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HERITABILITIES OF AND GENETIC, ENVIRONMENTAL AND PHENOTYPIC CORRELATIONS AMONG SERUM POTASSIUM AND SODIUM AND WEIGHT AT WEANING IN AN ANGUS BRAHMAN MULTIBREED HERD

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Introduction

Sodium (Na) and potassium (K) are essential elements in animals. They are involved in osmotic balance, acid base regulation and water balance (Underwood, 1981). Potassium also is involved in ionic balance controlling cellular excitability and activation of several enzyme systems (Underwood, 1981), including that of amino acid chain elongation during protein synthesis (Lewin, 1970). Increased K also causes release of insulin (Church, 1988) which is a growth factor for cells (Darnell, 1990). In ruminants Na neutralizes acidic compounds produced by rumen fermentation (Payne and Payne, 1987). Both K and Na are constituents of milk (Underwood, 1981; Beede et al., 1983) and thus are available to calves through their dams.

Sodium supplementation of grazing beef cattle in the form of common salt (sodium chloride) is a widely accepted practice in most countries (Minson, 1990); however, both K and Na also are critical in tropical countries because of higher loss of these elements in sweat (Underwood, 1981; Beede et al., 1983; McDowell et al., 1983). Furthermore, under heat stress conditions such as experienced in subtropical and tropical conditions, homeostatic mechanisms attempt to maintain body temperature by reducing feed consumption (McDowell, 1972); consequently, intake of essential

[1]Animal Breeding Mimeo, University of Florida, 1992, pp 1-15.

nutrients including K and Na can be reduced. Potassium and Na may be important under these conditions since they are major regulators of water balance (Vander, 1980).

Supplementation of K and Na is limited in tropical and subtopical developing countries because of exorbitant cost and/or unavailability. Thus, losses due to deficiencies of these elements are more pronounced in tropical and subtropical countries relative to temperate countries.

Frequently salt is used as a regulator of intake of supplements provided free choice to animals on range. Strategic placement of salt or salt meal mixture on range also is purported to give better distribution of grazing.

Weaning weight (WW) is an important selection criterion in beef animals because it reflects the preweaning growth of the calf. It also is moderately inherited and has moderate to high genetic correlation with postweaning weight and carcass traits. Thus, genetic improvement of WW is necessary. Genetic improvement of WW is influenced among other factors by heritability of the trait and by genetic, environmental and phenotypic correlations with correlated traits. Traits correlated with WW can increase accuracy of selection for WW, thus enabling genetic progress of WW to increase.

Despite the nutritional and physiological significance of K and Na macrominerals, there are apparently no genetic studies that relate them to growth. Thus, objectives of this study were:

i. to estimate heritabilities of amounts of serum K and Na at weaning and WW and

ii. to estimate additive genetic, environmental and phenotypic correlations among K and Na at weaning and WW.

Materials and Methods

Animals

In two years of research, 1989 and 1990, six herds of cows representing a multibreed herd was maintained. The herds were composed of: 65, 76, 18, 38 and 46 cows representing Angus (A), Brahman (B), .75A.25B, .5A.5B and Brangus, respectively. Paternal half sibs were produced by mating all the six breed group of sires across breed groups of dams in a diallel type of mating . The animals were located at Pine Acres Research Center, Citra, Florida. The 243 cows ranged between 3 and 8 years of age. They were bred artificially (in March for A and AxB dams and April for B dams) following estrus synchronization with prostaglandin $F_{2\alpha}$ and subsequently assigned to six clean up herds for 60 days with one bull representing each breed group. Connectedness across years and herds was created by assigning at least one bull from each breed group to sire calves in both years. In the two years, the largest number of sires (Table 1) were from purebred sires (7 for Brangus, 5 for B and 5 for A). Correspondingly, the largest number of progeny were from the purebred sires (92 for B, 85 for Brangus and 66 for A).

The six cow herds were maintained on bahiagrass pastures (Paspalum notatum) with a complete free choice mineral supplement containing 20% calcium, 9% phosphorus, .25% magnesium, 6.12% sodium and 18.18% chlorine. In winter and early spring (Mid-December to March), the dams were assigned to six replicated forage supplementation regimens and a control herd. The diet consisted of molasses and bermudagrass (Cynodon dactylon) hay fortified with urea (32% Nitrogen).

Records

Blood was taken from a total of 380 calves and serum was extracted from it. Weight at weaning (WW) was measured concurrently with blood sampling. Since colostrum was not of interest, the first blood sample was taken after about 7 days postpartum. Mineral concentrations of K and Na were determined from solutions made from serum (Fick et al., 1979). The atomic absorption spectrophotometry method was used to determine the mineral concentrations. All calves were weaned at approximately 7 months of age.

