



Sire by region interactions in Simmental sired calves  
by Michael Walter Tess

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:

Field records from the American Simmental Association were used to evaluate sire x region interaction effects on weaning weight. Records were from 1/2- and 3/4-Simmental bulls and heifers born and weaned in the same herd and raised by their own dams. Two basic data sets were used. The A-data set was analyzed by least-squares procedures using a mixed model containing region, herd/region, sire, age of dam, sex, percent Simmental, sire x region (SXR) interaction effects and a regression on weaning age. Four large regions were outlined with each region including several states. Sire and SXR interaction effects were both significant and their variance components comprised 1.0 and .2% of the total variance, respectively. The confidence interval for the genetic correlation overlapped unity. Rankings of the least-squares SXR means in each region indicated little changing of rank of the sires among regions. The B-data sets included only heifer records and 1/2- and 3/4-Simmental records were analyzed separately. The B-data sets were analyzed by least-squares procedures using a model containing region, herd/region, sire, age of dam, SXR, and sire x herd/region (SXH/R) interaction effects with a regression on weaning age. Three smaller regions were outlined: Montana (MT), Midwest (MW=Iowa + Illinois), and Texas (TX). Each region was analyzed separately in the 3/4-Simmental data sets by subdividing each region into two subregions in order to assess any subregion effects. Because of large subregion effects within TX, the West-TX subregion was deleted. Each combination of two regions was then analyzed in both 1/2- and 3/4-Simmental data sets. Sire effects were significant in all 3/4-Simmental analyses but not in any of the 1/2-Simmental analyses. The sire variance component comprised an average of 1.8% of the total variance. SXR interaction effects were generally not significant but did approach significance ( $P=.06$ ) in the 3/4-Simmental MW-TX analysis and was significant ( $P=.05$ ) in the 1/2-Simmental MW-TX analysis. The SXR interaction variance component comprised an average of .8% of the total variance. Confidence intervals for the genetic correlations in each analysis overlapped unity. Rankings of the least-squares SXR means in each region in each analysis indicated that some changing of rank of the sires was occurring but was not of such magnitude to be of practical importance. SXH/R interaction effects were significant in all B-data set analyses. The variance component for the SXH/R interaction comprised an average of 4.5% of the total variance and was consistently larger than the sire and SXR interaction variance components. Results indicated that SXR interaction effects are not important. SXH/R interaction effects, however, were significant sources of variation in weaning weights. Further evaluation of sire x herd interactions was suggested.

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A thesis submitted in partial fulfillment  
of the requirements for the degree

of

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in

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## ABSTRACT

Field records from the American Simmental Association were used to evaluate sire x region interaction effects on weaning weight. Records were from 1/2- and 3/4-Simmental bulls and heifers born and weaned in the same herd and raised by their own dams. Two basic data sets were used. The A-data set was analyzed by least-squares procedures using a mixed model containing region, herd/region, sire, age of dam, sex, percent Simmental, sire x region (SXR) interaction effects and a regression on weaning age. Four large regions were outlined with each region including several states. Sire and SXR interaction effects were both significant and their variance components comprised 1.0 and .2% of the total variance, respectively. The confidence interval for the genetic correlation overlapped unity. Rankings of the least-squares SXR means in each region indicated little changing of rank of the sires among regions. The B-data sets included only heifer records and 1/2- and 3/4-Simmental records were analyzed separately. The B-data sets were analyzed by least-squares procedures using a model containing region, herd/region, sire, age of dam, SXR, and sire x herd/region (SXH/R) interaction effects with a regression on weaning age. Three smaller regions were outlined: Montana (MT), Midwest (MW=Iowa + Illinois), and Texas (TX). Each region was analyzed separately in the 3/4-Simmental data sets by subdividing each region into two subregions in order to assess any subregion effects. Because of large subregion effects within TX, the West-TX subregion was deleted. Each combination of two regions was then analyzed in both 1/2- and 3/4-Simmental data sets. Sire effects were significant in all 3/4-Simmental analyses but not in any of the 1/2-Simmental analyses. The sire variance component comprised an average of 1.8% of the total variance. SXR interaction effects were generally not significant but did approach significance ( $P=.06$ ) in the 3/4-Simmental MW-TX analysis and was significant ( $P=.05$ ) in the 1/2-Simmental MW-TX analysis. The SXR interaction variance component comprised an average of .8% of the total variance. Confidence intervals for the genetic correlations in each analysis overlapped unity. Rankings of the least-squares SXR means in each region in each analysis indicated that some changing of rank of the sires was occurring but was not of such magnitude to be of practical importance. SXH/R interaction effects were significant in all B-data set analyses. The variance component for the SXH/R interaction comprised an average of 4.5% of the total variance and was consistently larger than the sire and SXR interaction variance components. Results indicated that SXR interaction effects are not important. SXH/R interaction effects, however, were significant sources of variation in weaning weights. Further evaluation of sire x herd interactions was suggested.

## INTRODUCTION

The ability to accurately identify those animals that are superior genetically is essential in order to obtain maximum progress from selection over time. Genotype x environment interactions may be defined as the failure of the effects of genotypes and environments to be additive, or in other words, the failure of genotype to have the same effect on phenotype in different environments.

Genotype x environment interactions are important because of the potential problems and opportunities they represent to animal breeders. If important genotype x environment interactions exist, progeny testing programs might need to be expanded to include progeny from all those environments among which important interactions exist. On the other hand, specific genotypes might be utilized to provide faster progress in specific environments.

Beef cattle are raised in many different climates and under a wide range of management conditions. With the increased use of artificial insemination in the United States, sires can produce progeny virtually anywhere in the country. If genotype x environment interactions do exist in beef cattle, specifically sire x region interactions, then use of sires in many different regions may need to be preceded by progeny testing in each region in which a sire is to be used. Studies in beef cattle are not conclusive as to the presence and/or importance of such interactions.

The purpose of this study was to determine if sire x region interactions exist in weaning weights of Simmental sired calves and if so to evaluate the importance of such interactions.

## LITERATURE REVIEW

### Introduction

The existence of genotype x environment interactions was proposed by several scientists before 1950, but little experimentation was conducted before that time. Wright (1939) stated "Where there are hidden systems of factor interactions, selection must be based on persistent combinations, and the method indicated is to start numerous isolated, strains, sufficiently widely founded to allow selection within each, . . . ." Lush (1945) recommended that selection should be carried out in the environment in which the animal is expected to perform, conceding the possible presence of important interactions between genotype and environment.

Dobzhansky (1960) stated "Heredity does not determine traits; it determines, . . . , the 'norm of reaction' of the organism to the environment. Different environments evoke different reactions in organisms with similar heredities; different hereditities engender different reactions in organisms which develop in similar environments."

An opposing view presented by Hammond (1947) seemed to be the catalyst for research in genotype x environment interactions. He stated "Since the actions of genes on the characters of an animal is limited to those effects which are physiologically possible, selection is most effective when carried out under environmental conditions which favour the fullest expression of the character that is particularly desired."

In a response to Hammond, Falconer (1952) restated the recommendations of Lush and said that situations involving genotype x environment interactions may be treated by methods of genetic correlation. In this manner performance in two environments is regarded as two characters genetically correlated. Falconer maintained that this procedure would give a specific answer as to whether selection should be done in an optimum environment or in one in which the animal is expected to live.

Robertson (1959) presented methods of estimating genetic correlations from the components of variance from a two way analysis of variance. He stated that interactions may be due to two completely separate biological phenomena. First, the between group variance may be different and second, the actual rankings of the genotypes may be different. He further proposed that a genetic correlation of .8 or less was of biological importance.

Dickerson (1962) expanded upon the work of Robertson and demonstrated similar methods of estimating genetic correlations from variance components in an analysis of variance. He proposed that one of the most probable kinds of genotype x environment interactions is a shift in emphasis between traits as environment changes. For example, selection for growth rate in a temperate climate might emphasize feed efficiency and/or appetite, whereas selection for growth rate in a humid climate might emphasize resistance to heat.

Yamada (1962) presented formulae for calculating genetic correlations in a mixed model situation, or in other words, when environments are considered as fixed rather than random in the model.

Falconer and Latyszewski (1952) reported on an experiment which supported the existence of genotype x environment interactions. Two strains of mice, derived from a single foundation population, were selected in the same manner for body weight at 6 weeks of age. One strain was fed ad libitum and the other fed at 75% of normal food intake. After several generations, portions of both strains exchanged diets. When both strains were fed on the restricted diet the 'restricted line' was superior, with the 'full line' showing no improvement over the unselected level. On the ad libitum diet the 'full line' was superior but the 'restricted line' was very close to the 'full line' performance and showed marked improvement over the unselected level. Falconer and Latyszewski concluded that their results contradicted Hammond's thesis.

Falconer (1960) reported on a similar experiment in which selection was made in two directions (increased and decreased growth) in mice raised on both high and low planes of nutrition. In mice selected for increased growth, growth on the high plane of nutrition was increased equally by selection at both nutritional levels, but growth on the low plane of nutrition was increased only by selection at the

low plane of nutrition. In mice selected for decreased growth, growth on the high plane of nutrition was reduced only by selection at the high plane of nutrition, but growth on the low plane of nutrition was reduced equally by selection at both nutritional levels. Falconer concluded that if good performance under a variety of conditions is desired, the selection should be made under the conditions least favorable to the desired expression of the trait.

Haldane (1946) demonstrated that with  $m$  genotypes and  $n$  environments there are  $\frac{(mn)!}{m! n!}$  possible kinds of interactions. Many individuals have attempted to classify these many combinations into more simple meaningful categories. Haldane (1946) put forth six basic types of interactions between two environments and two genotypes.

McBride (1958) and Dunlop (1962) proposed interaction classifications based on those combinations of environments with large or small differences and genotypes with large or small differences. Small environmental differences may be thought of as fluctuations within a general area in which a population lives and large differences are those of climate, management practices, or regions. Small genotype differences are those within a herd or related herds with large differences being those between breeds, strains or species. These interactions are illustrated in figure 1. McBride suggested that interactions of importance would be most often found involving large environmental differences and either large or small genetic differences.

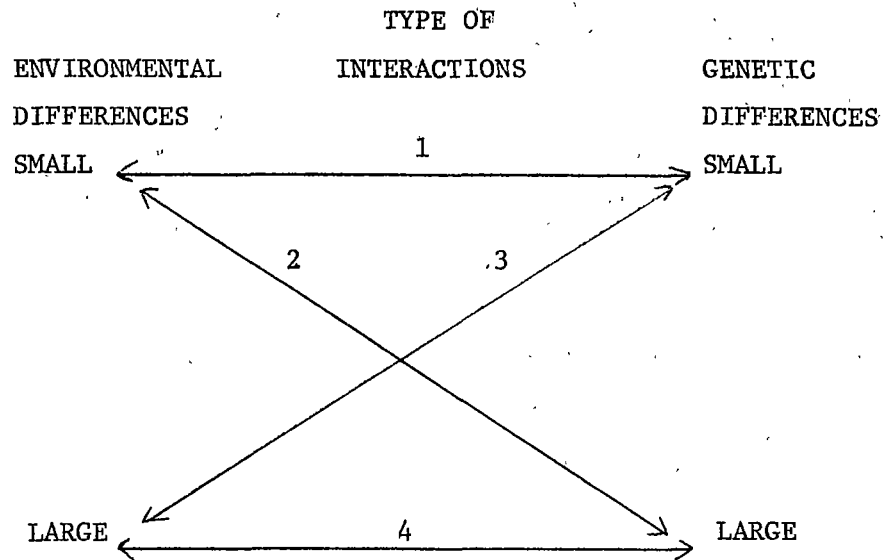


Figure 1. Types of heredity x environment interactions (Dunlop, 1962).

Pani and Lasley (1972) proposed a different classification of genotype x environment interactions involving two environments and two genotypes with consideration made for statistical significance of such interactions (figure 2). This classification makes a distinction between significant interactions involving changes in magnitude and those involving changes in rank. Differences in magnitude of interactions might suggest optimum environments in which selection might be made for detection of true genotype differences. Changes in rank are important when selection is performed in a different environment than which the animals or their progeny are expected to live.

#### Dairy Cattle

Extensive research in genotype x environment interactions has been done in dairy cattle. It might be argued that due to the intensive management of dairy cows compared to beef cattle that environmental differences within the dairy industry are of a different nature than those of the beef industry. Also, the traits most commonly investigated in dairy research are different than those of the beef industry. Conceding these differences, the limited amount of literature in preweaning traits in beef cattle makes the dairy literature of considerable value.

Milk yield and fat percent. Bonnier et al. (1948), in studies with identical twins, observed interactions between heredity and environment of growth, preweaning and postweaning, milk yield and fat

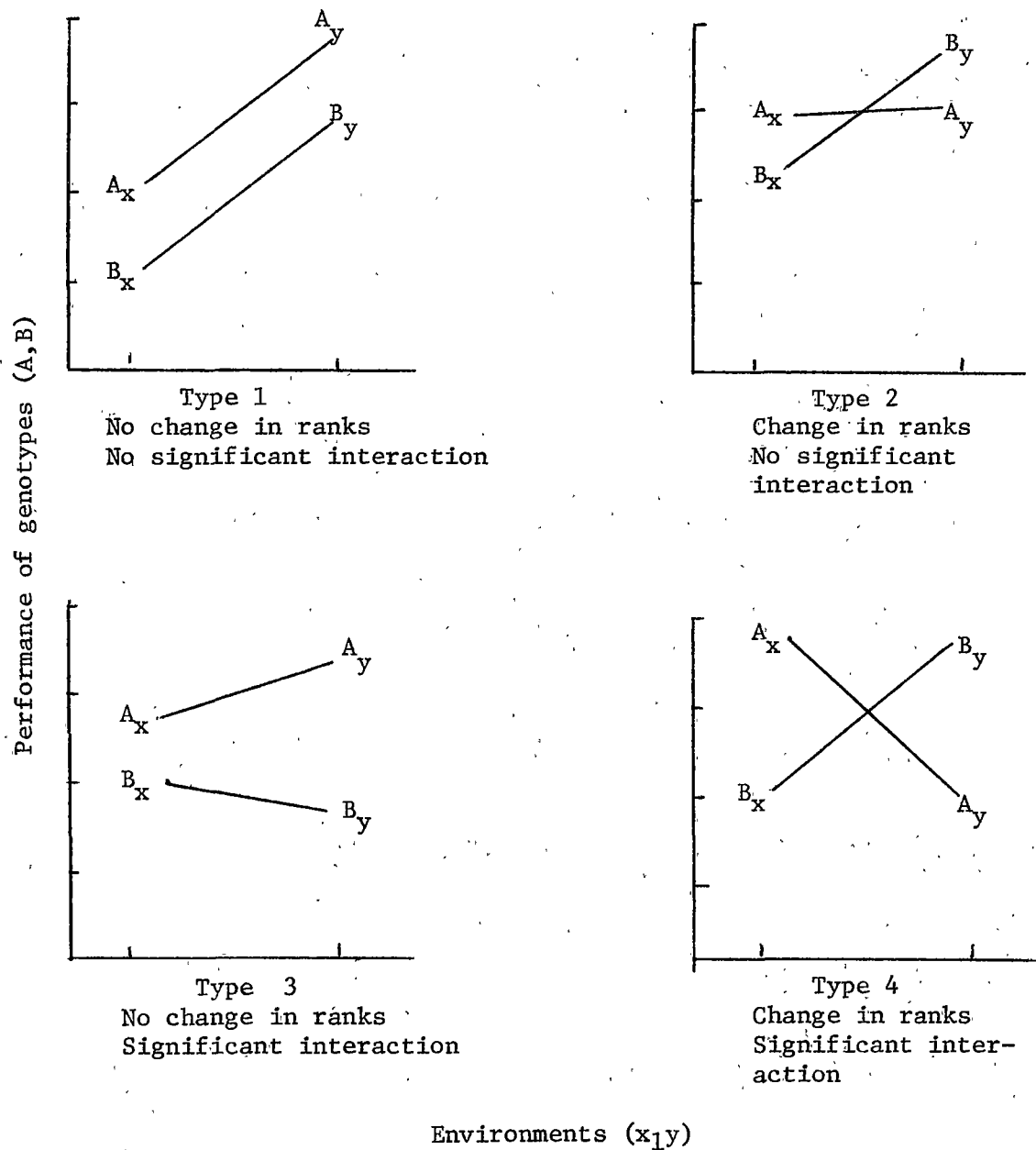


Figure 2. Classification of genotype x environment interaction (Pani and Lasley, 1972).

percent. He also observed non-linear interactions between age and heredity in weight and height of the shoulder, and between stage of lactation and heredity in milk yield.

In another study with identical twins, Brumby (1961) found evidence of interactions between herd environment and genotype which composed an appreciable source of variation.

Freeman (1969) studied identical and fraternal twins raised on two diets. The pair x ration interaction estimated from 30 to 55 identical pairs of various ages was zero for first lactation milk yield.

In studies of milk yield in Michigan DHIA records from 8,638 Holstein and 1,872 Guernsey cows, Burdick and McGilliard (1963), found no interactions of practical importance between sires and herd environments classified by level of production, location, days dry, calving interval, or type of housing.

Mao and Burnside (1969) studied the milk production records of AI sired cows and found no important interactions between sire proofs and herd environments classified with respect to use of AI sires, price received for milk, source of water on pasture, forage feeding method in winter and summer, amount of exercise in winter, and herd size. They did find an interaction ( $P < .01$ ) between sire proofs and level of grain feeding in summer.

Probably the most common type of genotype x environment interactions studied in dairy cattle are sire x herd interactions. Legates et al. (1956), in studying lactation production records of 24,754 daughters of Guernsey, Holstein, and Jersey sires used in U.S. AI associations, found sire x herd variances to be inconsequential for milk, fat percent, and fat yield.

Mason and Robertson (1956) studied 13,000 milk records of AI sired cows in Denmark. They divided herds on the basis of average production levels. No evidence was found of any sire x herd interactions for milk yield or fat content.

Van Vleck (1963) divided 45,876 first lactation and 39,261 second lactation records of New York AI sired cows into four groups on the basis of DHIA season averages. No important sire x herd interactions were found.

Age-corrected milk records of 40,374 Holstein cows tested in 1,073 herds divided on the basis of herd production levels were studied by Burnside and Rennie (1968). Correlations among contemporary comparison proofs of 19 sires, each evaluated on the production of at least 20 daughters at four levels of herd production ranged from .73 to 1.01 indicating little changing in rank.

