lactation (ME_l) are estimated as 1.25 Mcal for I kg of 4 percent fat corrected milk, and a value was given for mobilized tissue. Pregnancy requirements consider average birth weight per kid, day of gestation, and litter size. Previous protein requirements were given as crude (CP) or digestible crude protein. The new recommendation considers metabolizable protein (MP) for all functions. A conversion of MP to CP is given to facilitate its use. An estimate of rumen degraded intake protein is also given as a general guideline.

Key Words: Energy, Protein, Goats

454 Vitamin requirements of goats. B. W. Hess*, *University of Wyoming*, *Laramie*.

Vitamins are a group of complex organic nutrients that are essential for multiple metabolic processes but, unlike other organic nutrients, vitamins are required in minute amounts (µg to mg/d). Because estimates of endogenous vitamin losses are non-existent, vitamin requirements are based on animal responses during feeding trials. Recommendations for vitamin requirements are complicated by selection of the criteria by which the vitamins are judged adequate or inadequate. As in past NRC publications, vitamin requirements of goats are often derived from values for sheep. Unlike previous requirements for vitamin A, newly established requirements are based on the animal′s ability to maintain 20 µg of retinol/g of liver and are expressed as retinol equivalents (RE). Daily intake of 31.4 RE/kg of live BW is deemed necessary for animals at maintenance. Vitamin A requirements increase to 45.5 RE/kg of live BW for nannies during late gestation, 53.5 RE/kg of live BW for lactating nannies, and 100 RE/kg of live BW for growing kids. Due to insufficient data published to the contrary, the vitamin D requirements for all classifications of goats are comparable to previous recommendations. Daily vitamin E intake of 5.3 IU/kg of live BW is required to maintain blood α–tocopherol concentrations ≥ 2 µg/mL. Provision of 5.6 IU/kg of live BW during late gestation is recommended to increase serum α–tocopherol concentrations of the neonate. Vitamin E requirements increase to 10 IU of vitamin E/kg of live BW when the goal is to enhance immune response or extend the storage case life of meat. In general, vitamin K and water–soluble vitamin requirements of goats can be met by escape of dietary sources from ruminal metabolism and through endogenous synthesis (microbial or bodily). Although several studies have demonstrated production or health benefits when diets have been supplemented with water–soluble vitamins, the amounts of vitamins given to induce such responses are usually for specialized situations and may not necessarily reflect requirements for various production functions. Additional research is needed to establish recommendations for requirements of water-soluble vitamins for goats.

Key Words: Goats, Vitamins, Requirements

455 Revised guidelines for mineral requirements of goats. S. G. Solaiman*, *Tuskegee University*, *Tuskegee, AL*.

Mineral requirements of an animal largely reflect the nutritional demands during different physiological phases. Minerals are required for maintenance, growth, conceptus product formation, and milk production. Borderline mineral intake may compromise animal performance and longevity. Specific mineral deficiencies vary and animal may deplete the pool of tissue minerals before deficiency symptoms are exhibited. Inadequate mineral supplies may reduce production, prolong the duration of parturition, increase the number of stillbirths and result in a higher occurrence of skeletal problems. Many advances in mineral nutrition and metabolism have resulted in establishing guidelines for requirements of different species. However, there are relatively few original scientific research reported on mineral nutrition and metabolism of goats that can be used in establishing the guidelines for this species. Also most of the reported literature is largely speculation based on analogy with cattle and sheep, thus, made our task more challenging. However, few advances in recent years have allowed more specific recommendations for some macro and trace minerals based on goat data. The present report is an assessment of original research conducted on goats and where possible, mineral requirements are calculated by factorial methods using goats, cattle and sheep data. Therefore, the proposed requirements are generalizations and their application to specific breeds and conditions may vary.

Key Words: Goat, Minerals, Requirements

Growth and Development - Livestock and Poultry I

456 Specie and age effects on IGF mRNA expression in the amniotic and allantoic membranes and jejunum of developing avian species. D. M. Karcher* and T. J. Applegate, *Purdue University*, *West Lafayette, IN*.

