GROWTH AND DEVELOPMENT

105 Effect of steroid implant on GH responses after acute treatments with a GH secretagogue L-165,868 or GRF and on IGF-1 responses in steers. C. H. Chang*, E. L. Rickes, L. A. McGuire, J. Tata, A. Patchett, R. G. Smith, and G. J. Hickey, *Merck Research Labs, Rahway, New Jersey.*

We have demonstrated in a pilot study that the GH secretagogue L-165,868, administered iv bolus at 0, 10, and 30 μg/kg, resulted in dose-related increases in GH AUC s (ng.min/ml) of 316±73, 1,415±519, and 2,160±792, respectively in yearling steers. The objective was to determine the efficacy of L-165,868 or GRF in the presence or absence of anabolic steroid implants (Ralgro or Revalor) in steers. Eighteen yearling steers (initial weight=297 kg) were randomly allocated into three treatment groups (n=6 per group): no implant control, Ralgro (zeranol), and Revelor (trenbolone acetate and estradiol-17β). The steroid implants were inserted on Day 0. On Days –7, 7, and 28, all animals were administered an iv bolus dose of L-165,868 at 10 μg/kg to monitor GH response over 120 min. In addition, all animals were administered an iv bolus dose of hGRF(1-29)NH2 at 3 μg/kg on Days 0 and 22. Plasma IGF-1 levels on Days 0, 7, 22 and 28 were determined. Plasma GH AUC post L-165,868 treatment in the control group increased from 2,647±477 on Day –7 to 3,066±552 (NS) and 3,134±564 (+18%,NS) on Days 7 and 28, respectively. In the Revelor group, GH AUC increased from 2,209±398 to 3,134±564 (NS) and 3,429±617 (+55%,P<0.10) over the respective days. In the Ralgro group, GH AUC increased from 1,751±315 to 2,276±410 (NS) and 2,864±516 (+63%,P<0.10), respectively. Plasma GH AUC post GRF treatment in the control group increased from 1,326±385 on Day 0 to 1,713±502 (NS) on Day 22. In the Revelor group, GH AUC was 982±288 on Day 0 and increased to 2,298±673 (P<0.05) on Day 22. No significant increase in GH AUC was noted in the Ralgro group (904±265 vs 1,033±303, NS). Compared to Day 0 level, both Revelor and Ralgro treatments resulted in significantly greater IGF-1 increases (1.9- and 1.6-fold, both at p<0.05) than that of the control group (1.2-fold increase) by Day 28. Results of this and the preliminary studies indicated that L-165,868 is efficacious in stimulating GH secretion in control and steroid implanted steers. Although there were increases in GH responses in all groups over the 35 study days, both Revelor and Ralgro treatments appeared to increase L-165,868-stimulated GH response on Day 28 after implant insertion when compared to their respective Day –7 GH responses. GRF-stimulated GH response was significantly increased in the Revelor group only.

Key Words: GH secretagogues, IGF-1, Steroid Implant

106 Effects of a growth hormone secretagogue L-163,255 fed in the diet over three weeks with a two week withdrawal period on growth performance and carcass characteristics of finishing swine. L. McNamara*, C. H. Chang, E. Rickes, D. Zhang, R. Nargund, R. G. Smith, and G. J. Hickey, *Merck Research Laboratories, Rahway, New Jersey.*

A trial was conducted to evaluate the efficacy of the growth hormone secretagogue L-163,255, provided in feed to growing swine for three weeks, followed by a two week withdrawal period on feed/gain ratio, average daily gain, and carcass characteristics in swine. Eighteen male castrate swine, with an average weight of 60 kg were randomly allocated into 3 treatment groups (n = 6/group): unmedicated control, and L-163,255 at 30 or 360 ppm. Animals were fed the above diets *ad libitum* for three weeks, followed by two weeks of non-medicated diet. Feed consumption and body weight were measured weekly during the five week period. Animals were necropsied at the completion of week five to determine carcass characteristics. Compared to unmedicated control, L-163,255 at 30 ppm decreased feed/gain ratio 4.6, 6.8, and 1.0% during the three week treatment regimen, and decreased 9.5, 12.9, and 15.9% at 360 ppm over the same period. Average daily gain at 30 ppm was 5.9, 4.6, and –7.0%, while at 360 ppm it was, 0, 9.2, and 9.3%. Mean feed/gain ratio for 0–3 weeks decreased 3.6% (NS), 13.1% (P < 0.05) for 30 and 360 ppm respectively. Mean average daily gains were –1% (NS), and 6.3% (NS) for 30 and 360 ppm, respectively. During the withdrawal period (weeks 4 and 5) feed/gain ratio increased 3.4 (NS) and 13.8% (NS) at 30 ppm, and 3.4 (NS) and 3.1 (NS) at 360 ppm for weeks four and five, respectively. Overall mean feed/gain ratio for weeks 0–5 were 1.5% (NS) and 5.9% (NS) for 30 and 360 ppm, respectively. Overall daily gains (week 0–5) were –3.7% (NS) and +1.1% (NS) for 30 and 360 ppm, respectively. Carcass characteristics are reported in the following table.

Carcass Effect	Unmedicated Control	L-163,255 30 ppm	L-163,255 360 ppm	SEM LSM
Backfat at 10th rib, cm	2.47	2.45 (–0.8%)	2.06 (–16.6%)	0.21
Kidney/pelvic fat, kg	0.95	0.88 (–7.4%)	1.01 (6.3%)	0.09
Loin-eye area at 10th rib, cm2	34.71	34.19 (–1.5%)	35.48 (2.2%)	1.80

Liver, heart and kidney weights were not effected by treatment. In summary, L-163,255 when administered in feed improves average daily gain and feed efficiency in a dose dependent manner, but its effects are reduced upon withdrawal. Treatment at 30 or 360 ppm of L-163,255 in the feed for three weeks followed by a two week withdrawal period did not significantly improve carcass or organ characteristics.

Key Words: L-163, 255, Growth, Swine

107 The effect of two peptidomimetic growth hormone secretagogues L-163,255 and L-164,139 on performance and carcass composition in swine. E. L. Rickes*, C. H. Chang, L. A. McNamara, R. Nargund, and G. J. Hickey, *Merck Research Laboratories, Rahway, New Jersey.*

Two GH secretagogues were evaluated for performance and carcass effects during a five week grow-out. Thirty-six crossbred swine, same sex litter mates, (initial body weight 61 kg) were randomly allocated to three treatment groups. Treatments were unmedicated controls, L-163,255 and L-164,139 at 100 ppm in the diet for five weeks (n = 12 per treatment group). Compared to unmedicated controls, average daily gain for L-163,255 over the five week period were 16.3, –1.9, 4.6, –0.8 and 11% while feed/gain ratios were –19.4, –1.3, –7.3, –0.8, and –8.5%, respectively. Compared to unmedicated controls, average daily gain for L-164,139 was 4.8, –8.3, –3.6, –1.0 and 13.9% while feed/gain ratios were –7.6, 2.3, –3.3, –2.2, and –13.9%, respectively. Carcass characteristics are reported in the following table:

	Unmedicated control	L-163,255 100 ppm	L-164,139 100 ppm	SEM LSM
Cold carcass wt. kg	70.1	71.6 (P = 0.04)	70.5	0.5
Backfat at 10th rib, cm	2.97	2.92	2.71	0.05
Kidney/pelvic fat, kg	1.18	1.17	1.12	0.04
Loin-eye area at 10th rib. cm^2	30.1	30.9	31.6 (P = 0.08)	0.04

Overall for the five week period L-163,255 improved average daily gain 6.2± 2.3% (P = 0.07) and improved feed efficiency 7.7 ± 2.0% (P = 0.01). Over the same period L-163,139 did not improve average daily gain, but feed efficiency did improve 5.2 ± 2.0% (P = 0.08). L-163,255 improved both final body and cold carcass wt 2.2% (P = 0.07) and 2.2% (P = 0.04) respectively compared to the unmedicated controls. L-164,139 appeared to reduce both backfat and kidney/pelvic fat 9.0% and 5.1% (both ns) respectively, while loin-eye area was increased 5.2% (P = 0.08) when compared to the unmedicated controls. In summary, at the dose level tested, L-163,255 was efficacious in improving weight gain and feed efficiency, with little effect on carcass characteristics. L-164,139 improved feed efficiency and loin-eye area.

