

Genetic and Environmental Factors Affecting Serum Macrominerals and Weights in an Angus-Brahman Multibreed Herd: II. Heritabilities of and Genetic, Environmental, and Phenotypic Correlations Among Serum Calcium, Phosphorus, and Magnesium and Weight at Weaning¹

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ABSTRACT: Heritabilities of and genetic, environmental, and phenotypic correlations among serum amounts of calcium, phosphorus, and magnesium and weight at weaning (WCa, WP, WMg, and WW, respectively) were estimated for an Angus (A)-Brahman(B) multibreed herd located at the Pine Acres Research Station of the University of Florida, Citra. Records were obtained from 380 calves produced by mating A, .75A .25B, .5A .5B, .25A .75B, B, and Brangus sires across dams of the same breed groups, except for .25A .75B, during 1989 and 1990. Restricted maximum likelihood procedures were used to compute variance and

covariance components. Estimates of heritability were .39 (WCa), .40 (WP), .36 (WMg), and .35 (WW). Estimates of genetic, environmental, and phenotypic correlations were .66, .55, .57 (WCa, WP), .70, .71, .70 (WCa, WMg), 1.00, .86, .88 (WCa, WW), .50, .51, .51 (WP, WMg), .78, .60, .63 (WP, WW), and .86, .73, .75 (WMg, WW). These correlations indicate that serum Ca, P, and Mg could be used in multiple-trait genetic evaluation procedures to help identify animals that require low amounts of these macrominerals for preweaning growth. This may prove advantageous in mineral-deficient regions.

Key Words: Beef Cattle, Heritability, Genetic Correlation, Minerals, Weaning Weight, Variance Components

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Introduction

Identification and study of components of growth suitable for genetic evaluation of animals in multibreed populations is needed to improve the accuracy of prediction of genetic values for growth traits, especially in small populations. Primary candidates are traits with known biochemical and physiological links to growth, such as macrominerals. Calcium, phosphorus, and magnesium are three macrominerals that have essential roles in

growth and development. These macrominerals are involved in the activation of enzymes for protein synthesis (Ca, P, Mg), bone formation (Ca, P), and possibly, hypothalamic regulation (Mg) of feed intake (Lewin, 1970; Ammerman et al., 1971; Seoane et al., 1975; Horowitz and Weistein, 1983; Reeds, 1989; Arnaud and Sanchez, 1990; Brostrom and Brostrom, 1990; Darnell et al., 1990).

Beef cattle requirements of Ca, P, and Mg for preweaning growth are normally met using a supplement in the form of mineral blocks or licks. The cost of mineral supplementation is higher in subtropical and tropical areas than in temperate zones, rendering mineral supplementation prohibitively expensive in some developing countries (McDowell et al., 1983). Incidence of deficiencies of Ca and P is higher in subtropical and tropical than in temperate regions (McDowell et al., 1983). Deficiencies of Ca, P, and Mg are not only clinical

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but also subclinical, thus are difficult to detect and can result in reduced weaning weights (Hardt et al., 1989). Amounts of Ca, P, and Mg in serum at weaning are three traits that may aid in the selection of animals for preweaning growth. To use these traits to evaluate animals genetically using multiple-trait mixed-model procedures (Henderson and Quaas, 1976; Quaas and Pollak, 1980), genetic, environmental, and phenotypic variances of and covariances among all these traits need to be estimated. Thus, the objectives of this research were 1) to estimate the heritabilities of the amounts of serum Ca, serum P, serum Mg, and weight at weaning (WCa, WP, WMg, and WW) and 2) to estimate additive genetic, environmental, and phenotypic correlations among WCa, WP, WMg, and WW.

Materials and Methods

Records of macrominerals in serum (WCa, WP, and WMg) and weight at weaning (WW) from 380 calves produced by the matings of five Angus (A), five Brahman (B), three .75A .25B, four .5A .5B, four .25A .75B, and seven Brangus (.625A .375B) sires across 65 A, 76 B, 18 .75A .25B, 38 .5A .5B, and 46 Brangus dams were collected in 1989 and 1990 at the Pine Acres Research Station of the University of Florida, Citra. Except for two .5A .5B bulls that were half-sibs, all the other bulls were unrelated. Calf age at weaning ranged between 151 and 275 d; 91% of the calves were weaned between 210 and 270 d of age. All records were adjusted to 205 d using the Beef Improvement Federation (BIF, 1990) recommended procedures for adjusting weights, with values obtained in the first sampling after birth substituted for the values obtained at the sampling at birth in the BIF adjustment formula because blood samples were not collected at birth. Age at first sampling ranged from 1 to 85 d; 97% of calves were sampled within 70 d of birth.