McDaniel and Corley (1967) studied the first lactation records of AI progeny of 40 Holstein sires, each with at least 1000 daughters.

Correlations among sire progeny averages at different herd-mate levels were all very high (.88 to .96) suggesting bulls ranked in about the same order at all levels.

Records of 57 Friesian, 8 English Ayrshire, and 11 Scottish Ayrshire AI sires were used by Robertson et al. (1960) to compile contemporary comparisons. For each bull, herd-years were divided into three groups on the basis of yield with comparisons being made at each level. Correlations between true breeding values of the bulls at different levels were close to unity. They concluded that no sire x herd interaction was indicated.

Wiggans and Van Vleck (1970) classified over 1,000 Holstein herds in New York's Dairy Herd Improvement Cooperative as to the type of housing system used (free stall or stanchion). A total of 21,285 first-lactation records were analyzed. The genetic correlation between sire effects in the two systems was near unity suggesting essentially complete agreement between sire rankings in the two housing systems.

Sire x region interactions in first lactation records of 10,548 daughters of 46 Holstein sires born in the North and the South were investigated by Lytton and Legates (1966). Correlations of average breeding values of sires in the two regions were essentially unity. Estimates of the sire x region interaction variance were also zero.

They concluded that influences associated with a particular region should not unduly confuse the ranking of sires in the different regions.

Comparisons of AI sired heifers to non-AI sired heifers were made by Wadell and McGilliard (1959) from Michigan DHIA records. No interaction between AI sires and herds existed when each daughter's record was expressed as a deviation from the average fat production of all non-AI cows in the same herd.

Van Vleck et al. (1961), in studies of first and second lactation records of daughters of Holstein AI sires, found that sire x herd and sire x year-season interactions were both small indicating little genotype and environment interaction. Kelleher et al. (1967) also studied bull x herd-year season interactions and found that the interaction component only accounted for 2% of the variation in milk yield.

Branton et al. (1974) studied season of calving and its interactions with genotype in five herds in Louisiana. The sire x season interaction accounted for less than 1% of the total variation in both milk yield and milk fat.

Heritability. In his paper on genotype x environment interactions, Falconer (1952) stated that it is possible for a correlated response to be greater than direct response to selection if the heritability of the correlated character is greater than the heritability of the character in questions and the genetic correlation between the two

characters is large. The correlated character in the present context is the expression of the trait in a different environment. This has stimulated several experiments and studies into the heritability of milking traits in different environments. Considerable attention has also been given to the nature of phenotypic and genetic variances in different environments, which of course are closely related to heritability.

Milk production records from 5,740 first lactation Holstein daughter-dam pairs were analyzed by Van Vleck and Bradford (1964) to determine if heritability was related to herd production level. Heritability of milk yield from daughter-dam regressions was essentially constant at ten environmental levels. Estimates of heritability from paternal half-sib correlations over four environment levels and based on data from 2,568 daughters of AI sires generally increased as herd level of production increased. Daughter-dam estimates of heritability from the same data were essentially constant over the four levels. Total variance generally increased as herd level of production increased.

Mason and Robertson (1956) reported that heritability of milk yield and fat content and the variance of yield within herds increased as yield increased. Also the genetic variance was five times as large in high-yielding herds as in low-yielding herds. Van Vleck (1963) also found that higher producing herds had greater variability and increased heritability. Robertson et al. (1960) reported the

variance of yield within groups and the variance between groups increased with production level, but heritability remained the same.

Touchberry (1963) analyzed the records of 20,024 Holstein daughter-dam pairs from 1,703 herds. Herds were divided into 20 classes on the basis of production average. Heritability estimates for milk yield did not change with production level, although both phenotypic and genetic variances increased. Heritability for percent fat increased significantly with production level, but phenotypic variance decreased while genetic variance increased. Heritability for milk-fat decreased as production level increased, while both phenotypic and genetic variances increased.

Records of 1,243 Swedish red-and white cattle from 12 low- and 17 high-producing herds for butterfat were studied by Johansson (1953). Bulls of the same or related lines were used in both herd types so it was assumed that genetic differences were small. Heritabilities for yield and fat percent did not change significantly between herd levels.

Heritability estimates were calculated by Legates (1962) to examine the relationship between these values and the herd level of fat yield for 1,825 Guernsey, 5,458 Holstein, and 3,465 Jersey daughter-dam pairs. He reported that phenotypic and additive genetic variances increased as mean fat production for herd increased, but there was no significant relationship between heritability values and production levels for the groups of herds within any of the breeds.

## Sheep

Regional environmental differences in the sheep industry would seem to be more similar to those in the beef industry than is the case in dairy cattle. Variation in types of management practices in both the sheep and the beef industry appear to be much greater than in the dairy industry. Based on this assumption, Pani and Lasley (1972) proposed that genotype x environment interactions are more likely to be important in sheep and beef cattle than for dairy cattle and poultry. Studies of several traits of economic importance in sheep are reviewed below.

Birth Weight. Osman and Bradford (1965) collected data at two locations in California over 5 years. One location, Hopland, represented a poor environment, and the other location, Davis, represented a good environment. Results indicated that the heritable fraction of variance was larger at Davis than at Hopland. However, no significant genotype x environment interactions were observed for birth weight.

Half-sib progeny of five Merino rams, each from a different flock, were investigated in different flocks and at a progeny testing station by Radomska (1965). No interaction due to the different environments and types was found in birth weight.

Hohenboken et al. (1976b) reported genetic, environmental and interaction effects from a diallel cross among three breeds replicated

over 3 years and two grazing management systems (improved dryland hill pasture versus fertilized, irrigated pastures). No significant genotype x environment interactions were found for birth weight.

Two breed crosses were studied at both Ottawa, Canada, and Glade Springs, Virginia, by Carter et al. (1971a). The same rams were used at both locations during the test. A significant ( $P < .05$ ) ewe breed cross x location interaction was reported for birth weight, but differences were relatively small.

Weaning Weight and Preweaning Average Daily Gain. Five strains of Australian Merinos raised in three different wool-growing regions in Australia were evaluated by Dunlop (1963). Strain x location interactions were generally of moderate or small size and accounted for only a small fraction of the total variance in weaning weight. Radomska (1965) and Osman and Bradford (1965) also found genotype x location interactions not to be significant for weaning weight. Carter et al. (1971b) found the ewe breed cross x location interaction to be of marginal importance for weaning weight ( $P = .07$ ). Hohenboken et al. (1976b), however, reported a significant sire breed x management system interaction for weaning weight.

Ercanbrack and Price (1969) reported on a study designed to compare the effects of early weaning to regular weaning using 173 inbred and 397 non-inbred Rambouillet, Targhee, and Columbia sheep.

No significant interaction was observed between breed and weaning response in the inbred sheep but they did observe a significant interaction in the non-inbred sheep.

Postweaning Gain. Osman and Bradford (1965) and Carter et al. (1971b) both reported no evidence of important genotype x location interactions for average daily gain. Radomska (1965), however, found a significant genotype x environment interaction in development to 6 months of age in ram lambs and to 12 months of age in ewe lambs. Hohenboken et al. (1976b) found a significant sire breed x management system interaction for carcass weight per day of age.

Several studies of postweaning performance in sheep have classified environments according to the plane or type of nutrition. King and Young (1955) studied the reactions of three breeds of sheep (Blackface, Cheviot, and Wiltshire) to different environments classified according to temperature and plane of nutrition. Evidence was obtained that the three breeds reacted differently to these environments. No change in rank occurred between the environments but the Blackface grew relatively faster on a good plane of nutrition than the other two breeds.

Morely (1956) divided a number of groups of half-sibs into two lots, one on a high plane of nutrition and the second on a low plane of nutrition from 3 to 17 months of age. Genotype x treatment interactions were not important for 6-month body weight, but were

large and highly significant for weight at 12 and 17 months of age. Heritability did not vary with plane of nutrition.

Responses of 150 twin lambs of various breeds and crosses to different planes of nutrition were investigated by King et al. (1959). Results indicated that the different genotypes responded similarly to the different planes of nutrition. Few interactions were found of statistical significance.

Osman and Bradford (1967) used 40 ram lambs sired by five sires and 78 wether lambs sired by eight sires to study the effects of sire and two levels of nutrition over two, 7 week periods. Significant interactions between sire and plane of nutrition were found for average daily gain and daily feed intake in weathers in period one, and for carcass weight in rams during period two. Significant interactions were found in only five of 38 comparisons which led these researchers to conclude that this interaction was not a major source of variation.

The performance of 324 ram lambs from eight breeds averaging 84 days in age and 28 kg in weight were analyzed by Glimp (1971) to study the effects of breed and ration energy level on rate and efficiency of gain. Breeds used were Suffolk, Hampshire, Targhee, D-line, Fine Wool, Course Wool, Corriedale, and Navajo. Suffolk and Hampshire gained faster when the ration energy level was increased, but the other breeds showed no change, which produced a significant

( $P < .01$ ) breed x ration interaction.

Wool Traits. Radomska (1965) reported a significant interaction between genotype and location in wool fineness at the second shearing but found no important interactions for several other wool and fleece characters including fleece weight at the second shearing. Osman and Bradford (1967) in the same study mentioned above, out of several trait and period combinations, found only staple length in wethers during period one and clean fleece weight during period two to exhibit significant sire x plane of nutrition interactions. Morley (1956) reported genotype x plane of nutrition interactions were not important for any fleece characters.

Dunlop (1962) presented results for greasy fleece weight, clean fleece weight, percent clean scoured yield, number of fibers per unit area of skin, number of crimps per inch of staple, fiber diameter, staple length, gradings of count, character, color, soundness and handle from his experiment involving five strains of Merinos raised in three regions of Australia. Real interactions were found in most traits but were generally small and accounted for only a small fraction of the total variance. He concluded that specific adaptations in these characteristics should not be an important reason for the choice of the strain of sheep to be used in particular areas.

In a later study, Dunlop (1966) analyzed the records of the female progeny of the rams used in the previous experiment. Clean wool weight was analyzed for the presence of ram x year, ram x drop, and ram x station interactions. The ram x station interaction was found to be significant and its variance component was approximately half as large as the sire component of variance. The ram x drop and the ram x year interactions were not significant sources of variation.

Ewe Performance. Strain x location interactions were reported to be not important by Dunlop (1963) for the number of weight of lambs born and weaned. Carter et al. (1971a) found significant breed x location interactions for lambing date ( $P < .01$ ) and for weight of lamb weaned per ewe mated ( $P < .05$ ), and an interaction of marginal importance ( $P = .08$ ) for percentage of ewes lambing over a 5 year period. It should be noted that the breeds used in the study of Carter et al. (1971a) probably represented more diverse genotypes than the strains used by Dunlop (1963).

Hohenboken et al. (1976a) found no important sire breed x management system or sire breed x year interactions for ewe fertility and productivity. Dam breed x management system interactions, however, were found to be significant with changes in rank occurring between the breeds for ewe fertility and productivity.

Genotype x Sex Interactions. Sex is an important source of environmental variation when considering the progeny of a sire or dam. An interaction between genotype and sex would indicate a differential response to sex between genotypes.

Brown et al. (1961) analyzed the records of 121 inbred and 132 crossbred lambs to determine the effects of line, sex, type of birth, age of dam, and the sex x line interaction on birth weight, 30-day weight, 120-day weight and days required to reach 27 kilograms. Results indicated that the sex x line interaction was only significant in the case of days required to reach 27 kg in the inbred lambs. Interactions for all other traits were not important.

Data from 1,947 Rambouillet and Romnelet lambs sired by 75 rams was analyzed by Vesely and Robison (1969). Birth weight, weaning weight, grease and clean fleece weight, staple length, wool grade, wool yield, average daily gain, total gain, feed efficiency, and final weight were studied to determine the presence of genotype x sex interactions. All genotype x sex interactions were not significant in the Romnelet and only one sub group (10 sires within 1 year) had a significant ( $P < .05$ ) interaction in the Rambouillet. Nine of 11 traits gave higher heritabilities in females in the Romnelet, with all differences being small. The researchers concluded the similarity in heritability in the two sexes and the absence of important sire x sex interactions indicated that such interactions are not of sufficient

incidence or magnitude to be of concern in selection programs.

### Beef Cattle

Birth Weight. Differences between years often account for a considerable portion of the variation in growth traits. Years can reflect changes in many environmental factors such as rainfall, pasture conditions, and management practices. Ellis et al. (1965) analyzed birth weight data collected over 11 years in Texas, and reported a significant breed or cross x year interaction ( $P < .01$ ).

Turner and MacDonald (1969) studied the preweaning data from approximately 1,100 straightbred, singlecross, backcross, and three-breed-cross calves of Angus, Brahman, Brangus, and Hereford breeding and crossbred calves sired by Charolais bulls. The year x breed of sire interaction was not important for birth weight.

Brinks et al. (1967) analyzed the records of 241 bull and 228 heifer calves from five inbred lines produced over several years. Line of sire x year and line of dam x year interactions were not found to be significant for birth weight.

Sire x location interactions were studied by Woodward and Clark (1950) using the records of steer progeny produced at two locations in Montana and sired by 11 bulls. No significant interaction between sire and location was observed for birth weight.

The performance of 8,750 calves sired by Charolais and Hereford bulls out of Freisian, Ayrshire, Shorthorn, Jersey and Guernsey dams or purebred dairy was compared by Edwards et al. (1966). The calves were born in England and Wales. Birth weight was found to be significantly affected by the sire x region interaction.

Butts et al. (1971) reported on an experiment involving the reciprocal transfer of half of two herds of Hereford cattle between Brooksville, Florida, and Miles City, Montana. During the first 7 years of the experiment important ( $P < .01$ ) genotype x location-origin interactions were found for birth weight.

Field records of Simmental sired calves from several regions of the United states were analyzed by Nunn et al. (1978). They reported no significant sire x region interactions for birth weight.

Friedrich (1977) analyzed field records of non-creep fed Simmental-cross calves for sire x management unit interactions and analyzed records from creep fed and non-creep fed calves for sire x sex interactions. A significant sire x management unit interaction was found for birth weight in three-quarter Simmental calves, but not in half Simmental calves. Sire x sex interactions were significant in all analyses.

The effects of sex and sire were investigated by Bradley et al. (1966) in 34 Hereford and 33 Hereford x Red Poll steer and heifer calves sired by two Hereford sires. Interactions between sex and sire

and between sex and breed of dam were found to be small and not significant for birth weight. Ellis et al. (1965), however, found sex x breed or cross effects to be very important ( $P < .01$ ).

Records of Angus and Hereford calves sired over several years were analyzed by Kress and Webb (1972). Interactions between sex and year, dam, and sires within years were not significant for birth weight.

Pahnish et al. (1964) reported that the heritability of birth weight was .32 for bulls and .14 for heifers in a study involving 350 heifer and 370 bull calves produced over a 4 year period.

Weaning Weight and Preweaning Gain. Burnside et al. (1972) fed 48 pairs of male Holstein fraternal twin calves two different rations. Some pairs were fed uniformly and others were split between the two rations. No evidence was found for a pair x ration interaction in growth traits.

Heritability estimates for weaning weight at 240 days in two herds of similar breeding were calculated by Rollins and Wagnon (1956). One herd was supplemented; the other was not. They concluded that differences in nutritive levels between the two herds did not influence heritability.

Brinks et al. (1967) reported significant ( $P < .05$ ) line of sire x year effects for heifers but not for bulls in weaning weight. Turner

and MacDonald (1969) also found significant ( $P < .05$ ) breed of sire x year and breed of sire x mating type interactions for weaning weight, however, the ranking of the mating types generally was the same for each breed of sire. Similarly, Edwards et al. (1966) reported significant sire x year and sire x rearing method interactions for growth traits.

Woodward and Clark (1950) found no significant sire x location interaction for weaning weight in Montana. Butts, et al. (1971) found highly significant genotype x location-origin interactions between Montana and Florida. Nunn et al. (1978) also reported significant sire x region interactions over several regions of the United States.

Data on 228 male calves sired by 17 Flechvieh and 3 Gelbvieh sires in West Germany (144) and Central Texas (84) were analyzed by Aken et al. (1976). Calves in West Germany were purebred while the calves in Texas were crossbred. The sire x location interaction was not significant for weight at 196 days of age.

Sire x management unit effects were found to be significant for weaning weight and preweaning gain in three-quarter Simmental calves but not for half Simmental calves by Friedrich (1977).

Wilson et al. (1972) studied herd, sire, and herd x sire interaction effects in data from progeny tests of Angus and Hereford bulls, each replicated in different herds of each breed. Weaning records

obtained from 976 steers sired by 55 bulls. The herd x sire interaction was not significant.

Many researchers have investigated genotype x sex interactions in preweaning growth traits. Knapp et al. (1942) studied data collected in Montana over 3 years. They observed one sire which produced heifers averaging 12 kg heavier than male calves and this sire produced proportionally heavier heifers than steers when compared to other bulls. There was no significant sire x sex interaction for weaning score.

Weaning weights of 419 steers and 444 heifer calves were studied by Koger and Knox (1945) under range conditions over several years. No sire x sex interaction was observed for weaning weight. The sires in this study were related which led the authors to conclude that variation in sires was probably less than what would be obtained from a group of unrelated sires.

Bradley et al. (1966) reported no significant sire x sex interactions for preweaning average daily gain, weaning weight, and weaning type score. Edwards et al. (1966), however, reported important sire x sex interactions for growth traits. Similarly, Kress and Webb (1972) found significant sire x sex interactions for preweaning average daily gain in Angus calves ( $P < .01$ ) and for preweaning average daily gain and weaning weight in Hereford calves ( $P < .05$ ), with significant changes in rank of sires occurring. Friedrich (1977) also reported

significant sire x sex interactions for preweaning gain and weaning weight.

Pahnish et al. (1961) studied sex and sire influences on weaning weights of 329 bull and 332 heifer calves produced on two ranches over 6 years. The sire x sex interaction within years and ranches was not significant. Heritability of weaning weight was found to be .28 for bulls and .57 for heifers. In a later study, Pahnish et al. (1964) reported heritability of weaning weight to be .05 for bulls and .23 for heifers.

Sex differences in response to inbreeding in a single closed line of Hereford cattle were reported by Brinks et al. (1963). Data included 1,041 male and 986 female calves produced at the U. S. Range Livestock Experiment Station in Miles City, Montana. Partial and standard partial regressions, calculated within sire-year subclasses, indicated that inbreeding of the calf had a more pronounced effect on females and inbreeding of the dam had a greater effect on males.