Key Words: Growth Hormone Secretagogues, Swine

108 Effect of porcine somatotropin on skeletal muscle p94, calpastatin and α-actin gene expression in finishing pigs. S. Ji, G. R. Frank, S. G. Cornelius, G. M. Willis, and M. E. Spurlock*, *Swine Research Group, Purina Mills, Inc. St. Louis, MO.*

The objective of the study was to determine if the increased muscle growth associated with porcine somatotropin (pST) treatment requires altered expression of p94 (a muscle-specific calpain), calpastatin (the calpain-specific protease inhibitor), or α-actin. A total of 48 barrows (65.8 kg ± 2.5%) were assigned to 4 treatments arranged as a 2 × 2 factorial in a RCBD. The duration of treatment was 3 or 6 wk and pST administration (subcutaneous) was 0 or 3 mg/pig/day. Performance data (ADG, feed intake, gain:feed [G:F]) were evaluated weekly and overall. At the end of pST treatment (3 or 6 wk), longissimus muscle samples were obtained by surgical biopsy and RNA extracted. Plasma pST, insulin, urea nitrogen, creatinine and glucose levels were also measured 24 h after the first injection and at the end of treatment. Skeletal muscle α-actin mRNA abundance was quantified by slot blot analysis using a full-length human α-actin cDNA. Northern blot analysis of porcine calpastatin expression revealed 3 transcripts which were quantified individually. Both α-actin and calpastatin were standardized on rRNA (28S) abundance. The p94 mRNA was measured using a ribonuclease protection assay and standardized on _-actin. pST improved ADG (11% at 3 wk and 13.2% at 6 wk, P < .01), G:F (25.6% at 3 wk and 26.3% at 6 wk; P < .01) and decreased feed intake (11 and 10.3% at 3 and 6 wk, respectively, (P < .01). Administration of pST increased circulating level of growth hormone (2-fold at 24 h, P < .09; > 10-fold at 3 or 6 wk, P < .01), insulin (50% to 2-fold at 24 h, P < .02; 2 to 3 fold at 3 or 6 wk, P < .01), glucose (15% at week 3 and 10% at week 6, P < .01), but decreased plasma creatinine (8.9 and 8% at weeks 3 and 6, resp.; P < .01) and BUN (35.8 and 31.9% at weeks 3 and 6, resp.; P < .01). pST did not change a-actin or p94 mRNA abundance, but the second calpastatin transcript was decreased by pST (33% and 61%, 3 and 6 wk, respectively (P < .02). These data suggest that pST stimulated-muscle growth does not require altered expression of p94 or α-actin. However, decreased calpastatin expression (transcript 2) may be important.

Key Words: Growth Hormone, Calpain, Pig

109 Body weight gain and feed efficiency in growing beef cattle fed ad libitum and restricted rations, and supplemented with somatotropin (ST). M. W. Tripp*, T. A. Hoagland, and S. A. Zinn, *University of Connecticut, Storrs.*

To determine if restricted feeding and/or ST affects body weight gain (BW) or feed efficiency (FE; feed intake/ BW gain), 40 beef calves weighing 305 ± 2 kg were sorted by weight and randomly assigned to treatment in a 2×2 factorial with main effects of restricted feeding (ad libitum or 0.75 ad libitum) and ST (0 or 33μg/kg BW/d) for 98 days. Animals were grouped in eight pens (5 calves/pen; two pens/treatment). A corn silage-based diet supplemented with a 52% crude protein mix (80% soybean N and 20% urea N) was offered once daily at 0900h. Protein supplement (1 kg/head/day) was mixed with the silage. Feed intake was determined daily. BW was determined every two weeks. Amounts fed to the restricted feed groups were calculated as 0.75 intake of ad libitum groups. Quantities fed to the restricted feed groups were adjusted twice weekly. BW gain of ST-treated animals was increased over time (P<.001) compared with non-supplemented animals in both the full feed (142 ± 2 kg vs. 127 ± 2 kg) and the restricted feed groups (96 ± 2 kg vs. 87 ± 2 kg). ST improved (P<.05) FE in the full feed and restricted feed groups, 8.2% and 8.9%, respectively. Ad libitum feeding also improved FE (P<.05). In summary, ST supplementation improves BW gains and FE in full fed and restricted (0.75 ad libitum) fed growing cattle, and ad libitum feeding improves BW gains and FE compared with restricted feeding.

Key Words: Beef, Feeding, Somatotropin

110 Effect of growth hormone (GH) on body weight gain and bone development in young male swine. T. L. Veum[1], R. L. Matteri[2], J. A. Pardalos[1], J. A. Carroll[2], R. S. MacDonald[1], and L. S. Hillman[1], *[1]University of Missouri, Columbia and [2]Animal Physiology Research Unit, USDA/ARS, Columbia, MO.*

Young intact male swine (total n = 54) were used to study the effect of recombinant GH treatment (daily im injections of 200 μg/kg) for 2 wk on body weight gain and bone development. Pigs were allotted to one of three age groups (1, 4 or 9 wk of age) and one of two treatments (GH or vehicle injections for two wk) by litter and weight shortly after birth. There were 8 treated and 8 control animals/age group. At the end of GH treatment the pigs were sacrificed, blood samples were collected, and the right tibia removed for evaluation. The 1 wk age group remained with their dam and littermates. The 4 and 9 wk age groups were weaned at 3 wk of age and fed typical nursery and early grower diets. Mean starting and ending body weights (kg) for the 1, 4 and 9 wk age groups were 2.53 and 5.45, 7.05 and 15.46, and 27.12 and 39.84, respectively. GH treatment did not increase (P > .2 to .9) ADG for any age group, and did not increase (P > .5 to .7) gain:feed ratio for the 4 and 9 wk age groups. The effect of GH treatment on ADFI was inconsistent. GH treatment did not affect (P > .4 to .9) tibia fresh weight, length, midpoint width (narrow and wide measurements), breaking force (kg), breaking force in g/mm^2, or bone mineral content estimated by dual energy X-ray absorption. However, serum IGF-1 concentrations were increased (P < .01) by GH treatment. In conclusion, body weight gain, tibia measurements and tibia breaking strength in young male swine ranging from 3 to 11 wk of age (2.5 to 40 kg) were not responsive to a GH treatment administered daily for 2 wk.

Key Words: Swine, Growth hormone, Performance, Bone

111 Somatotropin decreases lipid synthesis from glucose in adipose tissue of neonatal pigs. Y. X. Wang*, S. K. Fried, and P. A. Schoknecht, *Rutgers, The State University of New Jersey, New Brunswick.*

Somatotropin (ST) is generally believed to have little function during the neonatal period because of its lack of effect on skeletal growth. However, its ability to influence lipid synthesis in neonatal adipose tissue has not been studied. Therefore, we tested this by culturing subscapular adipose tissue from 7 d- and 60 d-old pigs (n = 4) with or without ST (100 ng/ml) and insulin (42 ng/ml) in M199 for 24 h. Adipocytes prepared from fresh and cultured tissue were incubated in triplicate for 2 h in modified Krebs-Henseleit bicarbonate buffer containing [U-^{14}C]glucose. Glucose incorporation into total lipid and fatty acids was measured to assess lipid synthesis. Insulin maintained the lipogenic capacity of cultured tissue at levels comparable to those in fresh tissue. After 24 h of culture, ST decreased glucose incorporation into total lipid in adipose tissue from both 7 d- and 60 d-old pigs. ST decreased insulin-stimulated glucose incorporation into total lipid.