Insulin-like growth factor (IGF) concentrations change in amniotic and allantoic fluids during development in the chicken, duck, and turkey. However, IGF contribution by the embryo has not been evaluated. This study investigated mRNA transcript abundance in the amniotic and allantoic membranes and jejunum throughout development and among three avian species. Eggs were set (540/specie) and 5 embryos were sampled every other day during incubation through 7 days post-hatch. RNA was extracted and mRNA transcripts for IGF-I, IGF-II, and IGF-R were evaluated by quantitative PCR at d -7, -4, 0 (hatch), 1, 3. Statistical differences were detected using proc mixed in SAS. The starting abundance of chicken IGF-I mRNA in the allantois increased 25-fold from d -7 of incubation to d -4. Within d -4, chicken IGF-I transcript abundance was 8.6 times greater than turkey ($P<0.05$) in the allantoic membrane. However, no differences were detected in membranes for IGF-II or IGF-R among species. The jejunum was evaluated prior to hatch and both jejunum and jejunum mucosa post-hatch. IGF-I transcript abundance was 3.4 fold higher ($P<0.05$) in the chicken compared to turkey at d -7. Turkey and duck were significantly lower ($P<0.05$) than chicken at d -4 in the jejunum. The chicken jejunum IGF-I transcript peaked at 1 d post-hatch versus ($P<0.05$) hatch and 3 d post-hatch. Chicken IGF-I mRNA in the jejunum was significantly higher ($P<0.05$) than both duck and turkey at 1 d post-hatch. The IGF-I mRNA in the duck's jejunal mucosa peaked at 3 d post-hatch and was significantly greater ($P<0.05$) than turkey and chicken at 3 d post-hatch. Chicken jejunum contained significantly ($P<0.05$) more IGF-I transcript when compared to the jejunum mucosa at 1 d post-hatch, while duck jejunum mucosa was statistically ($P<0.05$)

greater than the jejunum at 3 d post-hatch. Greater transcript abundance in the mucosa at 3 d post-hatch may lead to higher IGF-I protein expression enhancing IGF-I effects on jejunum mucosa. No differences were observed in jejunum or jejunum mucosa for IGF-II or IGF-R during the incubation or post-hatch periods for all three species suggesting the majority of transcript is produced within the mucosa.

Key Words: IGF, Amnion, Small Intestine

457 The role of glypican-1 glycosaminoglycan chains in myogenic satellite cell proliferation, differentiation, and fibroblast growth factor 2 responsiveness. X. Zhang*[1], C. Liu[1], K. E. Nestor[1], D. C. McFarland[2], and S. G. Velleman[1], [1]*Ohio Agricultural Research and Development Center, The Ohio State University*, *Wooster*, [2]*South Dakota State University*, *Brookings*.

The glypicans are a family of cell-surface heparan sulfate proteoglycans consisting of a core protein covalently attached with glycosaminoglycans (GAG). Only glypican-1 is expressed in skeletal muscle and increases in expression during myoblast differentiation. Previous studies have suggested that glypican-1 influences fibroblast growth factor 2 (FGF2) signaling pathway by its heparan sulfate chains. A turkey glypican-1 full length cDNA (1,650 bp, GenBank acc. no. AY551002) with three potential GAG attachment sites at Ser483, Ser485, and Ser487 was cloned into the pCMS-EGFP vector. To investigate the functional contribution of each GAG chain, the wild type glypican-1, one-chain and no-chain mutants, and the pCMS-EGFP vector without an insert were transfected into turkey myogenic satellite cells. The transfected cell cultures were assayed for cell proliferation, differentiation, and FGF2 responsiveness. All the data were summarized as mean ± SEM analyzing by an ANOVA and two-sided P values of $P < 0.05$ were considered statistically significant. The overexpression of wild type glypican-1 increased FGF2 responsiveness during proliferation and increased the process of differentiation but did not affect proliferation when compared to the one-chain, no-chain mutants, and the pCMS-EGFP vector without an insert. To support the overexpression data, glypican-1 expression was reduced using a small interfering RNA against turkey glypican-1. Inhibition of glypican-1 expression decreased myogenic satellite cell proliferation, differentiation and FGF2 responsiveness during proliferation. We conclude that glypican-1 function requires all the GAG chains for myogenic satellite cells to increase FGF2 responsiveness during proliferation and to affect the process of differentiation.

Key Words: Glypican, Muscle, Turkey

458 Reduction in cell responsiveness to transforming growth factor-beta by decorin overexpression increases satellite cell proliferation and differentiation. X. Li*[1], D. C. McFarland[2], and S. G. Velleman[1], [1]*Ohio Agricultural Research and Development Center, The Ohio State University*, *Wooster*, [2]*South Dakota State University*, *Brookings*.