In a crossline experiment involving five inbred lines of Hereford cattle, Brinks et al. (1967) reported that greater heterosis was exhibited for preweaning daily gain and weaning weight in heifers than in bulls.

Harwin et al. (1966) analyzed weaning weight records of 1,627 inbred linecross Hereford calves. A significant sex x mating system interaction was found due to the greater expression of heterosis in heifers than in bulls.

Wilson et al. (1969) analyzed data from 80 steers and 94 heifers born from 1963 to 1966. The calves were all the progeny of 11 Polled Hereford bulls out of Angus-Holstein dams. A significant ( $P < .01$ ) sire x sex interaction in 205-day weight was observed with a true change in rank among the sires between sexes.

Sire x sex interactions and sex differences for preweaning growth rate and weaning weight were investigated by Tanner et al. (1969) using data from 487 bull, steer, and heifer calves sired by 24 bulls. No significant sire x sex interactions were observed for growth traits.

Postweaning Traits. Hereford (3/4)-Brahman (1/4) crossbred calves were compared to straightbred Hereford calves by Rollins et al. (1964) in the Imperial Valley of California which is characterized by extremely hot summers and mild winters. The crossbred calves outgained the straightbred calves in the summer on pasture and in the feedlot. The straightbred calves, however, performed best during the fall and winter. This was described as a 'breed' x season interaction.

Pani et al. (1973) investigated sire x year interactions in postweaning traits of 411 male and 465 female yearling sired by 17 bulls in Missouri. Traits studied were average daily gain in the feedlot, gain on pasture, conformation score, and weights at 392 and 550 days of age. No sire x year interactions were significant except for yearling weight in bulls.

Averdunk et al. (1968) studied the daily weight gains from 140 days of age to 500 kg live weight on 97 progeny of nine sires at two testing stations. The sire x station interaction was not significant.

One hundred-two progeny of five AI sires were used by Dillard et al. (1964) to study sire x location interaction effects between two locations in North Carolina. Half the cattle at each location were fed in a feedlot and half on pasture. A total of 25 traits and measurements were considered and in general little evidence of interaction between sires and locations or sires and rations was found.

In a similar experiment in North Carolina involving three locations and two different rations, Ahlschwede et al. (1969) reported sire x ration and sire x location interactions effects were both not significant. Sires constituted a wide sample of the Hereford breed and the rations were very different.

Aken et al. (1976) reported a significant sire x location interaction for weight at 364 days of age but not at 280, 420, or 500 days of age. The one significant interaction did not involve a change in rank of the sires and when sires within breed x location was substituted for the sires x location interaction in the model there were no significant interactions.

Butts et al. (1971) reported important ( $P < .01$ ) sire x location-origin effects for yearling weight, and Woodward and Clark (1950) reported significant ( $P < .05$ ) sire x location interactions for feedlot gain and efficiency.

Wilson et al. (1972) found sire x herd interaction effects not to be important for postweaning traits.

Progeny of 34 sires were compared by Lagos and Cartwright (1963) under two feeding regimes in two experiments for weight gain over 140 days. In the first experiment, 56 Santa Gertrudis heifers from 10 sires were split by sire into a high concentrate feedlot group or on pasture with a concentrate supplement. The second experiment involved 67 Hereford steers from nine sires and 120 F<sub>1</sub> Brahman-Hereford steers from 15 sires split by breed and sire into two feedlot groups based on high and low concentrate rations. All sire x ration interactions were not significant in both experiments, however, the additive variance increased under the higher plane of nutrition.

Warwich et al. (1964) studied the response of 25 pairs of identical twins to two rations (high and low concentrate) in gains to 800 pounds. Significant ( $P < .05$ ) pair x ration interactions were reported for average daily gain and feed efficiency.

In a similar study using identical and fraternal Holstein twins assigned to high and low concentrate rations, Freeman (1969) found pair x ration interactions small for growth traits.

Kress et al. (1971) collected data on 15 sets of identical twins and 14 sets of fraternal twins fed on high and low concentrate rations. Set x diet interactions were not significant for 10 body measurements taken from 210 to 701 days of age. Genetic correlations were all

positive and near one suggesting little change in rank of sets between diets.

Postweaning gains of 42 groups of progeny (408 performance tested bulls and 402 limited fed heifers) were studied by Brown and Gacula (1962). Management and sex were confounded and referred to as 'environment'. The sire x environment interaction was not significant for average daily gain.

Urick et al. (1968) reported on a followup study of the preweaning traits published by Brinks (1967). Data was collected from 229 bulls and 226 heifers at Miles City, Montana, to estimate the amount of heterosis in postweaning traits resulting from the crossing of five lines of inbred Herefords. Heifers showed more heterosis than bulls for weights at all ages.

Thrift et al. (1970) tested 78 progeny of eight bulls on a postweaning feeding trial. The sire x sex interaction was not important for growth traits.

Sire x sex and breed of dam x sex interactions were found to be not important for postweaning gain and final weight by Bradley et al. (1966). On the other hand, Knapp et al. (1942) found a significant sire x sex interaction for average daily gain.

Age and weight at puberty were studied by Wiltbank et al. (1969) in Angus, Hereford, and crossbred heifers raised under two different feed levels. Crossbreds on the high nutritional level were heaviest,

but lightest at the low level producing a significant ( $P < .01$ ) breed x nutrition interaction for weight at puberty.

Carcass Traits. Thrift et al. (1970), Tanner et al. (1970), and Wilson et al. (1969) all found sire x sex interactions not important for carcass traits.

Records of three calf crops produced by Hereford and Charolais cows bred to Hereford and Charolais bulls were studied by Klosterman et al. (1968). Half of the calves were creep fed, fattened immediately following weaning and slaughtered at 14 months of age. The other half of the calves were not creep fed, wintered, grazed for about 60 days, fattened in dry lot and slaughtered at 20 months of age. Significant interactions were found between breed and management system for weight of edible portion produced per day of age and in marbling score.

Forty-eight pairs of Holstein fraternal twins raised on two rations were used by Batra et al. (1973) to study ration x pair interactions for loin circumference, loin width, thurl width, pelvis length, and length from stifle to stifle. Carcass weights were also taken. No significant ration x pair interactions were found for the live measurements and the only important interactions in carcass traits were for percent kidneys, percent fat in shoulder, kidneys and minor cuts and bone in flank and breast.

## MATERIALS AND METHODS

Data used for this study were supplied by the American Simmental Association from their 1977 sire evaluation program. These records were the progeny records of Simmental sires used primarily by artificial insemination throughout the United States, representing 3 years data (1974 to 1976).

Two basic data sets were used, and were identified as A and B. The A-data set was divided into geographic regions and edited on a basis similar to that of an earlier study made at Montana State University by Nunn et al. (1978), in order to specifically compare analyses made over different years. The United States was divided into four regions as outlined in table 1.

In the B-data sets the United States was divided into geographic regions on the basis of elevation, soil type, and climate differences (Austin, 1972). Regions were outlined so that each region was separated by considerable distance from other regions to be as distinct from all other regions as possible. After consideration of the number of records available in each state four major region designations were made. It was not possible to outline regions in the far West and the East because of insufficient record numbers in both areas. Region designations were as follows: Montana, Midwest (Iowa and Illinois), Texas, and Southeast (Louisiana, Mississippi, Alabama, and Georgia).

TABLE 1. REGION DESIGNATIONS FOR THE A-DATA SET.

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|          |                                                                                     |
|----------|-------------------------------------------------------------------------------------|
| Region 1 | Minnesota<br>Iowa<br>Missouri<br>North Dakota<br>South Dakota<br>Nebraska<br>Kansas |
| Region 2 | Oklahoma<br>Texas                                                                   |
| Region 3 | Montana                                                                             |
| Region 4 | Idaho<br>Wyoming<br>Colorado<br>New Mexico<br>Arizona<br>Utah<br>Nevada             |

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Each region was further subdivided into two subregions on the basis of the same criteria as the major regions and with consideration for the number of records available in each region. This was accomplished by use of the zip code numbers corresponding to the owner location. Basically, all region subdivisions were made between East and West (figure 3).

Each region was analyzed separately to assess any subregion effects and/or interactions between sires and subregions. On the basis of the results from these analyses, modifications of the major regions were made to make each region as distinct as possible from other major regions and as uniform within as possible.

If regions are actually composed of two or more subregions which are very different, interpretation of any sire x region interaction effects becomes difficult. For example, it is possible that subregion effects opposite in sign (or direction) could be averaged when considered as only one region and could yield reduced region and/or sire x region interaction effects.

Each possible combination of two major regions was then analyzed to assess sire x region interaction effects.

Since the data were composed of field records collected without supervision, completeness of the records varies and the records may be subject to greater error than data collected in a designed and controlled experiment. For these reasons various edits were

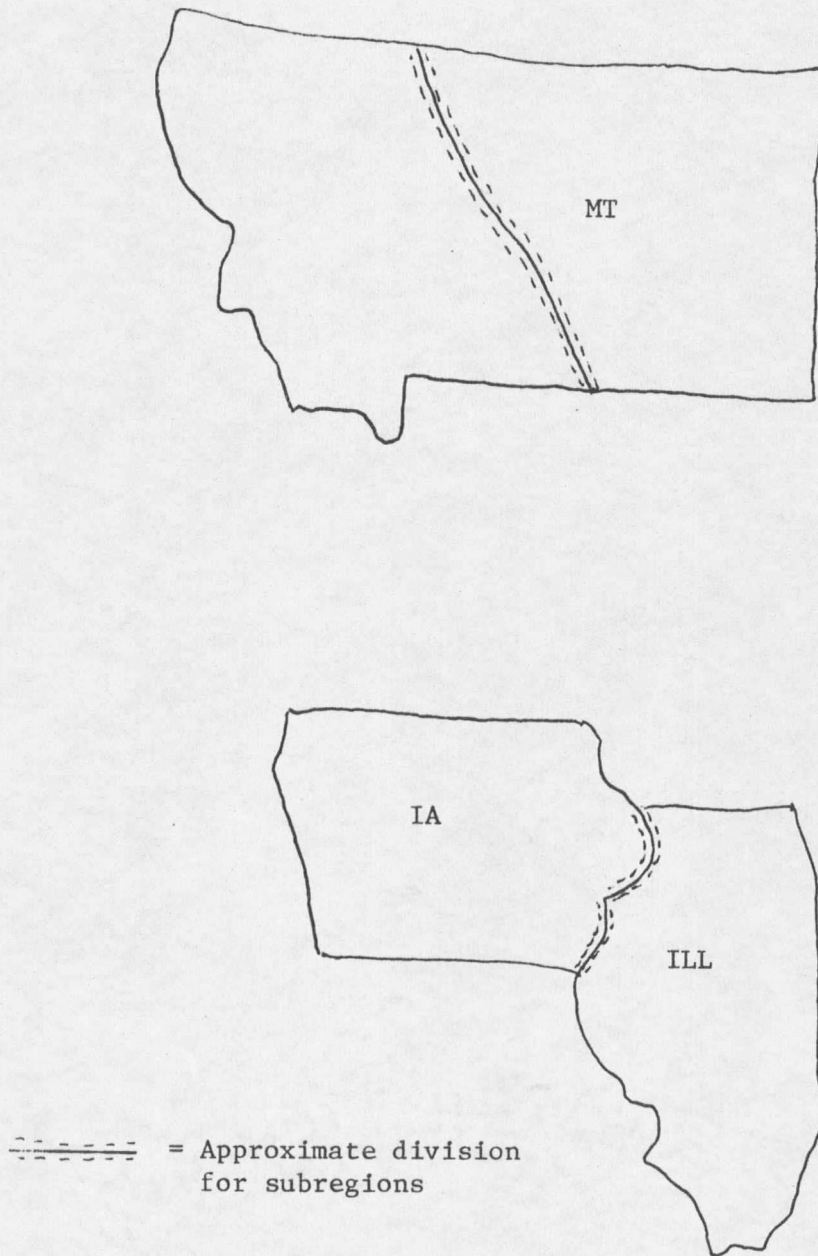


Figure 3. Region designations and subdivisions for the B-data sets.

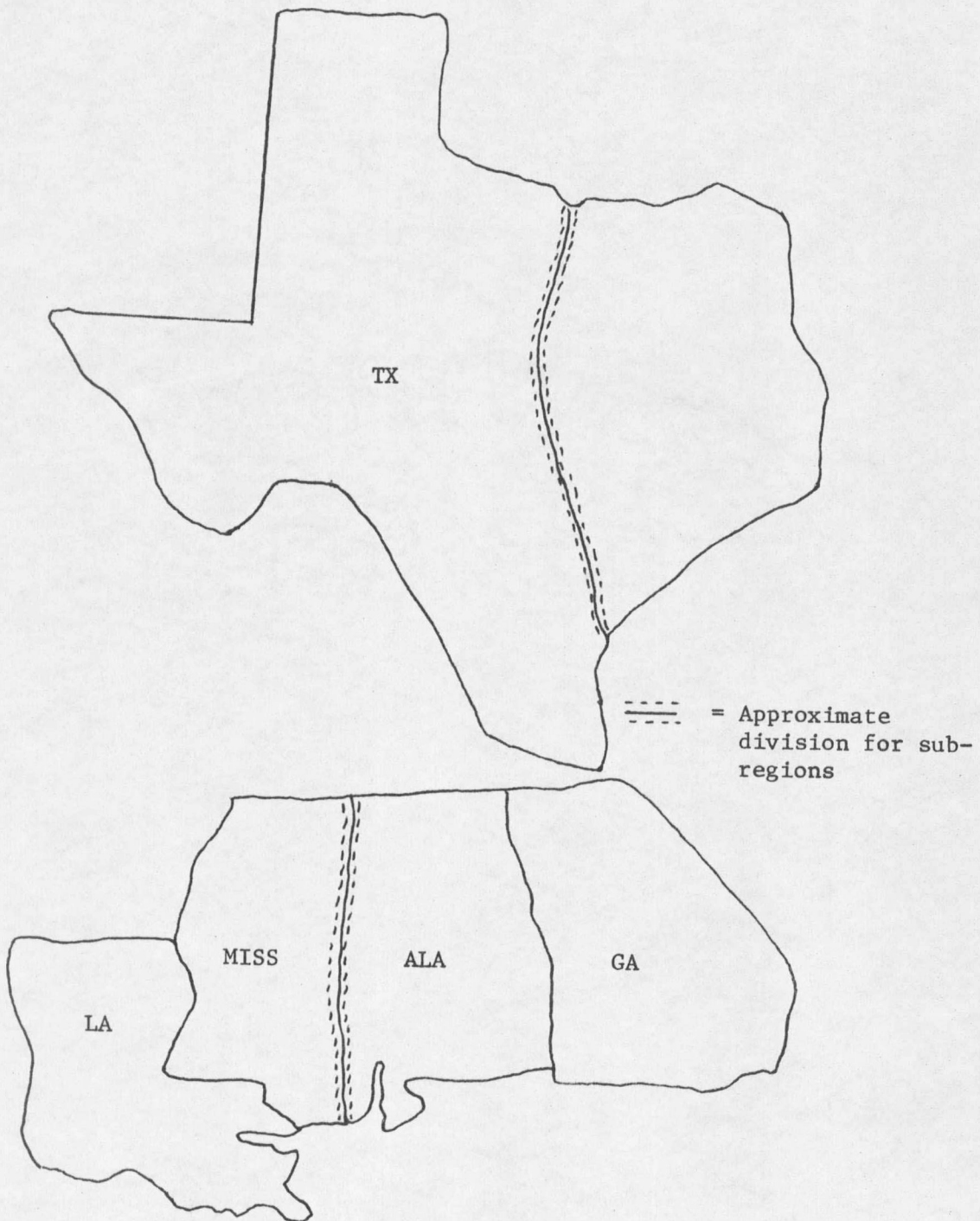


Figure 3. (Continued)

performed on the data in an attempt to remove as many of these problems as possible. These edits are summarized in table 2.

In both data set types, records were excluded if the owner number did not match the breeder number. This was to insure that calves were weaned in the same herd they were born in. In an effort to eliminate transcribing and keypunching errors, records were deleted if weaning weight was less than 91 or greater than 680 kilograms. All standardized weights were deleted. Records from calves weaned at less than 160 days or greater than 250 days of age were deleted because calf growth is not linear outside of this range (Cunningham and Henderson, 1965). Age of dam was calculated according to B.I.F. (1976) standards and records having ages of dam less than 1 year 9 months were deleted. Records from calves not raised by their own dams were deleted. Steer data was excluded because of insufficient numbers of steer records.

Progeny were assigned to management units (herds) on the basis of owner number and weaning weigh-date of the calf. Therefore, variation due to herd included effects of management (including nutrition), season of birth, breed of dam, and year. Each management unit was required to contain the progeny of at least two sires with one being a reference sire. A reference sire is a sire that has performance data through the weaning phase from more than 300 progeny located in 25 or more management units (American Simmental

TABLE 2. EDITS OF THE DATA

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All Data Sets

1. Non-matching breeder and owner numbers.
2. Weaning age < 160 or > 250 days.
3. Standardized weights and weights < 91 or > 680 kg.
4. Age of dam < 1 year 9 months.
5. Calves not raised by own dams.
6. Herds with < 2 sires or with no reference sire.
7. Calves not 1/2- or 3/4-Simmental.
8. Records previous to 1974.

A-data Set

1. Steers.
2. Sires not represented in at least 3 regions by 20 progeny in each region.

B-data Set

1. Steers and bulls.
  2. Sires not represented by at least 15 progeny in each region.
-

Association, 1977). Inclusion of a reference sire in every herd was to insure that several sires would be represented in the same herds. Two sires per herd were required in order to reduce the confounding of sire effects with herd effects.

The A-data set contained four age of dam classifications: 2, 3, 4, and 5 years and over. The B-data sets contained three age of dam classifications: 2, 3, and 4 years and over, which are the same as the classifications used by the American Simmental Association (1977) for age of dam adjustments for weaning weight.

The A-data set included records from 1/2- and 3/4-Simmental bulls and heifers. The number of bull records was far outnumbered by the number of heifer records and it is very likely that bull records represented considerable selection. To avoid any influence of this selection plus possible confounding of sex effects with herd effects, bull records were excluded from the B-data sets. Preliminary cell counts indicated that percent Simmental was severely confounded with herd classification, therefore 1/2- and 3/4-Simmental records were analyzed separately in the B-data sets. Records from calves greater than 3/4-Simmental were deleted due to insufficient records of this type in both data set types.