	Basal	Insulin	ST	Ins. + ST
	(nmoles/10^6 cells/2 h)			
7 d	17[a]	33[b]	6[c]	18[a]
60 d	172[a]	338[b]	64[c]	228[a,b]

[a,b,c]$P < .05$.

ST significantly decreased the percentage of glucose incorporation into the fatty acid component in both 7 d- and 60 d-old pigs. The present study is the first to demonstrate in neonatal pigs that, as in growing pigs, ST regulates the capacity of adipose tissue for lipid synthesis.

Key Words: Swine, Insulin, Glucose metabolism

112 Effects of alpha-2 adrenoceptor antagonists on nonesterified fatty acid and plasma urea nitrogen concentrations in pigs. R. M. Cleale*, J. M. Ingling, D. J. Search, J. R. Hadcock, and M. H. Pausch, *Fort Dodge Animal Health, Princeton, NJ.*

Four trials were performed with swine to evaluate effects of parenteral administration of alpha-2 adrenoceptor antagonists (A2AA) on plasma levels of NEFA and urea nitrogen (PUN). In Trial 1, barrows were given single i.v. doses of saline, 200 μg/kg BW of one of three A2AA (efaroxan (EF), idazoxan, methoxyidazoxan (METH)), or 25 μg/kg BW of isoproterenol (ISO). Concentrations of NEFA were determined in plasma harvested at 15 min intervals from 1 h before treatment to 2 h after treatment. Compared to saline-treated control pigs, areas under the curve (AUC) for NEFA were increased (P<.05) by EF, METH and ISO. In trial 2, barrows were given an i.v. injection of saline, EF (200 or 400 μg/kg BW) or METH (200 or 400 μg/kg BW). Quantitations of NEFA were performed on plasma from blood samples obtained every 15 min from 30 min pretreatment to 2 h posttreatment. Among pigs treated with METH at 400 μg/kg BW, mean NEFA AUC was more than three times greater (P<.05) than for saline-treated pigs. Trial 3 evaluated if NEFA changes in response to treatment with A2AA were due to direct effects on alpha-2 receptors or involved beta adrenoceptors. Pigs were first dosed i.v. with saline or the beta adrenoceptor antagonist propranolol (1 mg/kg BW). One hour later pigs within each group were dosed i.v. with either METH (400 μg/kg BW) or cimaterol (25 μg/kg BW). Compared to saline-treated controls, NEFA AUC among pigs dosed with saline then METH doubled (P>.05). Plasma NEFA AUC among pigs dosed with saline then cimaterol increased fourfold (P<.05) compared to saline-treated controls. Mean NEFA AUC among propranolol-treated pigs was comparable to saline-treated controls, suggesting beta adrenoceptor involvement in the effect of A2AA on NEFA. In Trial 4 pigs were treated s.c. 10 times at 8 h intervals with saline, METH (400 μg/(kg BW·injection)), cimaterol (20 μg/(kg BW·injection)) or porcine somatotropin (rpST; 1 mg/(pig·injection)). Following the 10th treatment only cimaterol increased NEFA AUC compared to saline-treated controls (P<.05). Mean PUN AUC was reduced (P<.05) by both METH and rpST compared to controls; PUN among rpST-treated pigs was lower than METH-treated pigs (P<.05). In summary, A2AA influence lipolysis in swine. Data suggest A2AA potentiate beta adrenoceptor control of lipolysis. Lower PUN levels suggest improved nitrogen utilization is also a result of dosing with A2AA.

Key Words: Swine, Adrenoceptors, Antagonists

113 Free-radical modulation of IGF-I downregulation in endotoxin (LPS)-induced disease stress in calves. T. H. Elsasser[1]*, S. Kahl[1], J. L. Sartin[2], and T. S. Rumsey[1], *[1]USDA, Agricultural Research Service, Beltsville, MD and [2]Auburn University, Auburn, AL.*

The objective was to determine the relative roles of tumor necrosis factor-alpha (TNF), cortisol (C), and nitrogen free radicals (NFR) in the downregulation of IGF-I in calves after iv LPS bolus challenge. Nine 4-mo old Holstein bull calves were assigned to LPS (E. coli, 055:B5) at doses of 0.2, 1.0 and 2.5 μg/kg BW. LPS was administered once daily for 4 consecutive days. On d 3, an infusion of arginine HCL (0.5 g/kg over 8 hours) was initiated with the LPS to amplify the nitric oxide (NO) response. On d 1 and 3, blood samples were obtained at 0, 1, 2, 3, 4, 6, 8, 12 and 24 h relative to LPS. After the last LPS challenge, all calves were euthanized for collection of liver samples for immunohistochemical staining. Plasma was assayed by RIA for TNF, C and IGF-I. NO production was assessed in terms of measurement of NO_3^-. The presence of nitrosylated proteins in tissue sections was used as evidence of peroxynitrite NFR formation and detected by immunohistochemical staining for nitrotyrosine (NT). Plasma TNF increased in response to dose of LPS (P<0.01). Tolerance to LPS was evident in the d-3 responses, the magnitude of the subsequent TNF responses inversely proportional to the LPS dose. Plasma C and NO_3^- concentrations increased at all doses of LPS, did not differ by LPS dose, but were significantly depressed with LPS on d-3 relative to d-1 in calves receiving 2.5 μg/kg LPS (P<0.05). Plasma IGF-I was depressed at 1 and 2.5 μg/kg LPS (P<0.2). Calves displaying large plasma IGF-I reductions after LPS showed positive immunostaining for NT. The presence of NT in liver of IGF-I downregulated calves suggests NFRs may participate in the pathophysiology of the somatotropic axis in disease stress.

Key Words: IGF-I, Endotoxin, Disease

114 Continuous and transient exposure to elevated GH in the mature oMt1a-oGH transgenic mouse. A. M. Oberbauer* and J. D. Murray, *University of California, Davis.*

Adolescent mice exposed to elevated growth hormone (GH) during active growth develop obesity upon withdrawal of the excess GH in the controllable oMT1a-oGH transgenic mouse model. Overall body lipid increased approximately threefold due to both adipocyte hyperplasia and hypertrophy. This study was designed to test the hypothesis that transient exposure to high levels of GH at maturity also induce increased body lipid once the elevated GH is withdrawn. In this model, transgene expression is initiated by 25 mM $ZnSO_4$ in the drinking water; withdrawal of Zn supplementation stops transgene expression. At 100 d of age, male and female oMt1a-oGH transgenic(T) and wildtype (W) mice were assigned to one of three treatment groups (8 of each sex and genotype per treatment): Zn from 100 to 156 d of age (T+ and W+), Zn from 100 to 128 d of age (T+/– and W +/–), and no Zn (T– and W–). At 156 d of age, animals were weighed and the mesenteric (MFP), right gonadal (GFP), and inguinal (IFP) adipose depots weighed. W values were pooled as there were no treatment effects (p>.1). Lipid deposition, assessed by adipose weight expressed as a percentage of body weight, significantly differed (p <.05) based upon the extent of transgene activity. Further, the proportion of GFP, MFP, and IFP exhibited sexual dimorphism in response to transiently elevated GH. In males, T– had the largest GFP% (3.12±.2%, 2.35±.2%, 2.4±.1%, 1.37±.2% p<.05, for T–, T+/–, W, T+, respectively) while transiently expressed GH was lipogenic for females (2.31±.3% 2.82±.3%, 1.8±.2%, .8±.3% p<.05 for T–, T+/–, W, T+, respectively). MFP and IFP responded in kind. Despite gender, continuously elevated GH reduced lipid content (p<.05). This study demonstrates that females, but not males, retain the ability to respond to transiently elevated GH with increased lipid accrual even when the elevated GH is provided at maturity.