Table 1. DISTRIBUTION OF SIRES AND CALVES BY BREED GROUP OF SIRE

Breed[a] group	Number of sires	Number of calves 1988	1989	per sire	Total
A	5	38	28	13.2	66
.75A.25B	3	26	25	17.0	51
.5A.5B	4	8	23	7.8	31
.25A.75B	4	29	26	13.8	55
B	5	46	46	18.4	92
Brangus	7	44	41	12.1	85
Total or average	28	191	189	13.6	380

[a]A = Angus, B = Brahman

The records were adjusted to 205 days using the Beef Improvement Federation (BIF, 1990) recommendations. Concentrations of K and Na of the first samples were taken to represent those at birth since no samples were taken at birth. The amounts of these minerals were estimated as a product of estimated serum volume and concentration. Serum volume was estimated as a product

of the weight of the calf, expected fraction of blood in cattle relative to weight (.077; Frandson, 1975) and expected fraction of serum in blood relative to blood volume (.6; Jesse, 1979).

Estimation of Variances, Covariances and Heritability

Estimates of variances and covariances were obtained using the restricted maximum likelihood (REML) method (Patterson and Thompson, 1971; Corbeil and Searle, 1976). Variance components procedure, single trait option, (SAS, 1985) was used for computation. Dependent variables included amount of K at weaning (WK) , amount of Na at weaning (WNa) and weight at weaning (WW). The mixed model contained fixed group environmental effects including: year of birth of calf, winter management within year, age at initial sampling after birth, sex, age of dam and interaction of sex and age of dam. Fixed genetic effects also included the interactions of breed group of sire and breed group of dam and those of breed group of maternal grandsire by breed group of maternal grandam. Random effects were sire within breed group of sire and residual. All the sires were unrelated except two that were half sibs. Fixed effects were assumed to have mean zero, common variance and to be uncorrelated. Assuming that sire differences are entirely genetic, variances of sires (σ^2_s) within sire groups represents .25 additive direct genetic variance (σ^2_A). That is $\sigma^2_A = 4\sigma^2_s$. This σ^2_A represents the component of variance for half sibs. The residual variance (σ^2_R) represented .75 additive direct genetic variance, additive maternal genetic variance and nonadditive (direct and maternal) genetic variances, covariances between direct and maternal genetic effects and variances due to random environmental effects (σ^2_E) . Thus, σ^2_E was computed as: $\sigma^2_R - 3\sigma^2_s$.

Covariances were estimated for additive genetic, phenotypic and environmental components using a linear function of the variance of the sum of two traits (X, Y) and the variance of the

individual traits (Searle and Rounsaville, 1974). Thus, the covariance of traits X and Y = .5[Var (X + Y)] -.5Var X - .5Var Y since Var (X + Y) = Var X + Var Y + 2Cov (X, Y). Thus, REML estimates of sire and residual components of variance were estimated as the sum of all possible pairs of traits (WNa + WK, WNa + WW, WK + WW). Environmental covariances were computed as the difference between residual covariance and three times the sire covariance, whereas phenotypic covariance was estimated as a sum of sire and residual covariances. The genetic, environmental and phenotypic correlations were computed as a ratio of the covariance of the traits to that of the square root of the product of the variance of the individual traits.

Results and Discussion

Restricted maximum likelihood estimates of variance components for WK, WNa and WW are shown in Table 2. Sire variance estimate for WW was 34.76 ± 25.00 kg^2. Thus, variation of WW due to sire was small. The estimate was within (21 to 52 kg^2) that reported by Kennedy and Henderson (1975) for the Angus. Residual variance of WW for 363.92 ± 32.11 kg^2 also was close to the 381 to 395 kg^2 reported by Kennedy and Henderson (1975) in Angus. The variance component due to sire for WK was large (11210.64 ± 21710.57 mg^2) but with a corresponding large standard error. The sire variance component for WNa was large with a smaller standard error (4209818.49 ± 2614974.72 kg^2) relative to that of WW and WK. The residual variances for WK and WNa were large with small standard errors (470293.06 ± 41545.17 mg^2 for WK, 32323947.63 ± 285633.99 mg^2 for WNa). The sire variance was relatively smaller than residual variance and accounted for only 2.33%, 11.52% and 8.72% of total variation in WK, WNa and WW respectively. No estimates of variance components for WK and WNa were found in the literature. Residual

variances were estimated with higher accuracy than sire variances in all the traits. The type of feed on which the animals were maintained might have not been good enough to produce maximum milk production and thus enable calves to express more fully their genetic potential.