In order to obtain a better estimate of the sire x region interaction variance, records from sires were included only if the sire was represented by at least 20 progeny in three of the four

regions in the A-data set. In the B-data sets, each sire was required to be represented by at least 15 progeny in each region in each analysis. Because this edit was performed before the 'herd edit', which required two sires per herd with a reference sire, a few sires in each analysis had less than 15 progeny per region.

After editing, the Southeast region in the B-data sets did not have enough sires represented by sufficient progeny to be analyzed, so the Southeast region was excluded from further consideration. The final composition of each data set is listed in table 3.

The A-data sets were analyzed by mixed model least-squares procedures as outlined by Harvey (1975). The statistical model for this analysis (Model A) was:

$$Y_{ijklmno} = \mu + R_i + H/R_{ij} + S_k + SXR_{ik} + X_l + A_m + P_n + b(W_{ijklmno} - W_{.....}) + E_{ijklmno}$$

where:  $Y_{ijklmno}$  = weaning weight of the  $o^{th}$  calf of the  $j^{th}$  herd within the  $i^{th}$  region,  $k^{th}$  sire,  $l^{th}$  sex,  $m^{th}$  age of dam class, and the  $n^{th}$  percent Simmental.

$\mu$  = overall mean

$R_i$  = effect of the  $i^{th}$  region

$H/R_{ij}$  = effect of the  $j^{th}$  herd within the  $i^{th}$  region

$S_k$  = effect of the  $k^{th}$  sire

TABLE 3. COMPOSITION OF THE DATA SETS

| Data Set                            | Number of<br>observations |
|-------------------------------------|---------------------------|
| A-data set (total)                  | 23260                     |
| Region 1                            | 11153                     |
| 2                                   | 4827                      |
| 3                                   | 4479                      |
| 4                                   | 2801                      |
| B-data sets - 3/4-Simmental         |                           |
| Within Montana (total)              | 3109                      |
| East                                | 1733                      |
| West                                | 1376                      |
| Within Midwest (total)              | 993                       |
| Iowa                                | 396                       |
| Illinois                            | 597                       |
| Within Texas (total)                | 1637                      |
| East                                | 782                       |
| West                                | 855                       |
| Between Montana and Texas (total)   | 3471                      |
| Montana                             | 2328                      |
| Texas                               | 1143                      |
| Between Montana and Midwest (total) | 4391                      |
| Montana                             | 2895                      |
| Midwest                             | 1496                      |
| Between Midwest and Texas (total)   | 2182                      |
| Midwest                             | 1246                      |
| Texas                               | 936                       |
| B-data sets - 1/2 Simmental         |                           |
| Between Montana and Midwest (total) | 1206                      |
| Montana                             | 660                       |
| Midwest                             | 546                       |

TABLE 3. (CONTINUED)

| Data Set                          | Number of<br>observations |
|-----------------------------------|---------------------------|
| Between Montana and Texas (total) | 1044                      |
| Montana                           | 553                       |
| Texas                             | 491                       |
| Between Midwest and Texas (total) | 974                       |
| Midwest                           | 479                       |
| Texas                             | 495                       |

$SXR_{ik}$  = interaction of the  $k^{th}$  sire with the  $i^{th}$  region

$X_1$  = effect of the  $1^{th}$  sex

$A_m$  = effect of the  $m^{th}$  age of dam

$P_n$  = effect of the  $n^{th}$  percent Simmental

$b$  = partial regression coefficient for weaning  
weight on age at weaning for calf  $W_{ijklmno}$

$W_{ijklmno}$  = continuous variable for age at weaning of the  $o^{th}$   
calf of the  $j^{th}$  herd, etc.

$E_{ijklmno}$  = random error

The effects of herd/region ( $H/R_{ij}$ ), sires ( $S_k$ ), sire x region interaction ( $SXR_{ik}$ ), and random error ( $E_{ijklmno}$ ) were regarded as random with the following assumptions:  $H/R_{ij} = N(0, \sigma_{H/R}^2)$ ;  $S_k = N(0, \sigma_S^2)$ ;  $SXR_{ik} = N(0, \sigma_{SXR}^2)$ ;  $E_{ijklmno} = N(0, \sigma_E^2)$ . All other effects were regarded as fixed.

The expectations of the mean squares for the mixed model with unequal subclass numbers are shown in table 4.

TABLE 4. EXPECTED MEAN SQUARES FOR MODEL A

| Source        | E.M.S.                                                                         |
|---------------|--------------------------------------------------------------------------------|
| Region        | $\sigma^2_E + k_8\sigma^2_{S \times R} + k_9\sigma^2_{H/R} + k_{10}\sigma^2_R$ |
| Herd/region   | $\sigma^2_E + k_7\sigma^2_{H/R}$                                               |
| Sires         | $\sigma^2_E + k_5\sigma^{2a}_{S \times R} + k_6\sigma^2_S$                     |
| Sire x region | $\sigma^2_E + k_4\sigma^2_{S \times R}$                                        |
| Sex           | $\sigma^2_E + k_3\sigma^2_X$                                                   |
| Age of dam    | $\sigma^2_E + k_2\sigma^2_A$                                                   |
| Percent       | $\sigma^2_E + k_1\sigma^2_P$                                                   |
| Residual      | $\sigma^2_E$                                                                   |

<sup>a</sup>Not in expectation with equal subclass numbers.

The B-data sets were also analyzed by mixed model least-squares procedures (Harvey, 1975). The statistical model used for these analyses (Model B) was:

$$Y_{ijklm} = \mu + R_i + H/R_{ij} + S_k + SXR_{ik} + SXH/R_{ijk} + A_1 + b(W_{ijklm} - W_{.....}) + E_{ijklm}$$

where:  $Y_{ijklm}$  = weaning weight of the  $m^{th}$  calf of the  $j^{th}$  herd within the  $i^{th}$  region,  $k^{th}$  sire, and  $l^{th}$  age of dam class.

$\mu$  = overall mean

$R_i$  = effect of the  $i^{th}$  region

$H/R_{ij}$  = effect of the  $j^{th}$  herd within the  $i^{th}$  region

$S_k$  = effect of the  $k^{th}$  sire

$SXR_{ik}$  = interaction of the  $k^{th}$  sire with the  $i^{th}$  region

$SXH/R_{ijk}$  = interaction of the  $k^{th}$  sire with the  $j^{th}$  herd within the  $k^{th}$  region

$A_1$  = effect of the  $l^{th}$  age of dam class

$b$  = partial regression coefficient for weaning weight on age at weaning for calf  $W_{ijklm}$

$W_{ijklm}$  = continuous variable for age of the  $m^{th}$  calf of the  $j^{th}$  herd, etc.

$E_{ijklm}$  = random error.

The effects of herd/region ( $H/R_{ij}$ ), sire ( $S_k$ ), sire x region interaction ( $SXR_{ik}$ ), sire x herd/region interaction ( $SXH/R_{ijk}$ ), and random error ( $E_{ijklm}$ ) were regarded as random with the following assumptions:  $H/R_{ij} = N(0, \sigma_{H/R}^2)$ ;  $S_k = N(0, \sigma_S^2)$ ;  $SXR_{ik} = N(0, \sigma_{SXR}^2)$ ;  $SXH/R_{ijk} = N(0, \sigma_{SXH/R}^2)$ ;  $E_{ijklm} = N(0, \sigma_E^2)$ . All other effects were regarded as fixed.

Sire effects were analyzed in the least-squares program as 'fixed' effects with variance components calculated by the program from the inverse elements of the reduced coefficient matrix. The expectation of the region mean square is not the same when sires are fixed as when random, however this mean square is not used again in the analysis. The error term for the region mean square is the herd/region mean square in both models. The expected mean squares with equal subclass numbers for the sire and sire x region interaction effects remain the same whether sires are fixed or random. However, with unequal subclass numbers the sire variance component is biased due to the interaction with the fixed region effect in the mixed model when sires are random. This bias is due to linear functions of the fixed effects contained in the sire mean square and any correlations between sires and the fixed effects (Harvey, 1970; Searle and Henderson, 1961). Because editing was done in such a manner as to increase the accuracy of the estimate of the sire x region interaction (i.e., minimize any correlation of sire effects

with region effects), bias in the sire variance component is outweighed by the severe biasing that would be present in the herd/region and sire x herd/region interaction variance components if sires were, instead, fit as a random variable.

When the analysis is made using sires as fixed, biases in the random variance components (H/R and SXH/R) are adjusted for by the mixed model program. These biases are due to linear functions of the fixed effects contained in the random variance components and any correlations between random and fixed effects in the data (Harvey, 1970; Searle and Henderson, 1961).

This procedure (fitting sires as fixed) more accurately represents the true state of the data for several reasons. First, a limited number of sires qualified after editing in any of the analyses. Second, sires that qualified after editing were generally sires that had produced tremendous numbers of progeny in the 3 years analyzed, so to some extent represent a selected group of the sires actually in use in the Simmental breed and hence are not truly a representative or random sample. This fact is born out to some extent by the low sire variances exhibited in the data which will be discussed later. Third, despite editing, herd effects were correlated with fixed effects in many instances, especially in those herds having small numbers of progeny, plus each sire was represented in only a small fraction of the herds used. By fitting sires as a

fixed effect, these correlations (for example, correlations between sires and herds) were adjusted for in the herd/region and the sire x herd/region interaction variance component calculations by the mixed model program. Finally, Harvey's (1975) mixed model programs, at present, do not allow inclusion of two random effects, one of which interacts with a fixed effect. Therefore, the only way to fit sires as a random variable would be to exclude the herd effects from the model. This procedure would require the assumption that all variation due to herds would be reflected in the error term. With field data and unequal subclass numbers this assumption is not justified, since herd effects are correlated with fixed effects in the data.

The expectations of the mean squares for the mixed model with unequal subclass numbers for model B are shown in table 5.

Variance components and their coefficients were computed as described by Harvey (1975) for each of the random effects in both models. In model A, the total variance was estimated as:

$$\sigma_T^2 = \sigma_{H/R}^2 + \sigma_S^2 + \sigma_{SXR}^2 + \sigma_E^2$$

The total variance in model B was estimated as:

$$\sigma_T^2 = \sigma_{H/R}^2 + \sigma_S^2 + \sigma_{SXR}^2 + \sigma_{SXH/R}^2 + \sigma_E^2$$

TABLE 5. EXPECTED MEAN SQUARES FOR MODEL B

| Source             | E.M.S.                                                                                                               |
|--------------------|----------------------------------------------------------------------------------------------------------------------|
| Region             | $\sigma^2_E + k_{10}\sigma^2_{S \times H/R} + k_{11}\sigma^2_{S \times R} + k_{12}\sigma^2_{H/R} + k_{13}\sigma^2_R$ |
| Herd/region        | $\sigma^2_E + k_8\sigma^2_{S \times H/R} + k_9\sigma^2_{H/R}$                                                        |
| Sires              | $\sigma^2_E + k_5\sigma^2_{S \times H/R} + k_6\sigma^{2a}_{S \times R} + k_7\sigma^2_S$                              |
| Sire x region      | $\sigma^2_E + k_3\sigma^2_{S \times H/R} + k_4\sigma^2_{S \times R}$                                                 |
| Sire x herd/region | $\sigma^2_E + k_2\sigma^2_{S \times H/R}$                                                                            |
| Age of dam         | $\sigma^2_E + k_1\sigma^2_A$                                                                                         |
| Residual           | $\sigma^2_E$                                                                                                         |

<sup>a</sup>Not in expectation with equal subclass numbers.

In each analysis genetic correlations of the sires' progeny performance among the regions were calculated according to:

$$rg_{SXR} = \frac{\frac{\sigma_S^2}{S} - \frac{1}{k} \frac{\sigma_{SXR}^2}{S}}{\frac{\sigma_S^2}{S} + \frac{k-1}{k} \frac{\sigma_{SXR}^2}{S}}$$

as presented by Yamada (1962), where k is the number of regions in the mixed model analysis. Negative estimates of variance components were assumed to be zero for these calculations.

In the B-data sets genetic correlations of the sires' progeny performance among herds within regions were calculated according to:

$$rg_{SXH/R} = \frac{\frac{\sigma_S^2}{S}}{\frac{\sigma_S^2}{S} + \frac{\sigma_{SXH/R}^2}{S}}$$

as presented by Dickerson (1962).

If the interaction mean square is not significant, the usefulness of genetic correlation estimates is limited. When the interaction mean square is not significant the variance due to the interaction then becomes more correctly interpreted as sampling error. For example, if the sire variance component is small, the correlation estimate can be radically affected by small changes in the size of the interaction variance.

The sampling variance of the genetic correlation coefficient with only two environments in the model was calculated according to:

$$V_{rg} = \frac{[nt(1-rg^2) + (1-t)]^2 + rg^2(1-t)^2}{(N-1)n^2t^2} + \frac{rg^2(1-t)^2}{N(n-1)n^2t^2}$$

and in more than two environments according to:

$$V_{rg} = \frac{2\{[1-t + nt(1-rg^2)][1 + (p-1)rg]^2 + (p-1)rg^2(1-t^2)\}}{(N-1)p(p-1)n^2t^2} + \frac{2rg^2(1-t)^2}{N_{pn}^2(n-1)t^2}$$

as presented by Robertson (1959), where:

N = number of sires

n = k-value for the sire x environment interaction variance component

t = intraclass correlation, assumed to be the same in all environments and calculated as:

$$t = \frac{\sigma_S^2}{\sigma_T^2} \quad (\text{Falconer, 1960})$$

rg = genetic correlation

p = average number of environments (i.e., herds) that each sire is represented in

When two regions are fit in the model, the average number of herds in which each sire is represented was estimated as:

$$p = \frac{k_S}{k_{SXH/R}(2)}$$

$k_S$  = k-value for the sire variance component

$k_{SXH/R}$  = k-value for the sire x herd/region variance component

To further evaluate the sire x region interaction effects in the B-data sets, rank-order and residual correlations (Snedecor and Cochran, 1967) between the least-squares sire x region interaction means for each sire in each region were calculated in the B-data sets.

To evaluate the practical importance of any sire x region interactions in the B-data sets each sire was ranked in each region within each analysis on the basis of least-squares sire x region interaction means, and the percent of the sires ranked in the top third of the sires in one region and in the bottom third in the other region was calculated. The average difference between the lowest sire mean in the top third and the highest sire mean in the bottom third of the rankings was calculated to help further evaluate the practical implications of any interactions. This obviously is related to the size of the sire variance and the accuracy with which each sire mean is estimated.

## RESULTS AND DISCUSSION

### A-data Set

The purpose of performing the A-data set analysis was to compare more recent data to the years studied by Nunn et al. (1978). Procedures used by Nunn et al. (1978) were duplicated in the analysis of this data set as close as possible.

The least-squares analysis of variance for the A-data set is presented in table 6. All effects in the model were highly significant. Least-squares means for the regions, sexes, age of dams, and percent Simmental are presented in appendix table 1. Weaning weights were highest in the western regions, and lowest in the South. Bull calves averaged 19 kg heavier than heifers at weaning. Weaning weights increased with age of dam with little difference after 4 years of age. Three-quarter-Simmental calves averaged 17 kg more than 1/2-Simmental calves.

Variance components are presented in table 7. The sire variance component composed approximately 1% of the total random variance. The sire x region interaction variance component comprised less than .2% of the total variance and was less than 1/5 the size of the sire component. The herd/region variance component was by far the most important source of variation for weaning weight.

The estimate of the genetic correlation of the sires' progeny performance among the regions was calculated to be .84 with a standard error of .2. Robertson (1959) proposed that a genetic

TABLE 6. LEAST-SQUARES ANALYSIS OF VARIANCE FOR THE A-DATA SET

| Source            | df    | Mean square (kg <sup>2</sup> ) |
|-------------------|-------|--------------------------------|
| Region            | 3     | 58412**                        |
| Herd/region       | 3171  | 4394**                         |
| Sires             | 22    | 3545**                         |
| Sex               | 1     | 834705**                       |
| Age of dam        | 3     | 232009**                       |
| Percent Simmental | 1     | 264540**                       |
| Sire x region     | 66    | 888**                          |
| Weaning age       | 1     | 2993816**                      |
| Residual          | 19991 | 496                            |

\*\*P<.01.

TABLE 7. VARIANCE COMPONENT ESTIMATES FROM THE A-DATA SET

| Source        | k-value | Variance<br>component (kg <sup>2</sup> ) | Percent of<br>total variance |
|---------------|---------|------------------------------------------|------------------------------|
| Herd/region   | 7.0     | 553.1                                    | 52.1                         |
| Sires         | 297.3   | 10.2                                     | 1.0                          |
| Sire x region | 213.8   | 1.8                                      | .2                           |
| Residual      | -       | 496.3                                    | 46.8                         |
| Total         | -       | 1061.4                                   | 100.1                        |

$$rg_{SxR} = .84 \pm .2.$$

correlation less than .8 is of biological importance. A value of .84 suggests that no important changes in rank of the sires occurred among the regions. This fact was verified by ranking the least-squares sire x region means in each region (appendix table 3), which showed that only 3 sires (13%) ranked in the top third of one region and in the bottom third of another region.

Least-squares constants for the sire effects ranged from -7.8 to 7.5 kg, and the constants for the sire x region interaction effects ranged from -10.7 to 10.5 kilograms. Least-squares means for the sire and sire x region interaction effects are listed in appendix tables 2 and 3. Variances of the sire x region interaction means within each region were 22.2, 35.2, 19.2 and 35.1 kg<sup>2</sup> for regions 1, 2, 3, and 4, respectively, and were not significantly heterogenous.

Results reported by Nunn et al. (1978), using the same region designations and procedures, were quite similar. The sire and sire x region interaction variance components composed 2 and .7% of the total variance, in this earlier data, which were slightly larger than the present study. The genetic correlation of the sires' progeny performance among the regions was .73.

The results of both analyses indicated that sire x region interaction effects were consistently present, but were not of such magnitude as to bias sire selection. The standard error of the genetic correlation overlapped unity, indicating that important

changes in rank of the sires among the regions were not occurring. Sire x herd/region interactions may have inflated the sire x region interaction in this model, and may have been responsible for the significance of the sire x region interaction mean square. In a model which includes both interaction terms, the sire x herd/region interaction mean square is the correct error term for the sire x region interaction mean square. This inflation of the sire x region interaction was suggested strongly by the results of the B-data set analyses which are discussed later.