Key Words: Transgenic, Fat deposition, growth

115 Phenotypic and genetic parameters of muscle fiber number and size. I. Fiedler, C. Rehfeldt*, G. Dietl, and K. Ender, *Research Institute for Biology of Farm Animals, Dummerstorf, Germany.*

Numerous studies have reported on relationships between microstructure traits of muscle and criteria of growth, stress-susceptibility, and meat quality in cattle, swine, and poultry. Therefore, it could be efficient in improving animal performance to alter muscle fiber characteristics. To investigate whether the use muscle fiber number and fiber size could be efficient in selection, two experiments, one on 2940 mice and another on 2020 pigs, were conducted to estimate coefficients of heritability and of phenotypic and genetic correlations. The parameters were calculated by using statistic models of full-and-half-pairs-analysis (pig) and of father-son-regression (mouse). The coefficients of genetic variability for fiber number and fiber size were 9.3 and 8.2% in mice and 17.1 and 11.7% in pigs. The coefficients of heritability ranged from low to moderate (h^2=0.14 to 0.30). Phenotypic and genetic correlation coefficients revealed negative correlations between fiber size and total fiber number (r_p = –0.23 to –0.40; r_g = –0.50 to –0.80). Simulated selection by data from mice using an optimized index of fiber number and fiber size was able to increase fiber number and fiber size simultaneously against their antagonism. Moreover, muscle mass, body weight, and daily gain were increased. Genetic correlations were also apparent between fiber diameter and criteria of pork quality such as drip loss and colour (r_g = 0.40 to 0.78). Phenotypically extreme fiber hypertrophy was related to stress-susceptibility in pigs and to low endurance fitness in mice, whereas high fiber numbers had correspondingly positive effects. An increased grade of pale, soft, exudative meat (PSE) was associated with large fiber diameters and low total fiber numbers. Moreover, pigs with moderate or high marbling values in *longissimus* muscle had fewer muscle fibers than pigs with small marbling values. In conclusion, fiber characteristics of muscle are sufficiently variable and heritable, and they are correlated to animal performance. Consequently, they could be effectively used as criteria of selection in farm animals to affect performance and meat quality.

Key Words: Skeletal muscle, Muscle fiber, Genetic parameter, Pigs, Mice

116 Fetal and maternal responses to feed intake from d 29 to 45 of gestation. R. E. Musser, D. L. Davis*, R. D. Goodband, M. D. Tokach, and J. L. Nelssen, *Kansas State University, Manhattan.*

Parity-four sows were fed 1.82 kg/d (control, n = 6) and 6.36 kg/d (high, n = 9) from d 29 to 45 of gestation. Blood samples were taken from sows on d 43 of gestation two hours after morning and evening feeding for analysis of IGF-I concentration. On d 45 of gestation, sows were slaughtered and uteri collected for fetal and placental measurements. High feed intake sows had increased weight gain compared to controls (34.0 vs 4.32 kg, respectively; P =.0047). No differences were detected in number of fetuses, mummies, length of unoccupied uterus, implantation length, allantoic fluid volume, placental or fetal weight, and crown-rump length (P > .10). Residuals were tested to estimate the variation of fetal and placenta weight, and crown-rump length. No differences were observed between the fetuses from sows fed control or high feed in fetal weight variation (1.94 vs 2.02 g, respectively; P = .81), or placental weight variation (18.28 vs 15.58 g, respectively; P = .21). However, crown-rump length variation differed(4.77 vs 3.16 mm, respectively; P = .03). Sows fed high feed had increased IGF-I concentrations in plasma on d 43(32.35 vs 77.10 ng/ml, respectively; P = .006). Control fetuses demonstrated expected negative relationship between fetal number and fetal weight (wt = -1.02 × fetal no + 32; R^2 = .48), but fetuses from high sows did not show this relationship (R^2 = .003). Providing feed in excess of established requirements to gestating sow from d 29 to 45, increased IGF-I concentrations in maternal plasma and decreased crown-rump length variation of the fetus. We postulate the increased maternal IGF-I, or other maternal responses to high feed removed the maternal limit on fetal growth at this stage of gestation.

Key Words: Feed intake, Fetal growth, IGF-I

117 Isolation of porcine myoblasts by flow cytometry. J. R. Blanton, Jr.*, A. L. Grant, D. C. McFarland, J. P. Robinson, and C. A. Bidwell, *Purdue University, West Lafayette, IN.*

The capability to identify and isolate myoblasts readily would allow a broad range of muscle biology research in domestic animals. Cells isolated by flow cytometry retain most of their proliferative capacity, which is a characteristic that allows genetic manipulation and propagation of cells. The objective of this study was to determine parameters for isolating porcine myoblasts from mixed primary cell preparations. As a first step in characterizing cellular parameters for porcine myoblasts, adult myoblasts were clonally selected from *semimembranosus* muscle of 2 to 4 wk old pigs. Individual cells were collected at two separate times by a robotic cell manipulator and transferred to 96-well plates. Three hundred of 481 isolated cells survived collection. At this time, 42 cell lines have been confirmed to be myogenic by cell fusion and reverse transcriptase-PCR analysis of muscle specific mRNA. Non-myoblast clones are referred to as fibroblasts, however their specific cell types have not been characterized. A Coulter EPICS Elite flow cytometer with a 488 nm argon laser was used to characterize clonal myoblasts, clonal fibroblasts, and primary mixed cell preparations. Cell size and nuclear/cytoplasmic ratio were determined by forward scatter (FS) and ninety degree light scatter (90LS), respectively. There were no differences in FS and 90LS between second passage clonal myoblasts and clonal fibroblasts. However, mixed primary cultures that were proliferated on a single plate for 2, 3, 4, 5, 15 or 28 d had two distinct populations based on FS. The two populations were sorted (d 2, 4, 5, 28) and tested for cell fusion. The population of larger cells either detached or remained mononucleated, whereas the smaller cells readily fused to form multinucleated myotubes. Size differences between myoblasts and fibroblasts were lost after a single passage of mixed primary cultures. Therefore, porcine myoblasts can be isolated from mixed primary cultures prior to the first passage based on size alone.

Key Words: Pigs, Muscle Cell, Culture

118 Direct injection of DNA into skeletal muscle of pigs for delivery of recombinant protein. S. K. Jacobi*, D. E. Gerrard, C. A. Bidwell, and A. L. Grant, *Purdue University, West Lafayette, IN.*

One approach for genetically engineering skeletal muscle includes direct injection of DNA constructs into skeletal muscle. The objective of this study was to determine if intramuscular injection of DNA in porcine muscle is effective for obtaining production of recombinant protein. A commercial luciferase reporter plasmid, pGL3C (Promega Biotech Inc.), containing the firefly luciferase cDNA under control of the SV40 promoter and enhancer was used for injections. Preliminary studies were conducted using muscle cell cultures to demonstrate construct functionality. Four pigs (2 wk old) were used for determining effective doses of DNA and extent of DNA and (or) luciferase migration following DNA injection. DNA was suspended in saline containing 1% India ink. Each pig received four 250-ul injections in the longissimus muscles for delivery of 50, 100, 200, and 500 ug DNA/site. Seven days following injections, pigs were euthanized and injection sites were located by presence of India ink. Muscle samples (3 mm × 3 mm × 1 cm) were collected from each injection site and at 3 mm intervals anterior and posterior to the injection site. Luciferase activity was determined by chemiluminescence and samples from uninjected muscles served as negative controls to determine background activity. Amount of luciferase activity was dependent on sample site (P<.05). Greatest activities were detected at injection sites and activities decreased with distance from the injection sites. Luciferase activity was not detected in the most distal samples (>9 mm) from the injection sites. Greater doses of DNA appeared to increase the migration of luciferase to more distal sites, even though injection volume was constant. Luciferase activity was greater with 100 ug and 500 ug than with 50 ug (P<.05) or 200 ug (P<.07) DNA injections. Variation in luciferase activity may also reflect sampling accuracy. We have demonstrated that direct DNA injection can be used to deliver recombinant protein to porcine skeletal muscle.