Table 2. RESTRICTED MAXIMUM LIKELIHOOD ESTIMATES OF VARIANCE COMPONENTS FOR SERUM POTASSIUM AND SODIUM AND WEIGHT AT WEANING

	Variance component estimates[2]	
Trait[1]	Sire	Residual
WK	11210.64 ± 21710.57	470293.06 ± 41545.17
WNa	4209818.49 ± 2614974.72	32323947.63 ± 2856337.99
WW	34.76 ± 25.00	363.92 ± 32.11
WK + WNa	4693832.00 ± 95083.55	37928651.97 ± 33528.64
WK + WW	12673.95 ± 22960.23	486523.80 ± 42996.45
WNa + WW	4235060.60 ± 83184.52	32509670.02 ± 90844.85

[1]WK, WNa, WW = serum K, and weight at weaning.
[2]Estimates of variance components are expressed in mg^2 for WK and WNa, in kg^2 for WW, in $(mg + mg)^2$ for sums of macromineral traits and in $(mg + kg)^2$ for sums of macromineral traits and WW.

Heritability estimates (h^2) for WK, WNa and WW are presented in Table 3. The estimates were .09 for WK, .46 for WNa and .34 for WW. The estimate for WW agreed with those reported in the literature (.37; .4; .44; .25; Nelsen and Kress, 1979; Schaeffer and Wilton, 1981; Kennedy and Henderson, 1975; Bertrand and Benyshek, 1987). The low h^2 for WK indicates that the trait cannot be improved by selection based on individual's records. On the other hand, the moderate h^2 estimates of WNa and WW indicate that selection based on the individual's record could improve these traits.

Improved efficiency in utilization of WNa would be advantageous in deficiency situations and in tropical and subtropical areas because of heat stress that results in increased loss of endogenous Na (Underwood, 1981). The low h^2 estimate of WK (.09) confirms the property of K to be susceptible to environmental influences. For instance, hemolysis frequently occurs as a result of leakage of K from the erythrocytes during separation of serum from hematocrit.

Estimates of genetic, environmental and phenotypic correlations between WK, WNa and WW are presented in Table 3. Genetic correlation between WK and WNa was high, above unity and positive (1.03). This possibly was because of random errors associated with the few number of sires and corresponding few progeny per sire (Table 1).

Table 3. ESTIMATES OF HERITABILITIES (±SE) AND GENETIC (±SE), ENVIRONMENTAL AND PHENOTYPIC CORRELATIONS AMONG SERUM POTASSIUM AND SODIUM AND WEIGHT AT WEANING

Trait[2]	WK	WNa	WW
WK	.09 ± .10	1.03 ± NE	.94 ± .06
WNa	.65 (.67)	.46 ± .18	.94 ± .04
WW	.59 (.62)	.84 (.87)	.35 ± .16

[1]Heritabilities on the diagonal; genetic correlations above the diagonal; environmental and phenotypic (in parenthesis) correlations below the diagonal.
[2]WK, WNa, WW = Serum K, Na and weight at weaning.
NE = Not estimable.

However, the high positive genetic correlation indicates that many of the same alleles that affect WK also affect WNa. This observation is supported by the physiological functions that K and Na jointly perform. For instance, both minerals function in maintaining acid-base and osmotic balances within the animal cells (Underwood, 1981; Minson, 1990). During deficiency of Na, K can

replace Na (Underwood, 1981). This occurs as a result of increased secretion of aldosterone hormone by the adrenal glands and an increase in the sensitivity of the parotid glands (Underwood, 1981). Sodium is required by the kidney for K conservation and to balance bicarbonate excretion (Vander, 1980). The transport of Na and K ions across the cell membrane also is catalyzed by one enzyme, Na, K ATPase (Darnell et al., 1990). The transfer of these ions is stimulated by insulin (White et al., 1968). The synthesis of this enzyme is induced by aldosterone in combination with triiodothyronine (Morel and Doucet, 1986). The action of aldosterone requires the presence of thyroid hormone (Morel and Doucet, 1986). In rats glucocorticoids have been shown to sustain Na, K ATPase activity by inducing the synthesis of lipocortin (Morel and Doucet, 1986), a protein that inhibits phosphorylase A_2 (Reeds, 1989). Arachidonic acid then is released, stimulating production of prostaglandin $F_{2\alpha}$ and E_2, which are proposed to effect protein phosphorylation. This process results in protein accretion and dephosphorylation which in turn results in protein degradation (Reeds, 1989). It is plausible that aldosterone, triiodothyronine, glucocorticoid and insulin hormones have pleiotropic effects on K and Na. All these processes of metabolism of K and Na suggest that many of the same alleles that influence serum WK also influence serum WNa.