Muscle development is a highly organized process regulated by interactions between muscle cells and their extracellular matrix (ECM) environment. The ECM, through its regulation of growth factors, plays a pivotal role in muscle growth and repair. Transforming growth factor-beta (TGF-β) is a potent inhibitor of muscle cell proliferation and differentiation. Decorin, a small ECM proteoglycan, binds to TGF-β and modulates TGF-β activity during muscle cell growth and development. However, its interaction with TGF-β is not well characterized. The objective of this study was to examine the interaction of TGF-β and decorin during myogenesis. Chicken myogenic satellite cells isolated from the pectoralis major muscle were used to investigate the biological functions of TGF-β and decorin during myogenesis. Satellite cells are considered to be myogenic precursors for muscle growth and repair. In the present study, the satellite cells were transfected in vitro with a full-length chicken decorin cDNA. The effect of decorin on cell proliferation was monitored by measuring the DNA content of sample wells. The effect of decorin on cell differentiation was assessed by measuring changes in muscle-specific creatine kinase levels. Decorin overexpression increased both satellite cell proliferation and differentiation rates compared to the control cells. Furthermore, decorin overexpressing satellite cells were less sensitive to TGF-β during both proliferation and differentation. These results suggest that decorin reduces satellite cell responsiveness to TGF-β signaling, leading to an increase in satellite cell proliferation and differentiation.

Key Words: Decorin, Transforming Growth Factor-Beta, Satellite Cell

459 Bone mineralization in four Cobb pedigree lines of meat-type chickens. P. Talaty*[1], M. N. Katanbaf[2], and P. Y. Hester[1], [1]*Purdue University*, *West Lafayette, IN*, [2]*Cobb-Vantress, Inc.*, *Monticello, KY*.

Previous work in our laboratory showed that 4 strains of commercial broilers (Cobb 500, Cobb 500T, Ross 308, and Cobb 700) did not differ in bone mineralization (Talaty et al., 2006, Poultry Sci. 85: (suppl. 1): 16). The purpose of the current study was to determine the variability of bone mineral density (BMD) and bone mineral content (BMC) of the tibia and humerus of four pedigree lines of Cobb breeders from 6 to 24 wk of age. Four purebred lines (A, B,C, and D) of male and female Cobb breeders were each placed in littered floor pens of 3 replicates each from hatch to 24 wk of age at stocking densities similar to industry standards. Feed restriction was initiated at 6 wk of age. Healthy birds without lameness and broken bones were selected for scans at 6, 15, and 24 wk of age. Different birds were scanned at each age. Bone mineralization of 9 birds/line/sex/age was determined using dual energy X-ray absorptiometry (DEXA).Using the mixed model procedure of SAS, mineralization data were analyzed using an analysis of covariance with BW as a covariant. Results indicated that the CV for BMD and BMC ranged from 11 to 19%. The BMD was similar among pedigree lines. An age related increase ($P < 0.001$) in BMD occurred between 6 wk (mean = 0.224^{b} g/ sq cm, CV = 14%) and 15 wk (mean = 0.244^{a} g/sq cm, CV = 13%) with no further increase noted at 24 wk of age (mean = 0.244^{a} g/sq cm, CV = 17%). The BMC was similar among pure-bred lines of Cobb chickens at 6 and 15 wk of age; however, at 24 wk of age, Line C had higher BMC than Lines A and D, but did not differ from Line B resulting in a line × age interaction ($P < 0.01$).The higher BMC of Line C was mainly due to increase bone length and bone area. Since differences in BMC among lines did not occur until 24 wk of age and there were little to no differences in BMD among pedigree lines of chickens suggest that 6 to 8 wk old progeny derived from these lines may not differ in bone mineralization.

Key Words: Bone Mineralization, Bone Mineral Density, Pedigree Chickens

460 Identification of two novel chicken growth hormone-releasing hormone receptor (GHRHR) splice variants: Implications for the role of Asparagine residue (Asp^{56}) in receptor activation and direct ligand-receptor interaction. C. Y. Wang*, Y. Wang, A. H. Y. Kwok, and F. C. Leung, *The University of Hong Kong*, *Hong Kong, HK-SAR, China*.

