32 \pm .10$ for the first 15 generations, $.22 \pm .10$ for generations 16-30, and $.24 \pm .11$ 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)

^aGovernment owned and managed central performance test center

^bPrivately 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

^aStudies (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

^aAndersen 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

^aKoch 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				

^aStudies (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)