Amounts of macrominerals were obtained by multiplying estimated serum volume by concentration. Serum volume was computed as the product of the expected fraction of serum in blood (serum volume/blood volume = .6; Jesse, 1979) times the expected fraction of blood in cattle (blood weight/animal weight = .077; Frandson, 1975) times the weight of the animal. Serum concentrations of Ca and Mg were measured by flame absorption spectrophotometry (Model 306, Perkin-Elmer, Norwalk, CT) of serum samples deproteinized with 10% trichloroacetic acid, whereas the concentration of P was determined by colorimetry (Fick et al., 1979).

To ensure connectedness across years, at least one bull from each breed group was used to sire

calves both in 1989 and in 1990. The number of progeny per sire and year fluctuated between 2 and 34 (Table 1). Artificial insemination (first two cycles after synchronization with prostaglandin F_{2α}) and natural service were used in all breed groups of dams. There was one natural-service bull per breed group of sire, resulting in a total of six breeding herds. Natural-service bulls were kept with the cows for 60 d. Subsequently, dams were assigned to only two groups: A and all A × B crossbred groups in one herd and B in the other (June to mid-December). Both groups of cows were maintained on bahiagrass pastures (*Paspalum notatum*) with a complete free-choice mineral supplement only (i.e., no supplement of protein or energy). In winter (mid-December to March), dams were allocated into six replicated supplementation regimens consisting of bermudagrass (*Cynodon dactylon*) hay sun-dried to various DM percentages, molasses, and urea.

Estimation of Heritabilities and Genetic, Environmental, and Phenotypic Correlations

Variance components were estimated using the REML method (Patterson and Thompson, 1971; Corbeil and Searle, 1976). Because all traits were

Table 1. Number of progeny per sire

Breed group ^a	Sire no.	Year		Total
		1989	1990	
Angus	1	7	10	17
	2	8	5	13
	3	7	3	10
	4	16	0	16
.75A .25B	24	0	10	10
	5	20	18	38
	6	6	2	8
	25	0	5	5
.5A .5B	9	2	4	6
	10	6	0	6
	26	0	13	13
.25A .75B	27	0	6	6
	12	9	0	9
	13	4	1	5
	14	6	4	10
Brahman	15	10	21	31
	16	5	4	9
	17	34	0	34
	18	7	33	40
Brangus	19	0	4	4
	29	0	5	5
	20	11	0	11
	21	21	3	24
	22	7	4	11
	23	5	0	5
	30	0	6	6
31	0	4	4	
32	0	24	24	
Total	—	191	189	380

^aA = Angus; B = Brahman.

measured in all animals, a single-trait REML procedure was used to estimate variances and covariances. Computations were carried out using the REML option of the program PROC VARCOMP of SAS (1985). This program 1) uses the W transformation applied to a Newton-Raphson algorithm (Hemmerle and Hartley, 1973; Goodnight and Hemmerle, 1979) to compute variance components and 2) uses the inverse of the information matrix (Corbeil and Searle, 1976) to compute large sample variances of the resulting REML estimates of variance components (R. C. Littell, personal communication). In addition, large sample standard errors of the REML estimates of variance components were computed by taking the square root of the large sample variances.

The mixed model used contained year, winter management within year, natural service herd within year, age at first sampling after birth, and sex of calf \times age of dam subclass as environmental effects, breed group of sire \times breed group of dam subclass, and breed group of maternal grandsire \times breed group of maternal grandam subclass as group genetic effects, sire within breed group of sire, and residual. Subclass effects contained both main effects and the interaction between them. Environmental and group genetic effects were assumed to be fixed. Sires and residuals were assumed to be random, each with a mean equal to zero, common variance, and uncorrelated. The sire variance represented .25 additive direct genetic variance. The residual variance contained .75 additive direct genetic variance, additive maternal genetic variance, nonadditive direct and maternal genetic variances, covariances between direct and maternal random genetic effects, and variances due to random environmental effects. Variance components (sire, residual) for WCa, WP, WMg, and WW were estimated using the same mixed model.

Heritabilities were computed as four times the estimate of the sire variance divided by the phenotypic variance. Phenotypic variances were computed as the sum of the sire plus the residual variances.

Because the REML program of PROC VARCOMP is for a single trait only, covariances were estimated using the formula .5 (estimate of variance [trait 1 + trait 2] - estimate of variance [trait 1] - estimate of variance [trait 2]), as suggested by Searle and Rounsaville (1974). Consequently, REML estimates of sire and residual variance components were estimated for the sums of all possible pairs of traits (WCa + WP, WCa + WMg, etc.). Then, additive genetic, environmental, and phenotypic covariances were computed for all pairs of traits. Environmental covariances were computed as the difference between the estimate

of the residual covariance minus three times the sire covariance. Environmental variances were computed in the same fashion. Phenotypic covariances were obtained by adding sire covariances to residual covariances. Finally, genetic, environmental, and phenotypic correlations among pairs of traits were computed as the ratio of the appropriate covariances to the product of the standard deviations.