The numbers of progeny per region was very different between regions. Regions 1 and 4 were also very large geographic areas. These two facts make further interpretation of the interaction component difficult. Interactions involving region 4, with its small number of progeny and large area, could possibly represent interactions of specific sires with subregions (i.e., states) within region 4. The results from the within region analyses of the B-data sets would support this hypothesis. The possibility of averaging of the subregion effects within such large regions is also distinctly possible.

B-data Sets - Within Region Analyses (3/4-Simmental)

The purpose of the within region analyses was to evaluate any subregion effects within the major regions plus any sire x region interactions. As mentioned earlier the Southeast region was eliminated due to lack of sufficient record numbers after editing.

The least-squares analyses of variance for the within region data sets are shown in table 8. Herd/region, age of dam, weaning age, and the sire x herd/region interaction were highly significant in all three analyses. Region was important only in the within Texas analysis. Sires were highly significant within Montana and Midwest but not within Texas. The sire x region interaction was not important in any of the within region analyses.

Least-squares means for the fixed effects are presented in appendix table 4. Weaning weights generally increased with age of dam except within the Midwest where there was no difference between 2 and 3 year old dams. This was reflected in the smaller size of the age of dam mean square in the within Midwest analysis.

The highly significant difference between the subregions within Texas indicated that Texas was composed of at least more than one region. To avoid possible future difficulties in interpretation of interaction effects, the West-Texas subregion was excluded from future analyses. The West-Texas subregion was chosen because it had fewer records than the East-Texas region, and since the Southeast

TABLE 8. LEAST-SQUARES ANALYSES OF VARIANCE FOR THE WITHIN REGION  
B-DATA SETS (3/4-SIMMENTAL)

| Source             | Montana |                   | Midwest |         | Texas |          |
|--------------------|---------|-------------------|---------|---------|-------|----------|
|                    | df      | M.S. <sup>a</sup> | df      | M.S.    | df    | M.S.     |
| Region             | 1       | 348               | 1       | 705     | 1     | 30492**  |
| Herd/region        | 140     | 4765**            | 158     | 2165**  | 277   | 3564**   |
| Sires              | 31      | 1934**            | 13      | 1741**  | 21    | 643      |
| Sire x region      | 31      | 1017              | 13      | 848     | 21    | 347      |
| Sire x herd/region | 318     | 743**             | 220     | 484**   | 372   | 444**    |
| Age of dam         | 2       | 40631**           | 2       | 1827**  | 2     | 14505**  |
| Weaning age        | 1       | 308478**          | 1       | 76339** | 1     | 118929** |
| Residual           | 2584    | 486               | 584     | 365     | 941   | 362      |

<sup>a</sup>Mean Square (kg<sup>2</sup>).

\*\*P<.01.

region had to be excluded, it was hoped that the East-Texas subregion might better represent a hot, humid environment in contrast to the conditions of Montana and Midwest.

Variance components are presented in table 9. Herd/region was the most important source of variation in the model. The sire component of variance averaged approximately 3% of the total variance. The sire x region interaction variance component only comprised an average of 1% of the total variance.

Genetic correlation estimates of the sires' progeny performance among the two regions within the three analyses (table 10) were: .70, .71, and 1.0 for Montana, Midwest, and Texas, respectively. Standard errors calculated for Montana and Midwest were .2 and .3; therefore, confidence intervals for these genetic correlation coefficients overlapped unity. This indicated that the observed interactions of the sires' progeny mean performance among the regions could very well be interpreted as sampling error.

The intraclass correlation coefficient ( $t$ ) has a tremendous effect on the size of the sampling variance of the genetic correlation (Robertson, 1959). This is reflected in the calculation of the genetic correlation as well. If the sire variance component is small (which is directly related to  $t$ ) then the resulting genetic correlation coefficient can be much less than unity even if the interaction component is small and in fact has a mean square that is not

TABLE 9. VARIANCE COMPONENT ESTIMATES FROM THE WITHIN REGION ANALYSES (3/4-SIMMENTAL, B-DATA SETS)

| Source                | k-value | Variance component (kg <sup>2</sup> ) | Percent of total variance |
|-----------------------|---------|---------------------------------------|---------------------------|
| <u>Within Montana</u> |         |                                       |                           |
| Herd/region           | 15.7    | 272.5                                 | 31.8                      |
| Sires                 | 52.6    | 27.0                                  | 3.2                       |
| Sire x region         | 52.6    | 9.6                                   | 1.1                       |
| Sire x herd/region    | 4.2     | 61.0                                  | 7.0                       |
| Residual              | -       | 486.0                                 | 56.8                      |
| Total                 | -       | 856.1                                 | 100.0                     |
| <u>Within Midwest</u> |         |                                       |                           |
| Herd/region           | 5.4     | 334.9                                 | 40.6                      |
| Sires                 | 29.1    | 46.1                                  | 5.6                       |
| Sire x region         | 29.3    | 15.4                                  | 1.9                       |
| Sire x herd/region    | 1.9     | 62.5                                  | 7.6                       |
| Residual              | -       | 365.5                                 | 44.3                      |
| Total                 | -       | 824.4                                 | 100.0                     |
| <u>Within Texas</u>   |         |                                       |                           |
| Herd/region           | 5.2     | 615.9                                 | 60.0                      |
| Sires                 | 35.7    | 7.2                                   | .7                        |
| Sire x region         | 36.1    | -1.1                                  | 0.0                       |
| Sire x herd/region    | 2.0     | 41.9                                  | 4.1                       |
| Residual              | -       | 361.8                                 | 35.3                      |
| Total                 | -       | 1025.7                                | 100.1                     |

TABLE 10. GENETIC CORRELATION ESTIMATES FROM THE WITHIN REGION  
ANALYSES (3/4-SIMMENTAL, B-DATA SETS)

|            | Montana       | Midwest       | Texas         |
|------------|---------------|---------------|---------------|
| $r_{gSXR}$ | .70 $\pm$ .2  | .71 $\pm$ .3  | 1             |
| $r_{gSXR}$ | .31 $\pm$ 1.1 | .42 $\pm$ 1.9 | .15 $\pm$ 4.2 |

significant. Therefore, the interpretation of the F-test of the interaction mean square is consistent with the interpretation of the genetic correlation. Without calculating the standard errors of the genetic correlations, interpretation of these statistics would be much different since the values were less than .8, which is the value at which Robertson (1959) proposed interactions become important biologically.

Least-squares sire and sire x region interaction means are listed in appendix tables 5 and 6. Sire constants ranged from -19.8 to 17.6 kg and sire x region interaction constants ranged from -12.4 to 11.0 kilograms.

Rankings of the sires within each subregion indicated that 15, 14, and 9% of the sires ranked in the top third of one subregion and in the bottom third in the other subregion in Montana, Midwest, and Texas, respectively. Several of the sires showing this kind of rank change had lower progeny numbers than average and hence had larger standard errors associated with the sire x region interaction constants. The average difference between the lowest ranking sire in the top third and the highest ranking sire in the bottom third was 11.5, 9.0, and 6.0 kg for Montana, Midwest, and Texas, respectively. This is an indication of the practical importance of such rank changes. It should be noted that confidence intervals for the sire x region interaction means for many sires, however, would overlap these ranges.

Variances of the sire x region interaction means within each sub-region were: 84.5, 84.7; 189.5, 82.7; and 104.1, 33.2 for Montana, Midwest, and Texas, respectively. Variances for the within Texas analysis were significantly heterogeneous, which suggested that unequal genetic variances among the subregions might exist which would contribute to the interaction effects observed in this analysis (Dickerson, 1962).

Residual and rank correlations of the sire x region interaction means for the within region analyses are presented in appendix table 7. These estimates generally agree with the results of the rankings of the sire x region interaction means, indicating that changes in rank of the sires among subregions did occur with some consistency. These statistics, however, give little indication of the magnitude (i.e., kg) of the rank changes, especially the rank correlation coefficient. Interpretation of these correlations should be tempered by the results of the analysis of variances, which would say that such changes are best explained by sampling error.

The size of the sire x herd/region interaction variance components warrants considerable attention. In each analysis this interaction comprised a larger percent of the total variation than the sire component, more than twice as much within Montana and Texas. Genetic correlation estimates of the sires' progeny performance among herds within subregions (table 10) were: .31, .42, and .15 for Montana,

Midwest, and Texas, respectively. Estimates of the standard errors for these correlations were very high, reflecting the low intraclass correlation (t) and the small k-values for the sire x herd/region interaction variance component. Despite the size of these standard errors, the size of the interaction variance component would suggest that sire x herd interactions were of considerable magnitude. Since this interaction involved a random effect (herds), no sire x herd or herd means were output by the least-squares mixed model program. Interpretation of the sire x herd interactions, as classified in this study, was difficult primarily because the herd component reflects year, management, season, and breed of dam effects. In this study these effects were not separated.

B-data Sets - Between Region Analyses (3/4-Simmental)

Analyses of sire x region interaction effects in the between region B-data sets were done separately for 1/2- and 3/4-Simmental progeny. This was done for two reasons. First, preliminary cell counts indicated that herd effects (as designated by weaning weight) were severely confounded with percent Simmental, indicating that 1/2-Simmental calves were managed separately from 3/4-Simmental calves by ranchers raising cattle of both percentages. Second, by analyzing the two groups separately, some evaluation of the influence of breed of dam effects upon sire x region interactions might be made. It is possible that breed of dam effects may contribute to interaction effects to the extent that breed of dam differences may be confounded with region. Breed of dam effects should contribute more to 1/2-Simmental differences than 3/4-Simmental because a greater percent of the genotype is composed of or due to breeds other than Simmental.

Even though the West-Texas subregion was excluded in the between region analyses, records from East-Texas will still be referred to as Texas. Names of the analyses will be abbreviated as: MT-MW, MT-TX, and MW-TX for Montana versus Midwest, Montana versus Texas, and Midwest versus Texas, respectively. All three regions were not analyzed together because of the limited degrees of freedom available in the

least-squares mixed model program. If three regions were included at one time the number of sires included in the analysis would have to be reduced to be able to fit both sire and sire x region interaction effects.

The least-squares analyses of variance for the between region 3/4-Simmental B-data sets are presented in table 11. Herd/region, sires, age of dam, weaning age, and the sire x herd/region interaction were significant in all analyses. Region was significant in MT-TX and MW-TX but not in MT-MW. The sire x region interaction was not significant in any analysis, but did approach significance ( $P=.06$ ) in MW-TX.

Least-squares means for the fixed effects are presented in appendix table 8. Weaning weights in Montana and Midwest were significantly larger than in Texas, but no important difference was detected between Montana and Midwest. Weaning weight increased with age of dam in all analyses, though the magnitude of the differences was smaller in MW-TX. This was also reflected by the much smaller mean square for age of dam in the MW-TX analysis.

TABLE 11. LEAST-SQUARES ANALYSES OF VARIANCE FOR THE BETWEEN REGION  
B-DATA SETS (3/4-SIMMENTAL)

| Source             | Montana-<br>Midwest |                   | Montana-<br>Texas |          | Midwest-<br>Texas |          |
|--------------------|---------------------|-------------------|-------------------|----------|-------------------|----------|
|                    | df                  | M.S. <sup>a</sup> | df                | M.S.     | df                | M.S.     |
| Region             | 1                   | 9445              | 1                 | 52874**  | 1                 | 84704**  |
| Herd/region        | 483                 | 3375**            | 389               | 4686**   | 356               | 3332**   |
| Sires              | 34                  | 1249**            | 31                | 639*     | 27                | 1048**   |
| Sire x region      | 34                  | 568               | 31                | 586      | 27                | 649      |
| Sire x herd/region | 841                 | 451**             | 633               | 435*     | 537               | 438**    |
| Age of dam         | 2                   | 49782**           | 2                 | 44498**  | 2                 | 5492**   |
| Weaning age        | 1                   | 375159**          | 1                 | 309366** | 1                 | 152695** |
| Residual           | 2994                | 394               | 2382              | 382      | 1230              | 366      |

<sup>a</sup> Mean square (kg<sup>2</sup>).

\* P<.05.

\*\*P<.01.

Variance components are presented in table 12. Herd/region was the most important source of variation in the model. The sire variance component comprised an average of 1.4% of the total variance, though it was noticeably smaller in MT-TX. The generally small size of the sire variance component lends further support to the possibility that the sires used in the analyses represented a selected group from what was available in the industry. Unfortunately, it is extremely difficult to avoid this type of 'selection' in analyses of field data.

The sire x region interaction variance component was very small and comprised less than 1% of the total variance in each analysis with an average of .5%. Genetic correlation estimates of the sires' progeny performance among the two regions in each analysis (table 13) were: .83, .44, and .67 with standard errors of .3, .6, and .4 for MT-MW, MT-TX, and MW-TX, respectively. Confidence intervals for each correlation coefficient overlapped unity. Therefore, interpretation of the genetic correlations agreed with the results of the analysis of variance. Again, the impact of the sire variance component upon the genetic correlation estimate is emphasized.

TABLE 12. VARIANCE COMPONENT ESTIMATES FROM THE BETWEEN REGION ANALYSES (3/4-SIMMENTAL, B-DATA SETS)

| Source             | k-value | Variance component (kg <sup>2</sup> ) | Percent of total variance |
|--------------------|---------|---------------------------------------|---------------------------|
| <u>MT-MW</u>       |         |                                       |                           |
| Herd/region        | 8.1     | 369.4                                 | 46.0                      |
| Sires              | 59.1    | 14.3                                  | 1.8                       |
| Sire x region      | 59.2    | 2.7                                   | .3                        |
| Sire x herd/region | 2.5     | 23.0                                  | 2.9                       |
| Residual           | -       | 393.7                                 | 49.0                      |
| Total              | -       | 803.1                                 | 100.0                     |
| <u>MT-TX</u>       |         |                                       |                           |
| Herd/region        | 7.9     | 548.2                                 | 57.1                      |
| Sires              | 43.3    | 5.7                                   | .6                        |
| Sire x region      | 43.6    | 4.4                                   | .5                        |
| Sire x herd/region | 2.6     | 20.9                                  | 2.2                       |
| Residual           | -       | 381.5                                 | 39.7                      |
| Total              | -       | 960.7                                 | 100.1                     |
| <u>MW-TX</u>       |         |                                       |                           |
| Herd/region        | 5.4     | 548.4                                 | 58.1                      |
| Sires              | 36.8    | 17.9                                  | 1.8                       |
| Sire x region      | 37.0    | 7.1                                   | .7                        |
| Sire x herd/region | 1.9     | 38.7                                  | 4.0                       |
| Residual           | -       | 365.7                                 | 37.4                      |
| Total              | -       | 977.8                                 | 100.0                     |

TABLE 13. GENETIC CORRELATION ESTIMATES FROM THE BETWEEN REGION ANALYSES (3/4-SIMMENTAL, B-DATA SETS)

|                    | Montana-<br>Midwest | Montana-<br>Texas | Midwest-<br>Texas |
|--------------------|---------------------|-------------------|-------------------|
| $r_{\text{SXR}}$   | .83 $\pm$ .3        | .44 $\pm$ .6      | .67 $\pm$ .4      |
| $r_{\text{SXH/R}}$ | .38 $\pm$ 2.9       | .21 $\pm$ 2.8     | .32 $\pm$ 2.9     |

Least-squares sire and sire x region interaction means are listed in appendix tables 9 and 10. Sire constants ranged from -18.4 to 15.4 kg and sire x region interaction constants ranged from -16.1 to 16.1 kilograms. Rankings of the sires within each region indicated that 6, 19, and 11% of the sires ranked in the top third in one region and in the bottom third in the other region in MT-MW, MT-TX, and MW-TX, respectively. These percentages followed the same pattern as the genetic correlation estimates. Five of the six sires in MT-TX showing rank changes had low progeny numbers in at least one region. The average difference between the lowest ranking sire in the top third and the highest ranking sire in the bottom third was 8.0, 5.0 and 5.5 kg for MT-MW, MT-TX, and MW-TX, respectively. These small differences were a reflection of the small sire variances, and indicated that, even though changes in rank were occurring, most of these changes were not likely to be of practical importance.

Variances of the sire x region means for each region were: 45.8, 64.7; 34.7, 84.9; and 85.9, 84.5 for MT-MW, MT-TX, and MW-TX, respectively. Variances in MT-TX were significantly heterogeneous indicating that genetic variances may be different in these two regions. This was somewhat inconsistent, however, with the variances calculated for Montana and Texas in the other two analyses. Since sire x region interaction effects were not important for this analysis, any difference in genetic variance was most likely small.

Residual and rank correlations of the sire x region interaction means are presented in appendix table 11. The same relative order as for the genetic correlation estimates was present in these estimates. Recognizing the limited usefulness of these statistics mentioned earlier, the small values of these correlation estimates suggest the presence of some interaction effects.

As in the within region analyses, the sire x herd/region interaction variance component was a more important source of variation than sires. The percent of the total variance comprised by the sire x herd/region interaction was: 2.9, 2.2, and 4.0% for MT-MW, MT-TX, and MW-TX, respectively. Genetic correlation estimates of the sires progeny's performance among herds within regions (table 13) were: .38, .21, and .32 for MT-MW, MT-TX, and MW-TX, respectively. Standard errors of these statistics were very large due to the small intraclass correlation (t) and the small k-values for the sire x herd/region interaction variance components. Interpretation of these interactions was difficult, but it appeared that interactions between sires and herd environment factors were at least more important than sire x region interaction effects and possibly as important as sire differences.

B-data Sets - Between Region Analyses (1/2-Simmental)

There were not enough sires with enough progeny after editing to duplicate the within region analyses in the 1/2-Simmental data sets. Therefore, region designations used for the 3/4-Simmental between region analyses were also used for the 1/2-Simmental data sets. The assumption required was that region differences in weaning weights were composed in the same way for 1/2- and 3/4-Simmental progeny. The number of records available in each of the region combinations after editing were small, making results less reliable than the results of the 3/4-Simmental analyses.

The least-squares analyses of variance for the 1/2-Simmental data sets are presented in table 14. Herd/region and weaning age were significant in all analyses. Age of dam and the sire x herd/region interaction were significant in MT-MW and MT-TX but not for MW-TX. Sires were not important in any analysis. Region and the sire x region interaction were significant in MW-TX only.

Least-squares means for the fixed effects are presented in appendix table 11. Weaning weights were larger in the Midwest and Montana than in Texas, which was consistent with the 3/4-Simmental data sets. Weaning weights for 1/2-Simmental calves averaged approximately 15 kg less than 3/4-Simmental calves, which was consistent with results of the A-data set analysis which showed a 17 kg difference between 1/2- and 3/4-Simmental weaning weights.