Key Words: Pigs, Muscle, DNA

119 Changes in ribosomal recruitment during translation in differentiating C2C12 myogenic cells. J. G. Klaasmeyer*, C. W. Smith, D. Grant, T. L. Woods, and S. J. Jones, *University of Nebraska, Lincoln.*

During translation, ribosomes that are actively synthesizing protein attach to mRNA strands forming multi-ribosomal units. During differentiation the rate of ribosome initiation may vary. Mouse C2C12 myogenic cells were used determine the effects at differentiation on ribosome recruitment. Cells were plated at 100,000 cells per plate on 60 mm culture dishes in DMEM + 10% fetal bovine serum. Studies were initiated when cells were 80-85% confluent. Media was changed to DMEM with 2% horse serum 24 h after initiation of the study to stimulate differentiation. Plates were removed from the incubator washed with PBS and frozen at –70°C at: 0, 12, 24, 30, 36, 42, 48 h after initiation of the study. Plates were taken from the freezer and the cells were removed from the plates using a buffer to prevent RNase activity. Polyribosomes were fractionated by centrifugation on 15-60% sucrose gradients, and monitored at 254 nm. Percent polyribosomes were determined by measuring the area under the peaks for monoribosomes and polyribosomes. Creatine kinase was measured to determine the extent of differentiation. Creatine kinase increased ($p<.05$) after myoblasts were stimulated to differentiate. Myoblasts had higher polyribosome percentages than myotubes ($p<.05$). Polyribosome percent ($p<.05$) decreased after the cells fused. Monoribosome peak heights were highest at the time of differentiation and then declined ($p<.01$). Polyribosome peak height increased up to the time of differentiation and declined ($p<.01$). Total RNA was not different between treatments. Changes in the rate of protein synthesis during differentiation is due to the rate of initiation of polyribosomes and not to changes in the of amount rRNA.

Key Words: Polyribosome, C2C12 myogenic cells, Differentiation

120 Insulin, FGF, IGFI, IGFII, and PDGF alter the recruitment of ribosomes to polysomes for protein synthesis in C2C12 myogenic cells. C. W. Smith, J. G. Klaasmeyer, T. L. Woods, and S. J. Jones*, *University of Nebraska, Lincoln.*

To study mechanisms of how growth factors stimulate protein synthesis, C2C12 myogenic cells were treated with a variety of compounds and recruitment of free ribosomes to polysomes was quantified. After a 2 h incubation with either insulin, FGF, IGFI, IGFII, or PDGF-bb, cells were rinsed with PBS and quickly frozen at –80 C. Cell lysates were fractionated on 15-60% sucrose gradients by centrifugation. Absorbance at 254 nm was recorded continuously across the gradient. Protein and RNA concentrations were measured. With insulin treatment, monosome peak height decreased quadratically in myoblasts but not with myotubes. Polysome percentages increased quadratically with insulin ($p<.05$). H3-tyrosine uptake, measured in companion cultures, demonstrated a positive quadratic response ($p<.01$). The responses of IGFI, IGFII, and fibroblast growth factor (FGF) at 1, 10, and 100 ng/mL and platelet-derived growth factor (PDGF-bb) at 0.1, 1, and 10 ng/mL, paralleled that of insulin. All had a negative effect on monosome peak height and a positive effect on polysome percentage ($p<.05$). All responses were linear, except IGFI and FGF monosome peak height responses which were quadratic ($p<.05$). IGFI appears to have a plateau at 10 ng/mL. Protein synthesis responded to these growth factors by increasing linearly, but this response was only significant ($p<.05$) in IGFI and PDGF. No changes in protein accretion were seen except in the insulin treatment ($p<.05$). A 150% increase in total protein content, and a 180% increase in creatine kinase were seen between myoblasts and myotubes ($p<.01$). Total RNA was not different between treatments. In summary increased protein synthesis exhibited by growth factor treated cells is due to an increase in the activity of existing ribosomes.

Key Words: IGFI, IGFII, FGF, PDGF, Polysomes, Ribosomes

121 Myogenin and MyoD expression are more closely related to myosin heavy chain isoform composition than muscle mass. P. E. Mozdziak*, M. L. Greaser, and E. Schultz, *University of Wisconsin, Madison, WI.*

The myogenic regulatory factors (MRF) myogenin and MyoD are expressed at low levels in mature slow (myogenin) and fast (MyoD) skeletal muscles. However, there is little information regarding treatments that alter myosin heavy chain isoform (MHC) composition and muscle mass on MRF expression. The objective of these studies was to examine the potential roles of myogenin and MyoD in the slow MHC (Type I) to fast MHC (Type IIA, IIX, or IIB) transition that occurs in the rat soleus from two experimental treatments that have differing effects on muscle mass. In the first experiment, mature (n=10) female rats were supplemented with clenbuterol (CLEN) and 3,5,3′-triiodothyronine (T3) for 4 weeks. In the second experiment, mature female rats were hindlimb suspended (HS; n=4) for 14 days. Soleus muscles were removed from experimental and control animals for evaluation of MRF expression (Northern analysis or quantitative RT-PCR) or for electrophoretic separation of the MHC. CLEN/T3 treatment increased ($P<0.05$) soleus mass compared to untreated (n=13) animals (CLEN/T3, 197.5 ± 11 mg; control, 155.3 ± 8 mg), while HS decreased ($P<0.05$) soleus mass compared to weightbearing-control (n=5) animals (HS, 62.8 ± 4 mg; weightbearing, 124 ± 5 mg). CLEN/T3 treatment decreased ($P<0.05$) myogenin expression (Northern analysis) in the rat soleus corresponding with a decrease ($P<0.05$) in slow MHC Type I. CLEN/T3 treatment induced detectable levels of MyoD (Northern analysis) in the rat soleus corresponding with an ($P<0.05$) increase in fast MHC Type IIA/X. Northern analysis did not reveal any differences ($P>0.05$) in myogenin expression between HS and weightbearing soleus muscles. However, quantitative RT-PCR uncovered an upregulation in MyoD expression, following HS, that corresponded with previously reported increases in fast MHC. The results of these studies suggest that myogenin and MyoD expression are more closely related to MHC composition than muscle mass.

Key Words: RT-PCR, Northern Analysis, Electrophoresis

122 Effects of IGF's on Rb protein in primary skeletal muscle culture. E. Liu, R. L. Kelley, E. Huff-Lonergan, C. H. Rahe, and D. R. Mulvaney*, *Auburn University, AL.*

Because of the known relationships of IGF's to myogenic proliferation/ differentiation and the role of abundance level and phosphorylation (RbP or Rb hypo) state of the retinoblastoma (Rb) protein on the cell cycle control, a series of experiments were performed to examine the linkage of these factors in primary muscle culture. Cells were harvested from the hindlimb of 12 d chick embryos using routine procedures and subjected to myogenic enrichment by differential plating. Cells were transferred to multiwell plates and exposed to growth media (DMEM w/ 5% FBS and 5% dialyzed FBS (dFBS)) for 24 h prior to imposing one of five treatment medias. Treatment medias consisted of a control media (DMEM w/ 10% dFBS), control w/ 200 or 20 ng/ml IGF-I and control w/ 200 or 20 ng/ml IGF-II. Treatments were replicated 2× with 3× repeated observations within each treatment. Cells were harvested at 6, 9, 12, 24, 48 and 72 h after the addition of treatment media, with 1×/rep used for proliferation determination and 2×/rep used for protein isolation. Protein samples were isolated from cultures using TriPure Reagent (Boehringer Mannheim). Western Blot analysis was performed using a commercially available antibody (antiRB cat#14001A, Pharmingen). Rb levels and Rb state were found to be affected by both time and growth factor exposure. IGF-I (200 ng/ml) differed ($P<0.05$) from control with increased total Rb (0.85 vs 0.67 ± 0.07) and enhanced RbP (0.57 vs 0.45 ± 0.04) at 24 and 12 h post exposure, respectively. IGF-I (200 ng/ml) also increased ($P<0.01$) Rb levels (1.03 vs 0.59 ± 0.07) at 72 h post exposure. IGF-II (200 ng/ml) also differed ($P<0.05$) from control with increased Rb levels at 9 h (1.09 vs 0.59 ± 0.07), 12 (1.05 vs 0.86 ± 0.07) and 72 (104 vs 0.59 ± 0.07). IGF-II at 20 ng/ml had similar results; however, from 9 h throughout, higher RB levels were observed. Demonstrated sensitivity of Rb to IGF s in primary muscle culture suggest significant roles for Rb in myogenesis.