In this study, two novel Growth Hormone-releasing Hormone Receptor (GHRHR) splice variants, named cGHRHR-v1 and cGHRHR-v2 respectively, were identified from chicken pituitary using RT-PCR assay. cGHRHR-v1 is a variant of 383 amino acids and characterized by an N-terminal deletion of 36 amino acid residues (encoded by exon 3) including an asparagine at position 56 (Asp^{56}) conserved in all members of subfamily B-III G protein-coupled receptor. cGHRHR-v2 is a C-terminally truncated receptor variant of 284 amino acids with 4 putative transmembrane domains, which arises from alternative usage of a splicing acceptor site located at the 3′ end of intron 8. Using pGL3-CRE-luciferase reporter system, the functionalities of the two variants were examined in CHO cells. cGHRHR-v2 could not transmit signal after agonist treatment. In contrast, cGHRHR-v1 is still likely a functional receptor. Both GHRH and pituitary adenylate cyclase-activating polypeptide (PACAP) could activate cGHRHR-v1 at high dosages (GHRH $\geq 10^{-8}$M; PACAP, $\geq 10^{-6}$M) and GHRH appeared to be much more potent than PACAP, suggesting that cGHRHR-v1 is a membrane-spanning receptor with an impairment in high affinity ligand binding, rather than in receptor activation or ligand-binding specificity. Meanwhile, this finding points out the possibility that Asp^{56} is not critical for receptor activation and direct ligand-receptor interaction. To substantiate this hypothesis, using site-directed mutagenesis, two receptor mutants with replacement of Asp^{56} by Ala or Gly were generated. Expectedly, GHRH and PACAP could activate both receptor mutants with slightly, but significant, reduced potencies. Taken together, our findings not only suggest that cGHRHR variants may play a role in controlling normal pituitary functions, but also support the notion that Asp^{56} is nonessential for receptor activation and direct ligand-receptor interaction.

Key Words: GHRH, GHRHR, Pituitary

461 Feed restriction alters the temporal expression of skeletal fast myosin isoforms in the breast muscle of diverse lines of turkeys. K. M. Huffman*, J. M. Reddish, M. S. Lilburn, and M. Wick, *The Ohio State University*, *Columbus*.

Significant increases for body weight and breast muscle proportion in commercial broiler and turkey strains have been made by genetic selection; however, the mechanisms of breast muscle growth and effects of such selection have not been fully explained. Our hypothesis is that feed restriction alters the temporal expression pattern of neonatal fast skeletal and adult fast skeletal myosin isoforms in the Pectoralis major (PM) of developing poults. We evaluated this hypothesis with a poultry growth model consisting of a random bred control line (RBC2) and a line selected for body weight at 16 weeks of age (F-line). The F-line has significantly heavier breast muscle weight than the RBC2 but the RBC2 breast muscle in proportion to body weight is similar to the F-line. Physiological differences between the lines have been normalized in previous research by restricted intake. We duplicated this approach to compare the temporal expression of neonatal and adult myosin isoforms in both restrict fed and ad libitum fed F and RBC2 poults. Our objective, using a quantitative indirect enzyme linked immunosorbent assay (ELISA) with fast skeletal myosin isoform specific monoclonal antibodies, was to investigate the affect of feed restriction on the temporal expression of neonatal and adult myosin isoforms in developing poults. Conclusions were made by comparing the ratios of the neonatal and adult myosin isoforms in the PM from the control line of poults (RBC2) and the F-line poults under ad libitum and restrict fed nutritional environments. Our results demonstrate that adult myosin isoform expression is delayed in both the F- and RBC2-lines undergoing feed restriction ($p<0.05$). Similarly, feed restriction resulted in a delay in the down-regulation of the neonatal myosin isoform at 14 and 21 d of age in both lines ($p<0.05$). These results confirm our hypothesis, that feed restriction alters the age related expression pattern of both the neonatal and adult myosin isoforms in the pectoralis major of both turkey lines.

Key Words: Muscle, Turkey, Myosin

462 Expression of the carbohydrate response element binding protein gene and related genes involved in hepatic lipogenesis during post-hatch development of broiler chickens. M. Proszkowiec-Weglarz*[1], B. D. Humphrey[2], M. P. Richards[1], R. W. Rosebrough[1], J. P. McMurtry[1], and R. Angel[3], [1]*USDA-ARS*, *Beltsville, MD*, [2]*California Polytechnic State University*, *San Luis Obispo*, [3]*University of Maryland*, *College Park*.