TABLE 14. LEAST SQUARES ANALYSES OF VARIANCE FOR THE BETWEEN  
REGION B-DATA SETS (1/2-SIMMENTAL)

| Source             | Montana-<br>Midwest |                   | Montana-<br>Texas |         | Midwest-<br>Texas |         |
|--------------------|---------------------|-------------------|-------------------|---------|-------------------|---------|
|                    | df                  | M.S. <sup>a</sup> | df                | M.S.    | df                | M.S.    |
| Region             | 1                   | 7                 | 1                 | 15906   | 1                 | 16805*  |
| Herd/region        | 115                 | 3871**            | 114               | 4360**  | 144               | 3246**  |
| Sires              | 16                  | 863               | 14                | 710     | 14                | 519     |
| Sire x region      | 16                  | 541               | 14                | 796     | 14                | 904*    |
| Sire x herd/region | 149                 | 605**             | 151               | 520**   | 184               | 472     |
| Age of dam         | 2                   | 4710**            | 2                 | 1841**  | 2                 | 19      |
| Weaning age        | 1                   | 60451**           | 1                 | 49084** | 1                 | 45378** |
| Residual           | 905                 | 449               | 746               | 386     | 613               | 450     |

Weaning weights generally increased with age of dam except in MW-TX, where there was little difference in age of dam means. It should be noted that by far the greatest number of records were from older cows (4 years and older) in the 1/2-Simmental data sets. Therefore, the estimates for the younger age of dam classes lacked the precision to make these results very meaningful. Standard errors for the age of dam means in the 1/2-Simmental analyses were more than twice the size of those obtained in the 3/4-Simmental analyses. Consistent, however, with the 3/4-Simmental data was the decreased importance of age of dam in the Midwest. It may have been that age of dam differences were smaller in the Midwest, which suggested a possible region x age of dam interaction. Most likely, however, it would seem that this region difference in age of dam may have reflected a greater incidence or use of creep-feeding in the Midwest. Cell counts indicated that creep-feeding was more common in the Midwest than in Montana or Texas. Creep-feeding, especially of the calves of the young cows, could potentially reduce the differences in weaning weights due to age of dam.

Variance components are presented in table 15. Herd/region was the most important source of variation fit in the model, which was consistent with results of the 3/4-Simmental analyses. The sire variance components comprised an average of only 1% of the total variance in the three analyses. Approximately half as many sires were included in the 1/2-Simmental data sets as in the 3/4-Simmental data sets,

TABLE 15. VARIANCE COMPONENT ESTIMATES FROM THE BETWEEN REGION ANALYSES (1/2-SIMMENTAL)

| Source             | k-value | Variance component (kg <sup>2</sup> ) | Percent of total variance |
|--------------------|---------|---------------------------------------|---------------------------|
| <u>MT-MW</u>       |         |                                       |                           |
| Herd/region        | 7.9     | 431.5                                 | 44.9                      |
| Sires              | 24.9    | 15.7                                  | 1.6                       |
| Sire x region      | 25.1    | 2.8                                   | .3                        |
| Sire x herd/region | 2.5     | 61.9                                  | 6.4                       |
| Residual           | -       | 449.0                                 | 46.7                      |
| Total              | -       | 960.9                                 | 99.9                      |
| <u>MT-TX</u>       |         |                                       |                           |
| Herd/region        | 7.1     | 556.9                                 | 54.5                      |
| Sires              | 27.6    | 10.9                                  | 1.1                       |
| Sire x region      | 27.8    | 14.0                                  | 1.4                       |
| Sire x herd/region | 2.4     | 54.6                                  | 5.3                       |
| Residual           | -       | 386.2                                 | 37.8                      |
| Total              | -       | 1022.6                                | 100.1                     |
| <u>MW-TX</u>       |         |                                       |                           |
| Herd/region        | 5.5     | 509.8                                 | 51.6                      |
| Sires              | 30.6    | 2.1                                   | .2                        |
| Sire x region      | 30.7    | 14.6                                  | 1.5                       |
| Sire x herd/region | 2.1     | 10.7                                  | 1.1                       |
| Residual           | -       | 450.0                                 | 45.6                      |
| Total              | -       | 987.2                                 | 100.0                     |

which may in part explain the extremely low sire variances. Selection, as discussed earlier, may have been also responsible for this.

The sire x region interaction variance components were also small and comprised an average of 1.1% of the total variance, which was slightly higher than the percent explained by sires, though probably not a real difference. Genetic correlation estimates of the sires' progeny performance among the two regions in each analysis (table 16) were: .84, .22, and -.55 for MT-MW, MT-TX, and MW-TX, respectively. The small sire variances, especially in MT-TX and MW-TX, drastically reduced the values of the correlation estimates compared to the 3/4-Simmental analyses, as well as the fact that the sire x region variance components were larger. The small intraclass correlations (t), smaller number of sires per analysis, and lower k-values for the sire x region interaction variance components all contributed to extremely large standard error estimates for the genetic correlation coefficients. Even though the sire x region interaction was significant in MW-TX, the extremely large standard error of the genetic correlation coefficient made interpretation of this statistic difficult.

Least-squares sire and sire x region interaction means are listed in appendix tables 12 and 13. Sire constants ranged from -13.4 to 16.1 kg and sire x region interaction constants ranged from -18.5 to 18.5 kilogram.

TABLE 16. GENETIC CORRELATION ESTIMATES FROM THE BETWEEN REGION ANALYSES (1/2-SIMMENTAL)

|                    | Montana-<br>Midwest | Montana-<br>Texas | Midwest-<br>Texas |
|--------------------|---------------------|-------------------|-------------------|
| $r_{\text{SXR}}$   | .84 $\pm$ .7        | .22 $\pm$ 1.2     | -.55 $\pm$ 5.1    |
| $r_{\text{SXH/R}}$ | .20 $\pm$ 2.5       | .17 $\pm$ 6.7     | .16 $\pm$ 29.7    |

Rankings of the sires within each region indicated that 18, 13, and 33% of the sires ranked in the top third in one region and in the bottom third in the other region in MT-MW, MT-TX, and MW-TX, respectively. The larger percentage in MW-TX agreed with the genetic correlation estimate and the F-test of the sire x region interaction mean square for this analysis. The average difference between the lowest ranking sire in the top third and the highest ranking sire in the bottom third was: 5.0, 7.5, and 5.0 kg for MT-MW, MT-TX, and MW-TX, respectively, which were smaller than those found in the 3/4-Simmental analyses, reflecting the smaller sire variances. It should be noted that standard errors for the sire x region interaction means were generally all larger than the differences (or distances in kg) required to jump from the top third to the bottom third in the rankings.

Variances of the sire x region interaction means for each region were: 44.6, 151.6; 63.6, 101.4; and 70.3, 120.1 for MT-MW, MT-TX, and MW-TX, respectively. Variances in MT-MW were significantly heterogeneous which suggested that genetic variances in Montana and Midwest may have been different. If this is true, then the interaction variance component in MT-MW may have been inflated (Dickerson, 1962).

Residual and rank correlations of the sire x region interaction means are presented in appendix table 14. These statistics suggested that a sire's rank in one region was not very reliable as a predictor of the sire's rank in another region. The limited value of these

correlation estimates are emphasized for the reasons mentioned earlier. Even though considerable changes in rank occurred, its doubtful that they represented a very practical concern, at least in these data, because of the narrow range in values (i.e., kg) over which the changes occurred.

The sire x herd/region interaction variance component comprised 6.4, 5.3, and 1.1% of the total variance in the 1/2-Simmental analyses for MT-MW, MT-TX, and MW-TX, respectively. The values were in general agreement with the results of the 3/4-Simmental analyses, except for MW-TX, which was markedly lower. The MW-TX data set had fewer records than any other data set, therefore, the differences in the results of this analysis may be best explained by sampling error. The consistency of the results of the other analyses (i.e., 1/2- and 3/4-Simmental both) suggested this.

The genetic correlation estimates of the sires' progeny performance among herds within regions (table 16) were .20, .17, and .16 for MT-MW, MT-TX, and MW-TX, respectively. Standard errors were extremely large due to the small intraclass correlation (t) and the small k-values for the sire x herd/region interaction variance components. Consistent with the results of all other B-data set analyses, however, interactions between sires and herds appeared to be more important than sire x region interactions.

### Discussion

Results of the within region analyses indicated the state of Texas was not uniform enough to be called one region whereas Iowa and Illinois were similar enough to be called a single region. Montana was also found to be fairly uniform, having no important subregion effects. These Montana results agreed with reports by Woodward and Clark (1950) and Nunn et al. (1978) who also found no region differences within Montana.

Weaning weights in Texas were consistently lower than weaning weights in Montana and Midwest. There was no evidence of region differences between Montana and Midwest.

Herd effects were very important ( $P < .01$ ) in all analyses and comprised an average of 49.5% of the total variance. Herds as classified in this study reflected the effects of year, season, management, and breed of dam; therefore are not exactly comparable to some other studies of herd effects. Studies by Burfening et al. (1978) and Friedrich et al. (1977) found herd effects to be very important and comprised an average of 46.9 and 53.4% of the total variance for weaning weight, respectively. Nunn et al. (1978) reported that management unit was highly significant in all analyses, but did not report it as a percentage of the total variance.

The importance of age of dam effects was not consistent between

regions. The reduced importance of age of dam effects was most noticeable in the Midwest. Analysis of the within Midwest data set and both analyses of the MW-TX data sets (1/2- and 3/4-Simmental) showed marked reduction in age of dam effects. Counts of the number of creep-fed calves and noncreep-fed calves indicated that a larger percentage of calves in the Midwest were creep-fed than in Montana with the percentage in Texas being intermediate. Cundiff et al. (1966) reported that although the age of dam x feeding (creep versus noncreep) interaction was not significant, creep-feeding tended to reduce the effect of age of dam. Calves out of 2-year-old dams that were creep-fed deviated significantly less from the mean than calves not creep-fed. Friedrich (1975) reported the age of dam x preweaning management (creep versus noncreep interaction approached significance ( $P=.08$ ) and stated that calves reared by 2-year-old dams utilized creep-feed to a greater advantage than 3-year-old dams (only 2- and 3-year-old 1/2-Simmental dams were studied). Schaeffer and Wilton (1974) reported age of dam x feeding (creep versus noncreep) interactions were not important in studies of Angus and Hereford calves. The consistency of the present data with respect to age of dam effects suggested the possibility of an age of dam interaction of some kind, either with region or preweaning management. Further study is needed in order to answer this question accurately.

Sire effects were generally important in the 3/4-Simmental data sets but not in the 1/2-Simmental data sets. Fewer sires were included in the 1/2-Simmental data sets and also fewer records. Sire variances were generally larger when more sires were included in the data set. The average percent of the total variance accounted for by sires effects in all analyses was 1.8% with a range of .2 to 5.6%. In a similar study on earlier Simmental records similar results were reported by Nunn et al. (1978) who found that sire variances comprised from .3 to 5.8% of the total variance for weaning weight. Studies by Friedrich (1977) in Simmental sired calves indicated that sire variances comprised from 1.4 to 4.0% of the total variance for weaning weight. Burfening et al. (1978), in studies of 1/2- and 3/4-Simmental calves reported that sire variance components comprised 5.6% of the total variance for weaning weight.

The size of the sire variance components indicated a lower heritability for weaning weight in Simmental-sired calves than is generally reported in the literature for beef cattle. Heritability summaries by Petty and Cartwright (1966) reported an unweighted average heritability of .31 and a weighted average of .28 for weaning weight. The lower heritability estimates for the Simmental data may be in part due to the fact that field data was used in the Simmental estimates. In more controlled experiments, as contrasted to field data, environmental sources of variation may be more

adequately accounted for in estimating the sire variance and the total variance.

Sire x region interaction effects were not large enough to be of practical importance. Results of the A-data set analysis indicated that the sire x region interaction was significant but only accounted for less than .2% of the total variation in weaning weight. The genetic correlation estimate (.84) indicated that sire x region interactions were not of practical importance.

Results of the B-data set analyses also indicated that sire x region interactions were not important. A more distinct estimate of the sire x region interaction was obtained in the B-data sets by including the sire x herd/region interaction in the statistical model. The sire x herd/region interaction is a component part of the sire x region interaction and is also the appropriate error term for the sire x region mean square. The sire x region interaction was generally not significant in the B-data set analyses. This interaction did, however, approach significance ( $P=.06$ ) in the MW-TX 3/4-Simmental data set and was significant in the MW-TX 1/2-Simmental data set ( $P=.05$ ). In all analyses, however, confidence intervals for the genetic correlations of the sires' progeny performance among regions overlapped unity and indicated that the interactions observed were best explained by sampling error. Sire x region interaction variances only accounted for approximately .8% of the total variance in weaning

weight.

The sire x region interaction variance components tended to comprise a slightly larger percent of the total variance in the 1/2-Simmental analyses than in the 3/4-Simmental analyses (.8 versus 1.1). Because the size of this difference was small and since the sire x region interaction was generally not significant, there was little evidence that breed of dam contributes significantly to sire x region interaction effects.

These results agree with results reported by Woodward and Clark (1950) in which no interactions were observed between sires and locations within Montana. Aken et al. (1976) also reported sire x location interaction effects to be not significant for weight at 196 days in studies of calves in Germany and Texas. Significant sire x region interactions, however, were found by Nunn et al. (1978) although the genetic correlation estimate was fairly high (>.73). Butts et al. (1971) reported important sire x location interactions for weaning weight in a reciprocal transfer of cattle between Florida and Montana.

Sire x herd/region interactions were significant in all B-data set analyses except MW-TX for the 1/2-Simmental data set. The sire x herd/region variance component comprised an average of 4.5% of the total variance being 2.5 times larger than the sire variance component. Despite the fact that confidence intervals for the genetic correlations

of the sires' progeny performance among herds within regions were very large, the sire x herd interaction appeared to be important. Herd effects as defined in this study were composed of year, season, management, and breed of dam effects so an exact interpretation of this interaction cannot be made. It may be that if herd effects were better or more distinctly classified, that this interaction could be partitioned into several parts, some or none of which would be significant statistically. The usefulness of further study in this area is emphasized.

Friedrich (1977) found sire x management interactions to be important for 3/4-Simmental but not for 1/2-Simmental weaning weights. Sire x herd interactions were found not to be important by Wilson et al. (1972) in studies of Angus and Hereford weaning weights in a limited number of herds. Sire x year interaction effects were reported to be significant, however, by Turner and MacDonald (1969) and Edwards et al. (1966). Brinks et al. (1967) also reported significant line of sire x year interaction effects in heifer progeny but not in bull progeny weaning weights.

## SUMMARY

Field data from the years 1974 to 1976 supplied by the American Simmental Association were analyzed to evaluate the importance of sire x region interaction effects in beef cattle weaning weights.

Two basic data sets were used. In the A-data set four large regions were outlined, each including several states. The data were edited to include records from 1/2- and 3/4-Simmental bull and heifer calves, raised by their own dams, born and weaned in the same herd, and only the progeny of sires that had at least 20 progeny in three of the four regions.

In the B-data sets 1/2- and 3/4-Simmental records were analyzed separately and only three regions were outlined (Montana, Midwest = Iowa + Illinois, and Texas). In the 3/4-Simmental B-data sets each region was first analyzed separately by dividing each region into two subregions to assess any subregion effects. Records were edited in the same manner as the A-data set except that sires were required to be represented by at least 15 progeny in each region and only heifers records were used. Due to significant region differences within Texas the West-Texas subregion was excluded. Each combination of two regions was then analyzed in both 1/2- and 3/4-Simmental B-data sets.

The A-data set was analyzed by least-squares mixed model procedures using a model which included region, herd/region, sires, age of dam, weaning age, sex, percent Simmental, and sire x region interaction effects. The B-data sets were also analyzed by least-squares mixed

model procedures and the model included region, herd/region, sires, age of dam, weaning age, sire x region interaction, and sire x herd/region interaction effects.

The least-squares analysis of variance for the A-data set indicated that sire and sire x region interaction effects were significant. The estimate of the genetic correlation of the sires' progeny performance among the regions was .84 and the sire x region interaction variance component accounted for less than .2% of the total variance indicating sire x region interaction effects were not of major importance and/or did not represent large changes in rank of the sires between regions. Rankings of the sire x region interaction means in each region confirmed that large changes in rank of the sires among the regions were not occurring.

Sire x region interaction effects were not significant in the 3/4-Simmental B-data set analyses. Sire affects were significant in all analyses. All confidence intervals for the genetic correlations of the sires' progeny performance among the regions overlapped unity. The sire x region interaction variance component comprised less than 1% of the total variance in each analysis. Ranking of the sire x region interaction means in each region indicated that some changing in rank was occurring but was not of such magnitude to be of practical importance.

Results of the 1/2-Simmental B-data set analyses indicated that

sire x region interaction effects were not significant except in the Midwest versus Texas analysis. Sire effects were not significant in any analysis. Due to smaller numbers of 1/2-Simmental records and fewer sires in each analysis, the results of these analyses were of limited value. The confidence intervals for the genetic correlations of the sires' progeny performance among the regions overlapped unity. The sire x region interaction variance component comprised an average of 1% of the total variance. Rankings of the sire x region interaction means in each region indicated that changes in rank were occurring but were of small magnitude and could not be distinguished from sampling error.

The sire x herd/region interaction was significant in all B-data set analyses except in the Midwest versus Texas 1/2-Simmental analysis. The variance component for this interaction was consistently larger than the sire x region interaction and sire variance components. Even though confidence intervals for the sires' progeny performance among herds within regions overlapped unity, it appeared that sire x herd interactions were more important than sire x region interactions in Simmental-sired calves. Herd effects as classified in this study included effects of management, year, season of birth, and breed of dam. Therefore, exact interpretation of the sire x herd/region interaction effects was difficult.