Key Words: IGF's, Retinoblastoma, Muscle, Cell proliferation

123 Identification and isolation of adipocyte membrane glycoproteins. J. T. Wright* and C. Mateus, *Georgia Southwestern State University, Americus.*

Adipocyte plasma membranes were isolated from the floating fraction of digested one week-old pig and three week-old rat adipose tissues. Fractions were either analyzed directly by SDS-PAGE and protein blotting, or subjected to affinity chromatography on Con A agarose before electrophoresis. Blots were screened using biotinylated Con A and avidin-peroxidase. In some experiments, the AD-1 adipocyte antigen was localized on blots using a previously prepared monoclonal antibody (Mab). Approximately 15 Con A-reactive glycoproteins were identified in both rat and pig whole plasma membrane preparations. Analysis of affinity-purified fractions revealed that the vast majority of the Con A-reactive glycoproteins also bound to Con A agarose. Lastly, immunoblots identified the AD-1 antigen as a glycoprotein in the lectin-reactive fraction. In summary, lectin affinity chromatography is useful in preparing plasma membrane fractions enriched for adipocyte surface glycoproteins, and will aid in identifying developmentally regulated cell surface glycoproteins expressed by cultured stromal vascular cells.

Key Words: Preadipocyte, Pig, Membrane Glycoproteins

124 Partial cloning of the bovine leptin gene and its expression in adipose depots and in cattle before and after finishing. S. Ji*, G. M. Willis, R. R. Scott[1], and M. E. Spurlock, *[1]Swine and Beef Research Groups, Purina Mills, Inc., St. Louis, MO.*

The objective of this study was to clone the coding region of the bovine leptin gene and to evaluate expression in several adipose depots and in cattle before and after the finishing phase. Reverse transcription (performed with adipose RNA) and cDNA amplification using polymerase chain reaction techniques (RT-PCR) gave a 449 bp product. The RT-PCR product was cloned into an expression vector (pASK75). Sequence analysis indicated that the bovine cDNA is 84% and 87% identical to the mouse and human leptin cDNAs, respectively. The predicted amino acid sequence was approximately 97% similar to the mouse and human sequences for 146 overlapping amino acids. The recombinant protein was expressed in *E. coli* and gel purified for N-terminal sequence analysis. The results (30 amino acid residues) confirmed the identity of the recombinant protein and showed 100% identity with mouse and human leptin. Northern blot analysis of poly A^+ mRNA showed that the bovine adipose tissue contains a single leptin transcript (approximately 3090 nt) and that its abundance is relatively low compared with the C57BL6J$^{ob/ob}$ mouse. Therefore, a more sensitive ribonuclease protection assay was established for quantitative and qualitative purposes. An evaluation of leptin expression in multiple tissues verified that the leptin gene is expressed only in adipose tissue. Abundance was similar in omental, perirenal, and subcutaneous fat. In a small preliminary trial with finishing steers, leptin expression in subcutaneous fat was numerically greater ($P < .16$) at finish than in samples collected at the start of the finishing period.

Key Words: Leptin, Growth, Adipose Tissue

125 Recombinant porcine leptin reduces feed intake in swine. T. G. Ramsay[1], X. Yan[1], J. B. Barrett[2], M. J. Azain[3], and C. R. Barb[2], *[1]Louisiana State University, Baton Rouge, [2]USDA-ARS, Athens, and [3]University of Georgia, Athens.*

Leptin is a protein produced by adipose tissue with significant effects on feed intake, reproduction and immune function in genetically obese mice. The present experiment was designed to determine if porcine leptin has any similar functions in swine. Recombinant leptin protein was synthesized using a pGEX-2T expression vector and GST-thrombin fusion protein purification. Porcine leptin (pLeptin) was administered to gilts (93 ± 2 kg bwt) through an intracerebroventricular (ICV) cannula. Six gilts were randomly assigned to a Latin square, replicated 3×3. Gilts were injected ICV with either 150 μl saline, 50 μg porcine somatotropin (pST, a protein control) or 50 μg porcine Leptin (pLeptin) with 4 day intervals between ICV injection periods. Four additional ICV cannulated animals served as non-injected controls. Prior to a feed challenge, animals were fasted for 20 hours. Animals were injected with the treatments at 16 hours into the fast. Animals were presented with feed 4 hours post-injection. Feed intake (FI) was monitored 4, 8, 20 and 44 hours after feed presentation. In general, ICV administration of any material (saline, etc.) resulted in a depression in FI. pGH did not have a FI effect when compared to the saline treated animals ($P > .05$). A single pLeptin administration resulted in a 51% reduction in FI relative to saline treatment at 4 hours after feed presentation ($p < .004$, $n = 6$). At 8 hours following feed presentation, pLeptin had maintained a 43% inhibition of FI ($P < .002$, $n=6$). Twenty hours after feeding, pLeptin continued to inhibit FI by 25%, relative to saline treatment ($P < .01$, $n = 6$). The effect of a single administration of pLeptin ICV on inhibition of FI dissipated by 44 hours post-feed presentation as intake returned to the level in saline treated animals. These data demonstrate that a single administration of recombinant pLeptin can acutely inhibit feed intake in swine.

Key Words: Leptin, Pig, Intake

126 Adipose tissue-specific effects of intracerebroventricular leptin in rats. M. J. Azain*, T. Wang, M. G. Hulsey, D. L. Hartzell, and C. A. Baile, *University of Georgia, Athens.*

Body composition involves complex interactions among genes, environment and development. It has been shown that leptin secreted from adipocytes has metabolic and central effects to inhibit feed intake and fat storage. Male Sprague-Dawley rats were implanted with intracerebroventricular (ICV) cannulas. Cannula placement was confirmed by monitoring drinking behavior in response to an ICV injection of angiotensin II. Rats were individually housed and had unlimited access to feed and water. Rats were treated with 0 or 2.5 μg rat leptin/d by ICV administration for 4 days. Feed intake and body weight were monitored daily through the treatment period and for 8 days of recovery. Feed intake in control rats averaged 22.7 g/d and was not affected by vehicle injection. Intake was decreased 57% (Control, 21.8 vs Leptin 9.4 g; $P <0.0001$) after the first leptin treatment and remained low through the treatment period. Intake was normalized within 72 h of the last injection. Body weight was reduced by leptin treatment (328 vs 374 g, $P < 0.001$), but did not recover during the recovery period (Control, 391 vs Leptin, 344; $P < 0.001$). Rats were sacrificed at the end of the recovery period. Despite the reduction in body and carcass weights, liver, kidney, heart and soleus muscle weights were not different between control and leptin treated groups when expressed on an absolute or relative basis. However, epididymal and retroperitoneal pad weights were reduced 56 (2.7 vs 1.2 g; $P < 0.01$) and 78 % (2.3 vs 0.5 g; $P < 0.01$), respectively, in rats that had previously been treated with leptin. Centrally administered leptin has potent effects on intake of non-obese rats and a sustained effect (> 8 d) on adipose tissue mass after withdrawal of treatment.