Carbohydrate response element binding protein (ChREBP) and sterol regulatory element binding protein-1c (SREBP-1c) are key regulators of glucose metabolism and lipid synthesis in mammals. In response to glucose (ChREBP) and insulin (SREBP-1c), these two transcription factors regulate expression of lipogenic genes such as acetyl-CoA carboxylase (ACC), fatty acid synthase (FAS), stearoyl-CoA desaturase 1 (SCD1), ATP citrate lyase (ACL), and malic enzyme (ME). ChREBP dimerizes with Max-like protein X (Mlx) and binds to carbohydrate response element sites in target gene promoter regions. Expression of ChREBP and SREBP-1c is regulated, in part, by the nuclear liver × receptor (LXR). Since the ChREBP gene has not been identified in birds, the aim of this work was to clone and determine the expression of ChREBP and related genes in broilers during post-hatch (PH) development. To determine mRNA expression by RT-PCR and capillary electrophoresis, total RNA was isolated from 10 different tissues from 3-wk-old birds and from the livers of birds at 0, 1, 2, 3, 4, 6, and 8 d PH that were fed or fasted for 48 h PH. ChREBP, SREBP-1c, Mlx, and LXR gene homologues were expressed in all tissues examined at 3 wk. ChREBP demonstrated significant tissue-specific expression with the highest mRNA levels in liver and duodenum. Fasting for 48h PH did not change the level of ChREBP or Mlx mRNAs in liver, whereas SREBP-1c mRNA was lower at 2 d in fasted compared to fed chicks. Hepatic ACC, FAS, SCD1, and ME mRNAs increased in response to feeding. Fasting for 48 h PH delayed the rise in lipogenic gene mRNAs but had no effect on plasma insulin or glucagon. We conclude that ChREBP and Mlx genes are expressed in chickens. However, the role of these transcription factors in the glucose-dependent regulation of lipogenesis remains to be shown in birds.

Key Words: ChREBP, Lipogenesis, Chicken

463 The activation of insulin and nutrient signaling components leading to translation initiation in skeletal muscle of neonatal pigs is developmentally regulated. A. Suryawan*, R. A. Orellana, A. S. Jeyapalan, H. V. Nguyen, J. R. Fleming, and T. A. Davis, *USDA/ARS Children's Nutr. Res. Ctr., Department Pediatrics, Baylor Coll. of Med.*, *Houston, TX*.

Insulin (INS) and amino acids (AA) act independently to stimulate protein synthesis in skeletal muscle of neonatal pigs and the responses decrease with development. The purpose of this study was to compare the effect of INS and AA on the activation of signaling components leading to translation initiation and how these responses change with development. To examine the independent role of INS, hyperinsulinemic-euglycemic-euaminoacidemic clamps were performed in fasted 6-d-old (n=4) and 26-d-old (n=6) pigs to raise plasma insulin from 5 (fasting level) to 30 (fed level) μU/ml while AA and glucose were maintained at fasting levels. To elucidate the independent role of AA, a balanced AA mixture was infused into fasted 6-d-old (n=4) and 26-d-old (n=6) pigs to raise branched-chain amino acids from 500 (fasting level) to 1000 μmol/L (fed level) while INS and glucose were maintained at fasting levels. INS, but not AA, increased the phosphorylation of protein kinase B. Both INS and AA increased the phosphorylation of mammalian target of rapamycin (mTOR), ribosomal protein S6 kinase-1, and eukaryotic initiation factor (eIF) 4E-binding protein 1 (4E-BP1) and these responses were higher in 6-d-old compared to 26-d-old pigs ($P<0.05$). In 6-d-old pigs, both INS and AA reduced the binding of raptor to mTOR ($P<0.05$). Both INS and AA decreased the binding of 4E-BP1 to eIF4E ($P<0.05$) and increased eIF4E binding to eIF4G ($P<0.05$); these effects were greater in 6-d-old than in 26-d-old pigs ($P < 0.05$). Furthermore, neither INS, AA, nor age had any effect on the phosphorylation of eukaryotic elongation factor 2. Our results suggest that the activation of many of the insulin and nutrient signaling components leading to translation initiation is developmentally regulated and parallels the developmental decline in protein synthesis in skeletal muscle of neonatal pigs.