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LITERATURE CITED

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## APPENDIX

APPENDIX TABLE 1. LEAST-SQUARES MEANS (kg) FOR THE A-DATA SET

| Effect            |    | No. observations | Mean |
|-------------------|----|------------------|------|
| Region            | 1  | 11,153           | 222  |
|                   | 2  | 4,827            | 214  |
|                   | 3  | 4,479            | 225  |
|                   | 4  | 2,801            | 225  |
| Bulls             |    | 6,095            | 231  |
| Heifers           |    | 17,165           | 212  |
| Age of dam        | 2  | 6,493            | 207  |
|                   | 3  | 5,847            | 220  |
|                   | 4  | 4,333            | 228  |
|                   | 5+ | 6,587            | 231  |
| Percent Simmental | 50 | 6,894            | 213  |
|                   | 75 | 16,366           | 230  |

APPENDIX TABLE 2. LEAST-SQUARES SIRE MEANS (kg) FOR THE A-DATA SET

| Sire | No. observations | Mean             |
|------|------------------|------------------|
| 1    | 665              | 218 <sup>a</sup> |
| 2    | 904              | 222              |
| 3    | 1625             | 222              |
| 4    | 1289             | 216              |
| 5    | 2122             | 226              |
| 6    | 551              | 222              |
| 7    | 1691             | 223              |
| 8    | 2069             | 224              |
| 9    | 522              | 225              |
| 10   | 885              | 224              |
| 11   | 784              | 221              |
| 12   | 1388             | 225              |
| 13   | 414              | 217              |
| 14   | 848              | 229              |
| 15   | 503              | 229              |
| 16   | 635              | 214              |
| 17   | 1413             | 219              |
| 18   | 528              | 219              |
| 19   | 1986             | 220              |
| 20   | 974              | 225              |
| 21   | 421              | 217              |
| 22   | 466              | 220              |
| 23   | 577              | 220              |

<sup>a</sup> Standard errors ranged from 1.7 to 2.8 kg, and were closely related to the number of progeny per sire.

APPENDIX TABLE 3. LEAST-SQUARES SIRE X REGION MEANS (kg) FOR THE  
A-DATA SET

| Sire | Region               |            |            |            |
|------|----------------------|------------|------------|------------|
|      | 1                    | 2          | 3          | 4          |
| 1    | 220(17) <sup>a</sup> | 211(17-18) | 222(18-19) | 220(17-18) |
| 2    | 225(6-10)            | 217(6-9)   | 225(10-14) | 220(17-18) |
| 3    | 225(6-10)            | 214(13-15) | 225(10-14) | 225(13)    |
| 4    | 218(19)              | 210(19-20) | 217(21)    | 219(19-20) |
| 5    | 226(5)               | 216(10-11) | 229(3-5)   | 231(5)     |
| 6    | 214(21-22)           | 219(4-5)   | 228(6-7)   | 227(10)    |
| 7    | 221(16)              | 217(6-9)   | 222(18-19) | 230(6)     |
| 8    | 227(3-4)             | 214(13-15) | 226(9)     | 229(7-9)   |
| 9    | 225(6-10)            | 217(6-9)   | 230(2)     | 229(7-9)   |
| 10   | 224(11-13)           | 210(19-20) | 229(3-5)   | 232(2-4)   |
| 11   | 223(14)              | 214(13-15) | 227(8)     | 219(19-20) |
| 12   | 227(3-4)             | 217(6-9)   | 228(6-7)   | 226(11-12) |
| 13   | 214(21-22)           | 206(21)    | 225(10-14) | 224(14)    |
| 14   | 228(2)               | 220(2-3)   | 233(1)     | 235(1)     |
| 15   | 230(1)               | 224(1)     | 229(3-5)   | 232(2-4)   |
| 16   | 213(23)              | 200(23)    | 216(22-23) | 226(11-12) |
| 17   | 224(11-13)           | 201(22)    | 224(15)    | 229(7-9)   |
| 18   | 217(20)              | 215(12)    | 221(20)    | 221(16)    |
| 19   | 222(15)              | 212(16)    | 225(10-14) | 222(15)    |
| 20   | 225(6-10)            | 219(4-5)   | 223(16-17) | 232(2-4)   |
| 21   | 219(18)              | 220(2-3)   | 216(22-23) | 214(23)    |
| 22   | 225(6-10)            | 211(17-18) | 225(10-14) | 217(21-22) |
| 23   | 224(11-13)           | 216(10-11) | 223(16-17) | 217(21-22) |

<sup>a</sup>Sire rank within region.

APPENDIX TABLE 4. LEAST-SQUARES MEANS (kg) FOR THE WITHIN REGION  
B-DATA SETS (3/4-SIMMENTAL)

| Effect         | No. observations | Mean |
|----------------|------------------|------|
| <u>Montana</u> |                  |      |
| $\mu$          | 3109             | 220  |
| East           | 1733             | 221  |
| West           | 1376             | 220  |
| Age of dam - 2 | 1320             | 212  |
| 3              | 909              | 220  |
| 4+             | 880              | 230  |
| <u>Midwest</u> |                  |      |
| $\mu$          | 993              | 230  |
| Iowa           | 396              | 229  |
| Illinois       | 597              | 231  |
| Age of dam - 2 | 276              | 228  |
| 3              | 265              | 228  |
| 4+             | 452              | 235  |
| <u>Texas</u>   |                  |      |
| $\mu$          | 1637             | 213  |
| East           | 782              | 205  |
| West           | 855              | 220  |
| Age of dam - 2 | 597              | 201  |
| 3              | 521              | 215  |
| 4+             | 519              | 222  |

APPENDIX TABLE 5. LEAST-SQUARES SIRE MEANS (kg) FOR THE WITHIN REGION  
B-DATA SETS (3/4 SIMMENTAL)<sup>a</sup>

| Sire | No. obs. | Montana |  | Sire | No. obs. | Mean |
|------|----------|---------|--|------|----------|------|
|      |          | Mean    |  |      |          |      |
| 1    | 58       | 223     |  | 17   | 80       | 211  |
| 2    | 99       | 227     |  | 18   | 271      | 218  |
| 3    | 96       | 215     |  | 19   | 39       | 217  |
| 4    | 269      | 222     |  | 20   | 36       | 216  |
| 5    | 132      | 218     |  | 21   | 193      | 217  |
| 6    | 393      | 219     |  | 22   | 46       | 220  |
| 7    | 62       | 238     |  | 23   | 42       | 224  |
| 8    | 139      | 213     |  | 24   | 83       | 208  |
| 9    | 32       | 221     |  | 25   | 44       | 213  |
| 10   | 86       | 226     |  | 26   | 43       | 215  |
| 11   | 114      | 222     |  | 27   | 20       | 228  |
| 12   | 47       | 219     |  | 28   | 49       | 211  |
| 13   | 58       | 236     |  | 29   | 67       | 225  |
| 14   | 63       | 225     |  | 30   | 124      | 208  |
| 15   | 155      | 225     |  | 31   | 67       | 216  |
| 16   | 21       | 238     |  | 32   | 81       | 221  |

APPENDIX TABLE 5. (CONTINUED)

|      |          |      | <u>Midwest</u> |          |      |
|------|----------|------|----------------|----------|------|
| Sire | No. obs. | Mean | Sire           | No. obs. | Mean |
| 1    | 47       | 233  | 8              | 35       | 240  |
| 2    | 50       | 242  | 9              | 118      | 238  |
| 3    | 75       | 210  | 10             | 26       | 215  |
| 4    | 132      | 235  | 11             | 160      | 228  |
| 5    | 50       | 218  | 12             | 20       | 238  |
| 6    | 111      | 233  | 13             | 30       | 229  |
| 7    | 114      | 228  | 14             | 25       | 235  |
|      |          |      | <u>Texas</u>   |          |      |
| 1    | 56       | 212  | 12             | 10       | 220  |
| 2    | 118      | 215  | 13             | 128      | 214  |
| 3    | 10       | 199  | 14             | 45       | 206  |
| 4    | 84       | 216  | 15             | 36       | 220  |
| 5    | 67       | 210  | 16             | 20       | 194  |
| 6    | 301      | 215  | 17             | 30       | 214  |
| 7    | 120      | 216  | 18             | 137      | 209  |
| 8    | 28       | 218  | 19             | 48       | 220  |
| 9    | 95       | 215  | 20             | 119      | 216  |
| 10   | 125      | 214  | 21             | 9        | 206  |
| 11   | 26       | 206  | 22             | 25       | 222  |

<sup>a</sup>Standard errors ranged from 4.0 to 12.3 kg, and were closely related to the number of progeny per sire.

APPENDIX TABLE 6. LEAST-SQUARES SIRE X REGION INTERACTION MEANS (kg)  
FOR THE WITHIN REGION B-DATA SETS (3/4-SIMMENTAL)<sup>a</sup>

| Sire | No. obs. | <u>Montana</u>          |          | West       |
|------|----------|-------------------------|----------|------------|
|      |          | East                    | No. obs. |            |
| 1    | 28       | 215(23-25) <sup>b</sup> | 30       | 230(4-5)   |
| 2    | 46       | 229(5-6)                | 53       | 225(11-12) |
| 3    | 75       | 219(18-19)              | 21       | 211(24-25) |
| 4    | 83       | 222(16)                 | 186      | 222(16)    |
| 5    | 106      | 215(23-25)              | 26       | 220(17)    |
| 6    | 217      | 219(18-19)              | 176      | 219(18)    |
| 7    | 25       | 244(1)                  | 37       | 231(3)     |
| 8    | 112      | 217(22)                 | 27       | 208(29-31) |
| 9    | 22       | 229(5-6)                | 10       | 212(22-23) |
| 10   | 58       | 224(10-12)              | 28       | 227(7-9)   |
| 11   | 86       | 218(20-21)              | 28       | 227(7-9)   |
| 12   | 23       | 210(28)                 | 24       | 228(6)     |
| 13   | 48       | 237(3)                  | 10       | 235(2)     |
| 14   | 36       | 223(13-15)              | 27       | 227(7-9)   |
| 15   | 99       | 223(13-15)              | 56       | 226(10)    |
| 16   | 20       | 238(2)                  | 1        | 238(1)     |
| 17   | 60       | 211(27)                 | 20       | 210(26-28) |
| 18   | 84       | 224(10-12)              | 187      | 212(22-23) |
| 19   | 14       | 223(13-15)              | 25       | 211(24-25) |
| 20   | 24       | 215(23-25)              | 12       | 217(20)    |
| 21   | 103      | 225(9)                  | 90       | 210(26-28) |
| 22   | 27       | 232(4)                  | 19       | 208(29-31) |
| 23   | 26       | 224(10-12)              | 16       | 224(13)    |
| 24   | 57       | 208(29-30)              | 26       | 208(29-31) |
| 25   | 15       | 208(29-30)              | 29       | 218(19)    |
| 26   | 9        | 206(32)                 | 34       | 223(14-15) |
| 27   | 9        | 227(8)                  | 11       | 230(4-5)   |
| 28   | 22       | 207(31)                 | 27       | 215(21)    |
| 29   | 32       | 226(7)                  | 35       | 223(14-15) |
| 30   | 100      | 214(26)                 | 24       | 201(32)    |
| 31   | 54       | 221(17)                 | 13       | 210(26-28) |
| 32   | 13       | 218(20-21)              | 68       | 225(11-12) |

APPENDIX TABLE 6. (CONTINUED)

| Sire | No. obs. | <u>Midwest</u> |  | No. obs. | Illinois   |
|------|----------|----------------|--|----------|------------|
|      |          | Iowa           |  |          |            |
| 1    | 40       | 232(7)         |  | 7        | 234(3-4)   |
| 2    | 7        | 251(1)         |  | 43       | 232(7)     |
| 3    | 25       | 209(12)        |  | 50       | 212(14)    |
| 4    | 30       | 237(4-5)       |  | 102      | 233(6)     |
| 5    | 7        | 207(13)        |  | 43       | 230(8)     |
| 6    | 67       | 237(4-5)       |  | 44       | 229(9-10)  |
| 7    | 54       | 226(9-10)      |  | 60       | 229(9-10)  |
| 8    | 15       | 226(9-10)      |  | 20       | 254(1)     |
| 9    | 47       | 241(3)         |  | 71       | 234(3-5)   |
| 10   | 5        | 206(14)        |  | 21       | 223(13)    |
| 11   | 51       | 222(11)        |  | 109      | 234(3-5)   |
| 12   | 7        | 236(6)         |  | 13       | 239(2)     |
| 13   | 23       | 230(8)         |  | 7        | 228(11-12) |
| 14   | 18       | 242(2)         |  | 7        | 228(11-12) |

APPENDIX TABLE 6. (CONTINUED)

| Sire | No. obs. | East        | Texas    |  | West        |
|------|----------|-------------|----------|--|-------------|
|      |          |             | No. obs. |  |             |
| 1    | 14       | 213 (6)     | 42       |  | 210 (21)    |
| 2    | 64       | 210 (7-9)   | 54       |  | 220 (12)    |
| 3    | 3        | 186 (21)    | 7        |  | 211 (19-20) |
| 4    | 55       | 203 (16)    | 29       |  | 228 (1-2)   |
| 5    | 45       | 206 (13-15) | 22       |  | 215 (18)    |
| 6    | 165      | 210 (7-9)   | 136      |  | 221 (10-11) |
| 7    | 53       | 208 (10-11) | 67       |  | 225 (4)     |
| 8    | 14       | 214 (5)     | 14       |  | 222 (8-9)   |
| 9    | 51       | 207 (12)    | 44       |  | 224 (5-7)   |
| 10   | 41       | 210 (7-9)   | 84       |  | 219 (13-15) |
| 11   | 17       | 192 (20)    | 9        |  | 219 (13-15) |
| 12   | 3        | 216 (2-3)   | 7        |  | 224 (5-7)   |
| 13   | 56       | 206 (13-15) | 72       |  | 221 (10-11) |
| 14   | 26       | 201 (18)    | 19       |  | 211 (19-20) |
| 15   | 11       | 215 (4)     | 25       |  | 226 (3)     |
| 16   | 10       | 179 (22)    | 10       |  | 208 (22)    |
| 17   | 25       | 206 (13-15) | 5        |  | 222 (8-9)   |
| 18   | 67       | 202 (17)    | 70       |  | 216 (17)    |
| 19   | 15       | 220 (1)     | 33       |  | 219 (13-15) |
| 20   | 30       | 208 (10-11) | 89       |  | 224 (5-7)   |
| 21   | 6        | 193 (19)    | 3        |  | 218 (16)    |
| 22   | 11       | 216 (2-3)   | 14       |  | 228 (1-2)   |

<sup>a</sup>Standard errors ranged from 2.4 to 26.6 kg and were closely related to the number of observations per subcell.

<sup>b</sup>Rank within the subregion.

APPENDIX TABLE 7. RESIDUAL AND RANK CORRELATIONS OF THE LEAST-SQUARES SIRE X REGION INTERACTION MEANS FOR THE WITHIN REGION B-DATA SETS (3/4-SIMMENTAL)

|            | Montana | Midwest | Texas |
|------------|---------|---------|-------|
| Residual r | .40**   | .57     | .36*  |
| Rank r     | .34**   | .49*    | .24** |

\* Different from 1.0 (P=.05).

\*\*Different from 1.0 (P=.01).

APPENDIX TABLE 8. LEAST-SQUARES MEANS (kg) FOR THE BETWEEN REGION  
B-DATA SETS (3/4-SIMMENTAL)

| Effect         | No. observations | Mean |
|----------------|------------------|------|
| <u>MT-MW</u>   |                  |      |
| $\mu$          | 4391             | 224  |
| Montana        | 2895             | 221  |
| Midwest        | 1496             | 226  |
| Age of dam - 2 | 1680             | 213  |
| 3              | 1252             | 223  |
| 4+             | 1459             | 235  |
| <u>MT-TX</u>   |                  |      |
| $\mu$          | 3471             | 214  |
| Montana        | 2328             | 221  |
| Texas          | 1143             | 207  |
| Age of dam - 2 | 1382             | 201  |
| 3              | 1065             | 215  |
| 4+             | 1024             | 226  |
| <u>MT-TX</u>   |                  |      |
| $\mu$          | 2182             | 218  |
| Midwest        | 1246             | 228  |
| Texas          | 936              | 209  |
| Age of dam - 2 | 662              | 212  |
| 3              | 674              | 218  |
| 4+             | 846              | 224  |

APPENDIX TABLE 9. LEAST-SQUARES SIRE MEANS (kg) FOR THE BETWEEN  
REGION B-DATA SETS (3/4-SIMMENTAL)<sup>a</sup>

| Sire | No. obs. | Mean | <u>MT-MW</u> |          |      |
|------|----------|------|--------------|----------|------|
|      |          |      | Sire         | No. obs. | Mean |
| 1    | 92       | 226  | 19           | 93       | 232  |
| 2    | 23       | 221  | 20           | 171      | 223  |
| 3    | 74       | 228  | 21           | 30       | 224  |
| 4    | 25       | 220  | 22           | 89       | 215  |
| 5    | 151      | 225  | 23           | 421      | 226  |
| 6    | 203      | 210  | 24           | 58       | 225  |
| 7    | 376      | 226  | 25           | 57       | 220  |
| 8    | 40       | 227  | 26           | 123      | 218  |
| 9    | 78       | 231  | 27           | 352      | 222  |
| 10   | 191      | 221  | 28           | 66       | 221  |
| 11   | 524      | 223  | 29           | 39       | 231  |
| 12   | 82       | 228  | 30           | 28       | 232  |
| 13   | 153      | 223  | 31           | 113      | 218  |
| 14   | 35       | 213  | 32           | 55       | 228  |
| 15   | 114      | 221  | 33           | 27       | 219  |
| 16   | 249      | 225  | 34           | 58       | 234  |
| 17   | 56       | 210  | 35           | 73       | 225  |
| 18   | 72       | 236  |              |          |      |

APPENDIX TABLE 9. (CONTINUED)

| <u>MT-TX</u> |          |      |      |          |      |
|--------------|----------|------|------|----------|------|
| Sire         | No. obs. | Mean | Sire | No. obs. | Mean |
| 1            | 64       | 207  | 17   | 90       | 226  |
| 2            | 31       | 211  | 18   | 189      | 216  |
| 3            | 90       | 218  | 19   | 75       | 210  |
| 4            | 9        | 204  | 20   | 83       | 223  |
| 5            | 26       | 212  | 21   | 68       | 207  |
| 6            | 153      | 214  | 22   | 113      | 221  |
| 7            | 153      | 211  | 23   | 59       | 219  |
| 8            | 424      | 216  | 24   | 53       | 216  |
| 9            | 29       | 206  | 25   | 106      | 207  |
| 10           | 78       | 218  | 26   | 265      | 211  |
| 11           | 71       | 221  | 27   | 72       | 216  |
| 12           | 175      | 213  | 28   | 20       | 216  |
| 13           | 392      | 215  | 29   | 78       | 211  |
| 14           | 55       | 212  | 30   | 189      | 215  |
| 15           | 123      | 210  | 31   | 19       | 218  |
| 16           | 49       | 209  | 32   | 70       | 217  |
| <u>MW-TX</u> |          |      |      |          |      |
| 1            | 43       | 215  | 15   | 24       | 234  |
| 2            | 24       | 222  | 16   | 173      | 218  |
| 3            | 113      | 223  | 17   | 40       | 200  |
| 4            | 17       | 206  | 18   | 60       | 230  |
| 5            | 108      | 221  | 19   | 46       | 223  |
| 6            | 125      | 209  | 20   | 45       | 214  |
| 7            | 313      | 223  | 21   | 40       | 215  |
| 8            | 75       | 218  | 22   | 38       | 211  |
| 9            | 55       | 226  | 23   | 269      | 217  |
| 10           | 30       | 223  | 24   | 43       | 213  |
| 11           | 117      | 218  | 25   | 34       | 220  |
| 12           | 150      | 218  | 26   | 40       | 218  |
| 13           | 32       | 220  | 27   | 26       | 225  |
| 14           | 51       | 215  | 28   | 51       | 219  |

<sup>a</sup>Standard errors ranged from 2.6 to 8.9 kg and were closely related to the number of progeny per sire.