Genetic correlations between WK and WW (.94) and between WNa and WW (.94) were high suggesting that many of the same alleles that affect WK and WNa also affect WW positively. This magnitude of genetic correlation between WK and WW and between WNa and WW support the physiological link that exists between these minerals and growth. Potassium activates chain elongation during protein synthesis (Lewin, 1970). Linderman and Pederson (1983) and Durand and Kawashima (1980) also have reported that K is required for protein synthesis. Potassium also activates pyruvate kinase which catalyses carbohydrate synthesis (Lehninger, 1984). Insulin

promotes: i) the conversion of carbohydrates into triacylglycerol, ii) amino acid uptake by muscle cells, iii) ribosome aggregation as polyribosomes, iv) aminoacyl-tRNA binding to ribosomes and v) the number and activity of ribosomes (Beitz, 1985). Thus, K may be contributing to growth through protein and fat synthesis and this might be the basis of high genetic correlation between WK and WW. On the other hand, Na is essential for cellular uptake of glucose through activation of the glucose carrier protein (NRC, 1984). The carrier protein must bind Na ions in order to bind glucose (White et al., 1968). Thus, the presence of Na may be a rate limiting factor in carbohydrate metabolism which in turn may limit growth. Lingrel et al. (1990) reported that increased intracellular Na stimulates Na, K-ATPase activity whereas Vandenburgh and Kaufman (1981) observed that Na, K-ATPase is one of the initiating events associated with stretch induced protein synthesis. Similarly, it has been observed that in cultured fibroblasts, lymphocytes and neuroblastoma cells that Na, K-ATPase activates deoxyribonucleic acid synthesis and cell hyperplasia (Kaplan, 1978; Rozengurt and Mendoza, 1980; Mummery et al., 1981). Thus, the high genetic correlation between WNa and WW may be through these physiological processes.

The high positive genetic correlations between these mineral traits and WW suggest that it might be possible to have animals that need lower amounts of WK and WNa to achieve the same weaning weight. Thus, a possible selection criterion could be to select calves with higher efficiency of WK and WNa utilization to achieve the same weaning weight. These would be animals with lower WK and WNa requirements and larger WW. This approach would take advantage of the animal's physiological homeostatic mechanism by resulting in an increase in aldosterone secretion which would reduce the amount of K and Na excreted. However, little genetic change would be expected from selecting animals with low WK since WK has low h^2. Thus, more emphasis would be placed

on WNa than WK. Since Na also is involved in carbohydrate synthesis which can be metabolized into fatty acids, single trait selection for WNa might increase fat deposition. A study by Evans (1954) elucidated this. In this study, fat tailed Lebanese sheep were found to have higher levels of K and Na than Merino sheep which are not fat tailed. Thus, selection for moderate amount of WNa may play an important role in energy conservation through storing energy reserves as fat when feed is abundant and mobilizing fat to supply energy in times of energy shortage. This selection procedure would be particularly advantageous in very extensive grazing conditions similar to those experienced in most tropical areas.

Estimates of environmental correlations among all the traits were high and positive. The values were .65 for WK and WNa which suggests that WK responds to many of the same environmental factors in a similar manner as WNa. The environmental correlation between WK and WW was .59 and that between WNa and WW was .84. Thus, WK and WNa respond to many of the same environmental factors affecting WW. These high environmental correlations might have been attributed to common environmental factors affecting all the three traits. For example, a decrease in feed intake due to nutritional changes might decrease thyroid hormone function which in turn would reduce the activity of Na, K-ATPase (Lingrel et al., 1990), thus resulting into reduced WK and WNa. Reduced activity of Na, K-ATPase would result in decreased energy available for metabolism (Beitz, 1985) , thus reducing WW. Similarly, decreased protein intake would decrease insulin production which would impair glucose utilization resulting in less pyruvate being converted to acetyl coA. This would result in less fatty acid synthesis which would in turn result in reduced WW. A decrease in insulin would result also in decreased Na, K-ATPase activity (Lingrel et al., 1990). Differences in milk yield which may be higher in crossbred A x B dams relative to

straightbred dams may result also in a high environmental effect because of larger quantities of milk and amount of K and Na that would be available to the calf.

Phenotypic correlations between the mineral traits and those between the mineral traits and WW also were high and positive. The values were .67 between WK and WNa, and .62 between WK and WW and .87 between WNa and WW. Thus, selection on phenotypic value for any one trait will result in a correlated phenotypic increase in the other traits.

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