Key Words: Adipose tissue, Feed intake, Ob protein

127 Intracerebroventricular (ICV) administration of leptin into rats and food intake, body weight and energy metabolism. C. A. Baile*, T. Wang, D. L. Hartzell, B. S. Rose, M. G. Hulsey, N. K. Menon, R. A. Makula, and W. P. Flatt, *University of Georgia, Athens.*

Body composition involves complex interactions among genes, environment and development. It has been shown that leptin secreted from adipocytes has metabolic and central effects to inhibit fat storage. The objective of Experiment 1 was to determine the dose response relationship of rat leptin (UGA lot #001) and changes in food intake, body weight and water intake. Male Sprague Dawley rats weighing between 225–250 g were prepared with ICV cannulas and assigned treatments according to a replicated 5 × 5 Latin square. Results are shown on the right. The objective of Experiment 2 was to determine changes in food intake, body weight, R.Q., metabolic rate (kcal/kg^{¾}) and water intake of rats administered 10 μg of rat leptin (5/Tr) into the lateral cerebroventricle. Table to the right shows the average response for the five days of leptin treatment. The objective of Experiment 3 was to determine the metabolic rate of rats made hypophagic by food restriction that was equal to the food intake of leptin treated rats in Experiment 2 (5/Tr). ICV leptin has a potent dose related effect on intake and body weight. ICV leptin not only causes reduced food intake, but the potential body weight losses are enhanced due to an increased metabolic rate; this is in contrast to the reduced metabolic rate associated with limited feeding.

Exp. 1

Treatment	FI (g/d)	ΔBW (g)	WI (ml/d)	B. Temp (C)
Control	25.4^{c}	0.91^{a}	45.1^{c}	100.1
0.156 μg	21.1^{b}	–6.52^{b}	35.0^{bc}	100.3
0.625 μg	19.4^{a}	–4.22^{ab}	36.1^{bc}	100.0
2.50 μg	18.7^{b}	–10.4^{b}	26.9^{ab}	100.1
10 μg	12.1^{a}	–18.3^{c}	24.0^{a}	100.1
p	<.001	<.001	<.01	>.9

Exp. 2

Treatment	FI (g/d)	ΔBW (g)	WI (ml/d)	R.Q.	kcal/kg^{¾}
Control	17.1	0.3	30.0	0.97	95
10 μg	6.7	–43.1	20.2	0.87	101
p	<.05	<.05	<.01	<.01	.066

Exp. 3

Treatment	FI (g/d)	ΔBW (g)	WI (ml/d)	R.Q.	kcal/kg^{¾}
Control	19.08	6.08	35.7	.98	91.22
Limited fed	7.24	–37.05	23.4	.85	80.3
p	<.001	<.01	<.01	<.01	<.01

Key Words: Ob protein, Energy balance, Obesity

128 Leptin (LEP) modulation of growth hormone (GH) secretion by pig pituitary cells in culture. C. R. Barb[1], J. B. Barrett[1]*, C. A. Baile[2], X. Yan[3], and T. G. Ramsay[3], *[1]USDA-ARS, Athens, GA, [2]University of Georgia, Athens, and [3]Pennington Biomedical Research Center, Baton Rouge, LA.*

Leptin is a protein produced by adipose tissue which suppresses feed intake in several mammals. We demonstrated that intracerebroventicular injection of LEP increased serum GH concentrations and suppressed feed intake in pigs. Pituitary cells from 160 to 170 day old pigs were studied in primary culture, to determine if LEP affects GH secretion at the level of the pituitary. On d 4 of culture, 10^{5} cells/well were challenged with 10^{-12}, 10^{-10}, 10^{-8} or 10^{-6} M [Ala^{15}]–h growth hormone-releasing factor-(1-29)NH_2 (GRF), 10^{-14}, 10^{-13}, 10^{-12}, 10^{-11}, 10^{-9}, 10^{-8}, 10^{-7} or 10^{-6} M recombinent pig LEP (pLEP) or rat LEP (UGA lot # 001;rLEP) individually or in combinations with 10^{-8} and 10^{-6} M GRF. Secreted GH was measured at 4 h after treatment. Basal GH secretion (control; n=12 wells) was 31 ± 2 ng/well. Relative to control at 4 h, 10^{-10}, 10^{-8} and 10^{-6} M GRF increased (P<.01) GH secretion by 131%, 156% and 170%, respectively. Only 10^{-6} M (143%) and 10^{-7} M (147%) pLEP increased (P<.01) GH secretion. However, all doses of rLEP increased (P<.05) GH secretion except for 10^{-14} and 10^{-12} M. Addition of 10^{-9} M pLEP or 10^{-11}, 10^{-9} and 10^{-7} M rLEP in combination with 10^{-6} M GRF suppressed (P<.05) GH secretion. However, 10^{-13}, 10^{-12}, 10^{-11} and 10^{-9} M pLEP or rLEP failed to alter GH response to 10^{-8} M GRF. These results suggest that LEP may directly modulate GH secretion at the level of the pituitary. Moreover, the dichotomous effects between pLEP and rLEP may in part be related to the presence of pLEP binding proteins.

Key Words: Pig, Leptin, GH, Pituitary

129 Pituitary hormone secretion and feed intake after intracerebro-ventricular (ICV) administration of recombinant pig leptin (LEP) in the gilt. C. R. Barb[1]*, T. G. Ramsay[2], X. Yan[2], M. J. Azain[3], R. R. Kraeling[1], and G. B. Rampacek[3], *[1]USDA-ARS, Athens, GA, [2]Pennington Biomedical Research Center, Baton Rouge, LA, and [3]University of Georgia, Athens.*

Leptin, a protein produced by adipose tissue, reduces feed intake and increases fecundity in rodents. To determine if LEP affects LH and GH secretion and feed intake at the level of the brain, prepuberal gilts received ICV LEP injections. Blood was collected every 15 min for 4 h before and 4 h after ICV injections of .9% saline (S; n=3), 10 ug (n=4), 50 ug (n=4) or 100 ug (n=4)of LEP in S. Gilts were fed each day at 0800 and 1700 h over a two week period prior to the experiment (EXP). On the d of the EXP, pigs were fed at 0800 h and blood sampling started at 0900 h. After the last sample, feeders were placed in all pens. Feed intake was monitored at 4, 20 and 44 hours after feed presentation. Serum LH concentrations were unaffected by LEP. Prior to injection, serum GH concentrations were similar (P>.1) among groups and averaged 1.6 ± 1.5 ng/mL. Serum GH concentrations increased (P<.005) after injection of 10 ug (21 ± 1 ng/mL) , 50 ug (9 ± 1 ng/mL) and 100 ug (13 ± 1 ng/mL) of LEP compared to S (1 ± 2 ng/mL) treated pigs. The GH response to LEP was greater (P<.001) in 10 ug than 50 or 100 ug LEP treated-pigs. By 20 h the 10, 50 and 100 ug doses of LEP reduced feed intake by 53% (P<.08), 76% and 90% (P.<05), respectively, compared to S pigs. These results indicate that, LEP acts at the brain to modulate GH secretion and as shown in other species LEP suppressed feed intake.

Key Words: Pig, Leptin, GH, Intake

130 Insulin regulation of leptin expression by porcine preadipocytes. G. J. Hausman[1], X. L. Chen[2], R. G. Dean[2], X. Yan[3], and T. G. Ramsay[3], *[1]USDA-ARS, Athens, GA, [2]University of Georgia, Athens, and [3]Pennington Biomedical Research Center, Baton Rouge, LA.*

Adipose tissue from seven day-old pigs was enzymatically digested and S-V cells seeded and plated for three days in fetal bovine serum (FBS) with dexamethasone (DEX) followed by six days(d3-9)in serum free medium with insulin(850 nm),transferrin and selenium. During FBS+DEX treatment(d0-3)a large number of preadipocytes develop with no lipid accretion. In contrast ,preadipocyte number does not change with lipid accretion during insulin treatment (d3-9). Total RNA was harvested from S-V cultures after periods with no insulin following FBS+DEX. RNA was probed with a riboprobe of pig leptin cDNA in Northern-blots and leptin mRNA signals were normalized to 18 signals. Insulin deprivation from d 3-5 reduced leptin mRNA levels to 53±5 %(mean ± SEM of 2 experiments)of values for control cultures.(+ insulin,d3-5) The absence of insulin from d 3-9 reduced leptin mRNA levels to 22±6 % (mean ± SEM of 3 experiments) of values for control cultures. After insulin deprivation from d 7-9 leptin mRNA levels were not reduced, ie.,95±8 %(mean ± SEM of 2 experiments) of that in control cultures (+ insulin,d3-9). Regardless of insulin concentration recombinant porcine leptin had no influence on lipid accretion or differentiation.For example,fat cell number in cultures treated from d 3-9 with 100 nm leptin was 108±6% of that in control cultures (mean ± SEM of 3 experiments).These results indicate that leptin expression by preadipocytes is dependent on insulin before but not after differentiation and lipid accretion.