APPENDIX TABLE 10. LEAST-SQUARES SIRE X REGION INTERACTION MEANS  
(kg) FOR THE BETWEEN REGION B-DATA SETS  
(3/4-SIMMENTAL)<sup>a</sup>

| Sire | No. obs. | Montana                 | MT-MW | No. obs. | Midwest    |
|------|----------|-------------------------|-------|----------|------------|
| 1    | 58       | 222(14-18) <sup>b</sup> |       | 34       | 231(9)     |
| 2    | 15       | 215(30)                 |       | 8        | 226(18-22) |
| 3    | 25       | 227(8-9)                |       | 49       | 229(12-14) |
| 4    | 12       | 217(26)                 |       | 13       | 222(26-28) |
| 5    | 96       | 221(19-21)              |       | 55       | 229(12-14) |
| 6    | 127      | 213(32)                 |       | 76       | 207(34)    |
| 7    | 240      | 223(13)                 |       | 136      | 230(10-11) |
| 8    | 20       | 228(7)                  |       | 20       | 226(18-22) |
| 9    | 59       | 231(3-4)                |       | 19       | 230(10-11) |
| 10   | 131      | 216(27-29)              |       | 60       | 226(18-22) |
| 11   | 392      | 222(14-18)              |       | 132      | 224(24)    |
| 12   | 59       | 224(11-12)              |       | 23       | 232(8)     |
| 13   | 126      | 221(19-21)              |       | 27       | 225(23)    |
| 14   | 22       | 216(27-29)              |       | 13       | 210(33)    |
| 15   | 92       | 220(22)                 |       | 22       | 223(25)    |
| 16   | 127      | 225(10)                 |       | 122      | 226(18-22) |
| 17   | 45       | 218(24-25)              |       | 11       | 203(35)    |
| 18   | 57       | 235(1)                  |       | 15       | 237(2-3)   |
| 19   | 56       | 227(8-9)                |       | 37       | 237(2-3)   |
| 20   | 137      | 224(11-12)              |       | 34       | 222(26-28) |
| 21   | 20       | 231(3-4)                |       | 10       | 217(32)    |
| 22   | 75       | 208(35)                 |       | 14       | 222(26-28) |
| 23   | 278      | 219(23)                 |       | 143      | 233(6-7)   |
| 24   | 24       | 214(31)                 |       | 34       | 236(4)     |
| 25   | 42       | 222(14-18)              |       | 15       | 219(31)    |
| 26   | 97       | 216(27-29)              |       | 26       | 220(29-30) |
| 27   | 178      | 218(24-25)              |       | 174      | 227(16-17) |
| 28   | 52       | 222(14-18)              |       | 14       | 220(29-30) |
| 29   | 11       | 230(5-6)                |       | 28       | 233(6-7)   |
| 30   | 14       | 234(2)                  |       | 14       | 229(12-13) |
| 31   | 82       | 209(34)                 |       | 31       | 226(18-22) |
| 32   | 43       | 221(19-21)              |       | 12       | 235(5)     |
| 33   | 10       | 211(33)                 |       | 17       | 227(16-17) |
| 34   | 27       | 230(5-6)                |       | 31       | 238(1)     |
| 35   | 46       | 222(14-18)              |       | 27       | 228(15)    |

APPENDIX TABLE 10. (CONTINUED)

| Sire | No. obs. | MT-TX       |          | Texas       |
|------|----------|-------------|----------|-------------|
|      |          | Montana     | No. obs. |             |
| 1    | 55       | 224 (8-10)  | 9        | 191 (30)    |
| 2    | 16       | 212 (29)    | 15       | 211 (7-9)   |
| 3    | 25       | 226 (5)     | 65       | 211 (7-9)   |
| 4    | 6        | 220 (21)    | 3        | 187 (32)    |
| 5    | 5        | 208 (31-32) | 21       | 216 (5)     |
| 6    | 92       | 222 (16-19) | 61       | 205 (22)    |
| 7    | 103      | 214 (27-28) | 50       | 207 (17-19) |
| 8    | 250      | 223 (11-15) | 174      | 210 (10-11) |
| 9    | 3        | 208 (31-32) | 26       | 203 (25-26) |
| 10   | 22       | 227 (3-4)   | 56       | 208 (13-16) |
| 11   | 60       | 231 (1-2)   | 11       | 210 (10-11) |
| 12   | 121      | 218 (23-24) | 54       | 208 (13-16) |
| 13   | 350      | 222 (16-19) | 42       | 209 (12)    |
| 14   | 45       | 222 (16-19) | 10       | 203 (25-26) |
| 15   | 99       | 221 (20)    | 24       | 198 (27-28) |
| 16   | 32       | 222 (16-19) | 17       | 196 (29)    |
| 17   | 86       | 218 (23-24) | 4        | 234 (1)     |
| 18   | 127      | 225 (6-7)   | 62       | 206 (20-21) |
| 19   | 49       | 216 (25)    | 26       | 204 (23-24) |
| 20   | 57       | 227 (3-4)   | 26       | 218 (3-4)   |
| 21   | 62       | 223 (11-15) | 6        | 190 (31)    |
| 22   | 101      | 223 (11-15) | 12       | 218 (3-4)   |
| 23   | 24       | 231 (1-2)   | 35       | 206 (20-21) |
| 24   | 28       | 224 (8-10)  | 25       | 208 (13-16) |
| 25   | 95       | 215 (26)    | 11       | 198 (27-28) |
| 26   | 192      | 219 (22)    | 73       | 204 (23-24) |
| 27   | 41       | 224 (8-10)  | 31       | 208 (13-16) |
| 28   | 8        | 225 (6-7)   | 12       | 207 (17-19) |
| 29   | 69       | 211 (30)    | 9        | 212 (6)     |
| 30   | 48       | 223 (11-15) | 141      | 207 (17-19) |
| 31   | 11       | 214 (27-28) | 8        | 221 (2)     |
| 32   | 46       | 223 (11-15) | 24       | 211 (7-9)   |

APPENDIX TABLE 10. (CONTINUED)

| Sire | No. obs. | <u>MW-TX</u> |  | No. obs. | Texas      |
|------|----------|--------------|--|----------|------------|
|      |          | Midwest      |  |          |            |
| 1    | 34       | 235(4-5)     |  | 9        | 195(27)    |
| 2    | 9        | 230(12-14)   |  | 15       | 213(7-8)   |
| 3    | 50       | 234(6-7)     |  | 63       | 212(9)     |
| 4    | 14       | 224(22)      |  | 3        | 188(28)    |
| 5    | 46       | 235(4-5)     |  | 62       | 207(17-19) |
| 6    | 73       | 210(27)      |  | 52       | 208(14-16) |
| 7    | 142      | 234(6-7)     |  | 171      | 213(7-8)   |
| 8    | 18       | 226(21)      |  | 57       | 209(12-13) |
| 9    | 32       | 236(3)       |  | 23       | 216(4-5)   |
| 10   | 19       | 231(9-11)    |  | 11       | 215(6)     |
| 11   | 63       | 229(15)      |  | 54       | 206(20-21) |
| 12   | 110      | 227(17-20)   |  | 40       | 210(10-11) |
| 13   | 22       | 239(2)       |  | 10       | 202(24)    |
| 14   | 27       | 230(12-14)   |  | 24       | 201(25-26) |
| 15   | 21       | 227(17-20)   |  | 3        | 241(1)     |
| 16   | 116      | 228(16)      |  | 57       | 207(17-19) |
| 17   | 12       | 196(28)      |  | 28       | 204(22-23) |
| 18   | 36       | 244(1)       |  | 24       | 216(4-5)   |
| 19   | 34       | 227(17-20)   |  | 12       | 220(2)     |
| 20   | 10       | 221(23-25)   |  | 35       | 206(20-21) |
| 21   | 16       | 221(23-25)   |  | 24       | 208(14-16) |
| 22   | 27       | 221(23-25)   |  | 11       | 201(25-26) |
| 23   | 204      | 230(12-14)   |  | 65       | 204(22-23) |
| 24   | 13       | 218(26)      |  | 30       | 207(17-19) |
| 25   | 22       | 232(8)       |  | 12       | 209(12-13) |
| 26   | 31       | 227(17-20)   |  | 9        | 210(10-11) |
| 27   | 18       | 231(9-11)    |  | 8        | 219(3)     |
| 28   | 27       | 231(9-11)    |  | 24       | 208(14-16) |

<sup>a</sup>Standard errors ranged from 1.6 to 14.3 kg and were closely related to the number of observations per subcell.

<sup>b</sup>Rank within the region.

APPENDIX TABLE 11. RESIDUAL AND RANK CORRELATIONS OF THE LEAST-SQUARES SIRE X REGION INTERACTION MEANS FOR THE BETWEEN REGION B-DATA SETS (3/4-SIMMENTAL)

|            | MT-MW | MT-TX  | MW-TX |
|------------|-------|--------|-------|
| Residual r | .38** | -.11** | .16** |
| Rank r     | .39** | .01**  | .24** |

\*\*Different from 1.0 (P=.01).

APPENDIX TABLE 12. LEAST-SQUARES MEANS (kg) FOR THE BETWEEN REGION  
B-DATA SETS (1/2-SIMMENTAL)

| Effect         | No. observations | Mean |
|----------------|------------------|------|
| <u>MT-MW</u>   |                  |      |
| $\mu$          | 1206             | 204  |
| Montana        | 660              | 203  |
| Midwest        | 546              | 204  |
| Age of dam - 2 | 88               | 194  |
| 3              | 126              | 204  |
| 4+             | 992              | 213  |
| <u>MT-TX</u>   |                  |      |
| $\mu$          | 1044             | 200  |
| Montana        | 553              | 206  |
| Texas          | 491              | 194  |
| Age of dam - 2 | 43               | 195  |
| 3              | 107              | 199  |
| 4+             | 894              | 206  |
| <u>MW-TX</u>   |                  |      |
| $\mu$          | 974              | 207  |
| Midwest        | 479              | 212  |
| Texas          | 495              | 202  |
| Age of dam - 2 | 41               | 208  |
| 3              | 94               | 207  |
| 4+             | 839              | 206  |

APPENDIX TABLE 13. LEAST-SQUARES SIRE MEANS (kg) FOR THE BETWEEN  
REGION B-DATA SETS (1/2-SIMMENTAL)<sup>a</sup>

| Sire         | No. obs. | Mean | <u>MT-MW</u> |          |      |
|--------------|----------|------|--------------|----------|------|
|              |          |      | Sire         | No. obs. | Mean |
| 1            | 96       | 201  | 10           | 37       | 210  |
| 2            | 74       | 199  | 11           | 125      | 202  |
| 3            | 56       | 204  | 12           | 24       | 201  |
| 4            | 25       | 205  | 13           | 44       | 190  |
| 5            | 60       | 199  | 14           | 213      | 202  |
| 6            | 73       | 211  | 15           | 50       | 202  |
| 7            | 195      | 203  | 16           | 7        | 220  |
| 8            | 42       | 216  | 17           | 37       | 194  |
| 9            | 48       | 201  |              |          |      |
| <u>MT-TX</u> |          |      |              |          |      |
| 1            | 132      | 202  | 9            | 59       | 190  |
| 2            | 78       | 199  | 10           | 36       | 201  |
| 3            | 26       | 199  | 11           | 93       | 195  |
| 4            | 79       | 194  | 12           | 29       | 194  |
| 5            | 83       | 208  | 13           | 43       | 205  |
| 6            | 27       | 192  | 14           | 182      | 202  |
| 7            | 124      | 207  | 15           | 21       | 209  |
| 8            | 32       | 206  |              |          |      |
| <u>MW-TX</u> |          |      |              |          |      |
| 1            | 74       | 206  | 9            | 92       | 200  |
| 2            | 140      | 207  | 10           | 17       | 194  |
| 3            | 26       | 207  | 11           | 41       | 206  |
| 4            | 74       | 206  | 12           | 33       | 203  |
| 5            | 88       | 209  | 13           | 142      | 206  |
| 6            | 54       | 214  | 14           | 48       | 207  |
| 7            | 67       | 219  | 15           | 38       | 210  |
| 8            | 40       | 209  |              |          |      |

<sup>a</sup>Standard errors ranged from 6.9 to 12.5 kg and were closely related to the number of observations per sire.

APPENDIX TABLE 14. LEAST-SQUARES SIRE X REGION INTERACTION MEANS (kg)  
FOR THE BETWEEN REGION B-DATA SETS (1/2-SIMMENTAL)<sup>a</sup>

| Sire | No. obs. | <u>MT-MW</u>          |  | No. obs. | Midwest    |
|------|----------|-----------------------|--|----------|------------|
|      |          | Montana               |  |          |            |
| 1    | 78       | 203(7-9) <sup>b</sup> |  | 18       | 199(15)    |
| 2    | 5        | 199(12-14)            |  | 69       | 200(13-14) |
| 3    | 9        | 203(7-9)              |  | 47       | 204(7-8)   |
| 4    | 14       | 201(10-11)            |  | 11       | 210(4)     |
| 5    | 37       | 195(17)               |  | 23       | 203(9-10)  |
| 6    | 35       | 218(2)                |  | 38       | 203(9-10)  |
| 7    | 126      | 204(5-6)              |  | 69       | 202(11-12) |
| 8    | 17       | 219(1)                |  | 25       | 213(2)     |
| 9    | 23       | 199(12-14)            |  | 25       | 202(11-12) |
| 10   | 29       | 210(3)                |  | 8        | 211(3)     |
| 11   | 85       | 199(12-14)            |  | 40       | 204(7-8)   |
| 12   | 8        | 197(16)               |  | 16       | 205(5-6)   |
| 13   | 27       | 203(7-9)              |  | 17       | 178(17)    |
| 14   | 137      | 205(4)                |  | 76       | 200(13-14) |
| 15   | 17       | 198(15)               |  | 33       | 205(5-6)   |
| 16   | 5        | 201(10-11)            |  | 2        | 238(1)     |
| 17   | 8        | 204(5-6)              |  | 29       | 185(16)    |

APPENDIX TABLE 14. (CONTINUED)

| Sire         | No. obs. | <u>MT-TX</u> |          |           |
|--------------|----------|--------------|----------|-----------|
|              |          | Montana      | No. obs. | Texas     |
| 1            | 78       | 204 (9-10)   | 54       | 199 (5)   |
| 2            | 5        | 199 (13)     | 73       | 200 (4)   |
| 3            | 14       | 207 (4-5)    | 12       | 191 (8-9) |
| 4            | 33       | 198 (14)     | 46       | 191 (8-9) |
| 5            | 35       | 219 (2-3)    | 48       | 196 (7)   |
| 6            | 8        | 195 (15)     | 19       | 189 (11)  |
| 7            | 113      | 204 (9-10)   | 11       | 210 (2)   |
| 8            | 17       | 222 (1)      | 15       | 190 (10)  |
| 9            | 14       | 206 (6-7)    | 45       | 174 (15)  |
| 10           | 31       | 219 (2-3)    | 5        | 183 (14)  |
| 11           | 30       | 202 (11)     | 63       | 187 (13)  |
| 12           | 8        | 200 (12)     | 21       | 188 (12)  |
| 13           | 27       | 206 (6-7)    | 16       | 204 (3)   |
| 14           | 137      | 207 (4-5)    | 45       | 197 (6)   |
| 15           | 3        | 205 (8)      | 18       | 212 (1)   |
| <u>MW-TX</u> |          |              |          |           |
| 1            | 18       | 210 (12)     | 56       | 203 (5-6) |
| 2            | 67       | 211 (11)     | 73       | 203 (5-6) |
| 3            | 11       | 224 (1)      | 15       | 191 (13)  |
| 4            | 36       | 212 (9-10)   | 38       | 201 (8)   |
| 5            | 39       | 216 (5)      | 49       | 202 (7)   |
| 6            | 21       | 217 (4)      | 33       | 210 (4)   |
| 7            | 54       | 213 (7-8)    | 13       | 224 (1)   |
| 8            | 26       | 223 (2)      | 14       | 195 (12)  |
| 9            | 25       | 212 (9-10)   | 67       | 188 (14)  |
| 10           | 13       | 207 (13)     | 4        | 182 (15)  |
| 11           | 19       | 214 (6)      | 22       | 198 (11)  |
| 12           | 17       | 195 (14-15)  | 16       | 211 (3)   |
| 13           | 87       | 213 (7-8)    | 55       | 199 (10)  |
| 14           | 30       | 195 (14-15)  | 18       | 218 (2)   |
| 15           | 16       | 220 (3)      | 22       | 200 (9)   |

<sup>a</sup>Standard error ranged from 4.0 to 19.8 kg and were closely related to the number of observations per subcell.

<sup>b</sup>Rank within region.

APPENDIX TABLE 15. RESIDUAL AND RANK CORRELATIONS OF THE LEAST-SQUARES SIRE X REGION INTERACTION MEANS FOR THE BETWEEN REGION B-DATA SETS (1/2-SIMMENTAL)

|            | MT-MW  | MT-TX  | MW-TX  |
|------------|--------|--------|--------|
| Residual r | .07**  | -.12** | -.39** |
| Rank r     | -.05** | -.06** | -.34** |

\*\*Different from 1.0(P=.01).



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Sire by region inter-  
actions in Simmental  
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[illegible]