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Key Words: Protein Synthesis, Skeletal Muscle, Pig

Immunology - Livestock and Poultry II

464 Effects of maternal nutrition and selenium supplementation on absorption of IgG and survival of lambs. C. J. Hammer*[1], K. A. Vonnahme[1], J. B. Taylor[2], D. A. Redmer[1], J. S. Luther[1], T. L. Neville[1], J. J. Reed[1], J. S. Caton[1], and L. P. Reynolds[1], [1]*North Dakota State University*, *Fargo*, [2]*USDA-ARS, U.S. Sheep Experiement Station*, *Dubois, ID*.

To examine the effects of maternal nutrition with or without additional selenium (Se) on absorption of IgG and survival of lambs, 82 Rambouillet ewe lambs were allotted randomly to one of six treatments in a 3 x 2 factorial design. Groups included dietary levels of Se [Adequate Se (ASe, 7.4 μg/kg BW) vs. High Se (HSe, 85 μg/kg BW)], and plane of nutrition [60% (RES), 100% (CON), and 140% (HIGH) of NRC requirements for gestating lambs]. Basal diets were fed once daily in a complete pelleted form and HSe ewes received a Se pellet to meet the required Se level. Upon parturition, lambs were immediately separated from their dams, weighed, and serum samples obtained. Lambs were fed artificial colostrum for the first 20 h after which lambs were fed milk replacer. The artificial colostrum contained 64.3 g IgG/L and lambs received 10.6 g IgG/kg BW divided into seven feedings. At 24 h post-parturition serum samples were obtained to assess IgG status. Lambs were reared similarly in a temperature controlled (12°C), and ventilated facility for the duration of the study. Signs of illness prompted treatment following protocol. Morbidity was assessed as number of days treated for respiratory or gastrointestinal symptoms. Mortality was calculated as days in flock. Plane of maternal nutrition affected ($P < 0.05$) ability of lambs to absorb IgG after birth, with 24 h IgG concentrations of 2276, 1586, and 1214 mg/dl for lambs from RES, CON, and HIGH respectively. Selenium supplementation of ewes decreased ($P < 0.01$) 24 h IgG concentrations in lambs from 1912 mg/dl for ASe to 1472 mg/dl for HSe. Morbidity was not different for lambs from ewes in any of the treatment groups. Mortality was greater ($P < 0.01$) for offspring of ewes in the HIGH group; this group also had the lowest 24 h IgG concentration. Lambs born from ewes on a high or low plane of nutrition or with high dietary Se appear to have an altered ability to absorb IgG after birth. Further research is needed to determine the mechanisms by which this occurs.

Key Words: IgG, Mortality, Lamb

465 Effect of supplementation with a *Bacillus*-based direct-fed microbial on immune development of dairy calves. K. Novak*[1], E. Davis[1], C. Wehnes[1], T. Rehberger[1], D. Shields[2], and J. Coalson[2], [1]*Agtech Products, Inc.*, *Waukesha, WI*, [2]*Merrick's, Inc.*, *Union Center, WI*.

Immune development was evaluated in 65 Holstein bull calves in response to the addition of a *Bacillus*-based direct-fed microbial (DFM) to electrolyte scour treatment. Calves were assigned to three treatments based on the presence of scours: non-scouring, electrolyte, and electrolyte+DFM. Scouring calves received electrolyte for a mandatory two days. Blood was sampled from eight calves from each treatment on d 3, 7, 14, 21, 28, and 42 post-placement for an analysis of leukocyte populations by flow cytometry. Immune cell populations were determined using a panel of monoclonal antibodies specific for various cell surface markers, including, CD4 (T helper cells), CD8 (cytotoxic T and natural killer cells), CD25 (IL-2 receptor), CD62L (L-selectin), TCR1 (γδ T cell receptor), AM-2 (activated γδ T cells), CD45RO (memory T cells), CD172a (monocytes), and CD14 (LPS receptor). Activated immune cells ($CD8^-CD25^+$) were greater ($P = 0.05$) in electrolyte+DFM calves compared to electrolyte and negative control calves. L-selectin expression on leukocytes ($CD8^-CD62L^+$) was greater ($P = 0.05$) in calves on either electrolyte treatment compared to negative control calves. Electrolyte+DFM calves had a greater ($P = 0.05$) γδ T cell population ($CD8^-TCR^+$) compared to electrolyte and negative control calves. Calves provided the electrolyte treatment had a greater ($P = 0.05$) cytotoxic memory T cell ($CD8^+CD45RO^+$) population than the negative control calves; whereas, the electrolyte+DFM calves