Results and Discussion

Estimates of sire and residual variances for all traits (WCa, WP, WMg, WW) and sums of pairs of traits (WCa + WP, WCa + WMg, etc.) are shown in Table 2 accompanied by the large sample standard errors. Estimates of residual variances were consistently estimated with higher accuracy than were sire variances. The mean of the 10 CV ($100 \times$ standard error of variance estimate/variance estimate) of the residual variance estimates ($8.83 \pm .01$) was 7.8 times smaller than that of the sire variance estimates (68.50 ± 2.75).

Heritability estimates were in the medium range (.39 WCa, .40 WP, .36 WMg, .35 WW; Table 3). Thus, selection of animals for or against WCa, WP, and WMg seems feasible. A possible selection goal could be to choose those animals that achieve the largest WW with the lowest requirements of Ca, P, and Mg in a given environment. This selection goal implies that selected animals make more efficient use of these minerals to reach a given WW than do the unselected ones. To

Table 2. Restricted maximum likelihood estimates of variance components for serum Ca, P, and Mg and weight at weaning

Trait ^a	Variance component estimate ^b			
	Sire		Residual	
WCa	5,458	\pm 3,621	50,224	\pm 4,429
WP	4,663	\pm 3,120	41,544	\pm 3,670
WMg	243.9	\pm 178.1	2,444	\pm 216.3
WW	34.76	\pm 25.00	363.9	\pm 32.11
WCa + WP	16,778	\pm 11,055	142,811	\pm 12,626
WCa + WMg	7,308	\pm 4,934	68,287	\pm 6,026
WCa + WW	6,364	\pm 4,206	58,036	\pm 5,118
WP + WMg	5,968	\pm 4,136	54,277	\pm 4,804
WP + WW	5,325	\pm 3,533	46,644	\pm 4,121
WMg + WW	437.6	\pm 313.4	4,205	\pm 372.3

^aWCa, WP, WMg, and WW = serum Ca, P, Mg, and weight at weaning.

^bEstimates of variance components are expressed in milligrams squared for WCa, WP, and WMg, in kilograms squared for WW, in (milligrams + milligrams)² for sums of macromineral traits and in (milligrams + kilograms)² for sums of macromineral traits and WW.

Table 3. Estimates of heritabilities of and genetic, environmental, and phenotypic correlations among serum Ca, P, and Mg and weight at weaning^a

Trait ^b	Trait			
	WCa	WP	WMg	WW
WCa	.39	.66	.70	1.00
WP	.55(.57)	.40	.50	.78
WMg	.71(.70)	.51(.51)	.36	.86
WW	.86(.88)	.60(.63)	.73(.75)	.35

^aHeritabilities are on the diagonal; genetic correlations are above the diagonal; environmental and phenotypic (in parentheses) correlations are below the diagonal.

^bWCa, WP, WMg, WW = serum Ca, P, Mg, and weight at weaning.

identify animals with these characteristics, a multiple-trait evaluation system for four traits (WCa, WP, WMg, WW) would need to be used. In addition to heritabilities, this genetic evaluation system would need the values of genetic and environmental correlations among all pairs of these four traits. Amounts of macrominerals in the various body tissues (e.g., muscle, bone, serum) have a biological part-whole relationship with weights. Thus, WCa, WP, and WMg were expected to be correlated with WW. However, because WW was used to predict WCa, WP, and WMg, estimates of genetic, environmental, and phenotypic correlations among these traits may have been higher than the ones that would have been obtained had actual measurements of amounts of macrominerals in serum been taken. This expected overestimation of these correlations could not be quantified here because it was not feasible to obtain direct measurements of amounts of serum Ca, P, and Mg. Estimates of genetic correlations between WCa, WP, and WMg and WW were high and positive (1.00, .78, and .86, Table 3). Also, all estimates of genetic correlations among macromineral traits were positive (.66 for [WCa, WP], .70 for [WCa, WMg], .50 for [WP, WMg], Table 4). The positive estimates of genetic correlations suggest that there could be animals that would need lower amounts of Ca, P, and Mg to achieve the same weaning weight. However, given the high values of the estimates of the genetic correlations between WW and WCa, WP, and WMg, the number of animals with high WW and low WCa, WP, and WMg is likely to be small.

High values of genetic correlations among WCa, WP, and WMg and WW were expected because of the known physiological relationships among these traits. The same hormones (parathyroid hormone, 1,25-dihydroxycholecalciferol [1,25-(OH)₂D₃], calcitonin) regulate their role in growth and development. Parathyroid hormone activates 1,25-(OH)₂D₃, which in turn

causes an increase in the absorption of Ca, P, and possibly Mg, in the intestine. Conversely, calcitonin increases the excretion of Ca, P, and Mg in the urine and(or) decreases their resorption from skeletal tissue (Littledike and Goff, 1987; Arnaud and Sanchez, 1990; Shils, 1990, Hardwick et al., 1991).

Estimates of environmental correlations among macromineral and weight traits at weaning, like the estimates computed for genetic correlations, were also positive, ranging from .51 between WP and WMg to .86 between WCa and WW (Table 3). External environmental stimuli may have caused these environmental correlations. For instance, irradiation of the skin with ultraviolet light from the sun initiates the conversion of 7-dehydrocholesterol to 1,25-(OH)₂D₃, which in turn increases the efficiency of intestinal absorption of Ca, P, and, perhaps, Mg (Littledike and Goff, 1987; Hardwick et al., 1991).

Estimates of phenotypic correlations (Table 3) fluctuated between .51 (WP, WMg) and .88 (WCa, WW) and generally were lower than the estimates of genetic correlations and larger than the environmental correlations.

No estimates of heritability for WCa, WP, and WMg and of genetic, environmental, and phenotypic correlations among these traits and with WW were found in the literature.

The estimate of heritability for WW (.35) obtained for this Angus-Brahman multibreed herd was smaller than the value of .44 reported for Angus by Kennedy and Henderson (1975), equal to the one computed by Nelsen and Kress (1979), also for Angus, and higher than the estimates of .26 calculated by Malagon and Duran (1985) for Brahman and of .25 calculated by Bertrand and Benyshek (1987) for Brangus.

The estimates of heritabilities and genetic, environmental, and phenotypic correlations were based on measurements taken on animals that had an adequate dietary supply of Ca, P, and Mg. However, these genetic parameters, especially correlations, may differ substantially under deficiency conditions. Thus, this research needs to be repeated under various nutritional regimens in which the supply of one or more of these macrominerals is insufficient to meet animal requirements. Because this may be infeasible, identification of animals that require lower amounts of Ca, P, and Mg for preweaning growth in a good nutritional environment may, in practice, be the first step in the identification of animals capable of adequate growth and development under conditions of limited availability of these minerals. Semen or sires, and dams if possible, with these characteristics could then be taken to areas with known deficiencies of Ca, P, and(or) Mg, and

progeny tested for WCa, WP, and WMg and WW under local conditions. The assumption here is that WW and WCa, WP, and WMg in these two environments (high and low nutritional environments) behave as two correlated sets of traits (the concept of treating a character measured in two different environments as two separate traits was first suggested by Falconer, 1952). In the event that weight and serum macromineral records were obtained in the high and the low nutritional environments, a multiple-trait analysis that considers information from both environments (Elzo and Bradford, 1985) could be conducted. Such analysis would require estimates of variances and covariances among WW and WCa, WP, and WMg measured within the high and the low nutritional environments as well as covariances between WW and WCa, WP, and WMg measured in the high nutritional environment with WW and WCa, WP, and WMg measured in the low nutritional environment.

In addition to Ca, P, and Mg, other macrominerals (e.g., Na, K), trace minerals (e.g., Se, I, Co), and vitamins (e.g., D, K) with known physiological effects on growth and development (Underwood, 1981; McDowell, 1989) also need to be studied as traits of potential use to aid in the selection of animals for growth or as target traits themselves. In the future, these nutritional traits could be used in conjunction with other biological traits (e.g., insulin-like growth factors) in a multiple-trait context to predict more accurately the growth and developmental behavior of individual animals. These traits need not only be studied at weaning, but at earlier ages, including birth. Of particular importance will be the genetic relationship between traits measured at birth and later in life. Having predictions of genetic values of a large number of biological traits (e.g., nutritional, physiological) as well as weights will allow the selection of animals that have much better-defined nutritional requirements and growth patterns than selecting animals based on weight traits alone. Because the number of traits may become very large, several multiple-trait analyses, each containing a subset of the total number of traits, may need to be conducted instead of a large analysis that includes all traits.

Implications

Macrominerals such as calcium, phosphorus, and magnesium have known physiological and biochemical links to growth and development of animals. The estimates of heritabilities and genetic correlations computed here indicate that amounts of calcium, phosphorus, and magnesium

in serum are heritable traits that are positively correlated with weaning weight. These macromineral traits could help identify animals that make more efficient use of calcium, phosphorus, and magnesium for preweaning growth, which would be especially advantageous in mineral-deficient areas.

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