Key Words: Leptin Expression, Porcine Preadipocytes, Insulin

131 Expression of the porcine β1-adrenergic receptor in Chinese hamster ovary cells. H. Cao*, C. A. Bidwell, S. K. Defoe, and S. E. Mills, *Purdue University, West Lafayette, IN.*

Beta-adrenergic agonists signal via beta-adrenergic receptors (βAR) and modify growth rate and body composition by affecting a variety of metabolic functions in adipose and muscle tissue. In order to identify subtype specific agonists and antagonists, and to determine which receptor subtypes effect specific metabolic events, we have cloned the porcine β1AR and expressed this clone in cell culture. A 4.2 kb Hind III fragment was isolated from a porcine cosmid library using a 243 bp porcine cDNA. Partial sequence of this clone indicated the presence of the full coding region of the pig gene. To confirm that the gene encodes a functional protein, the 4.2 kb Hind III fragment was ligated into an expression vector (pcDNA3.1) and used to transiently transfect CHO cells. Membranes from CHO cells bound ^{125}I-cyanopindolol in a saturable manner with an estimated Kd of 25 pM. No binding was detected in non-transfected CHO cells. Affinity constants for (-)isoproterenol and clenbuterol were determined by competitive displacement of the radioligand. The Ki for isoproterenol was 125 nM, which is equivalent to the value detected in β2AR-CHO cells and pig adipose and muscle membranes. In contrast, the Ki for clenbuterol was approximately 750 nM, which is 200-fold higher than the Ki for β2AR-CHO, and 5-6 fold higher than the Ki using membranes from pig tissues. Data is consistent with clenbuterol being β2AR-selective, and suggests that pig adipose and muscle tissue express a mixture of βAR subtypes. Kinetic characterization of the individual receptors in cell culture will generate the tools to characterize these receptors in intact tissues.

Key Words: Pig, β-adrenergic receptor, Cell culture

132 Structure and a kinetic characterization of the porcine β2–adrenergic receptor expressed in CHO cells. W. Liang*, C. A. Bidwell, and S. E. Mills, *Purdue University, West Lafayette, IN.*

Beta–adrenergic agonists are less effective in limiting fat accretion in pigs than other species. Pig beta-adrenergic receptors (βAR) are also more selective to the agonist to which they respond than are other species and we suggest that functional differences between species results from primary structural differences in receptor composition. Therefore, we have cloned the pig β2AR gene in order to identify specie differences and to design functional agonists for pigs. A 1.6 kb Xho I fragment containing the entire β2AR coding gene was isolated from a porcine genomic DNA library. The gene contains no introns and has an open reading frame of 1,254 nucleotides that encodes a protein of 417 amino acids, which is 15 nucleotides longer than that of human and 3 nucleotides shorter than that of a mouse. The nucleotide sequence is 87% identical to human and 83% identical to the mouse. The putative amino sequence is 90.8% similar to human and 90% similar to mouse. The 1.6 kb fragment was ligated into pcDNA3.1(+) expression vector and used to transfect CHO–K1 cells. Membranes from transient and stably transfected CHO cells bound ^{125}I–cyanopindolol in a saturable manner with an estimated Kd of 20 pM. Relative affinities for (–) isoproterenol and clenbuterol (CB) were 120 and 4 nM respectively. Affinity contents from intact porcine adipose and muscle membranes were about 100 nM for both ligands. The higher affinity by the cloned β2AR for CB is consistent with CB being β2AR selective.

Key Words: Pig, β-adrenergic receptor, Cell culture

133 Effect of endotoxin challenge on hepatic 5'-deiodinase activity in cattle. S. Kahl[1]*, T. H. Elsasser[1], and J. W. Blum[2], *[1]USDA, Agricultural Research Service, Beltsville, MD, [2]University of Berne, Berne, Switzerland.*

Thyroid status is compromised in a variety of acute and chronic nonthyroidal illness. Conversion of thyroxine (T_4) into the metabolically active hormone, triiodothyronine (T_3), is catalyzed by 5'-deiodinase (5'D). Our objective was to determine the effect of endotoxin challenge (EC) with and without L-arginine infusion (ARG) on hepatic 5'D and plasma concentration of T_4 and T_3. In a 2 × 2 factorial, crossbred beef heifers (9-10 mo; 275-310 kg BW) were fed low (8% CP; 6.5 kg/d) or high (14% CP; 7.2 kg/d) isocaloric protein diets (1.96 Mcal/kg DM) for 10 d before EC. L-Arginine in saline (0.5 g/kg BW) or saline alone was infused i.v. for 8 h starting 2 h before EC (*E. coli*, 055:B5; .2 μg/kg; i.v.). Blood samples were collected at –2, 0, 3, 6, 12 and 24 h relative to EC. Liver samples were obtained 24 h before, and then 6 and 24 h after EC using a commercial biopsy instrument. Plasma T_4 and T_3 concentrations were not affected by dietary CP or ARG. Compared with levels at 0 h (T_4: 75.5 ± 1.6; T_3: 1.92 ± 0.05 ng/ml), EC decreased plasma T_4 ($P < .01$) and T_3 ($P < .001$), respectively, 8.4% and 28.9% at 6 h and 19.7% and 31.3% at 24 h. As a result, the T_3:T_4 ratio decreased ($P < .001$) 22.0% at 6 h and 13.5% at 24 h. Hepatic 5'D activities 24 h before EC were 2.80 ± .11 nmol I^-/h per mg protein and decreased 24 h after EC, respectively, 45.4% ($P < .01$) and 17.6% ($P < .05$) in saline and ARG infused heifers. The results indicate that mild EC in cattle inhibits hepatic generation of T_3 and decreases plasma concentrations of thyroid hormones. The data also suggest that decreased 5'D activity in liver could be alleviated by ARG supplementation.

Key Words: Thyroid hormones, 5'-Deiodinase, Endotoxin

134 Towards defining the physiological and immunological mechanisms mediating improved performance in site–segregated early weaned pigs. A. G. Van Kessel*, A. Estrada, J. F. Patience, M. Tang, and B. Laarveld, *University of Saskatchewan, Saskatoon, Saskatchewan, Canada.*

Growth performance, endocrine and immunological parameters were examined to 56 d of age in 60 pigs assigned to one of three treatment groups including conventional on–site weaning at 21 days of age (21–ON), early on–site weaning at 12 days of age (12–ON) and early off–site weaning at 12 days of age (12–OFF). Nutrition and management were standardized among the three treatments and transfer of personnel and equipment between on–site and off–site facilities was restricted. At regular intervals between 12 and 56 d of age, a total of 14 serum samples were obtained from each of 10 pigs per group. Fecal samples and whole blood were collected from an additional 10 pigs per group using the same sampling schedule. Body weight at 56 d of age was greater ($P<0.01$; pooled SEM 0.30 kg) for 12–OFF pigs (26.24) versus 12–ON (20.87) or 21–ON (21.54). Mean (±SEM) serum insulin–like growth factor–I (IGF–I) was (54.4±4.8, 57.2±5.9, 75.9±4.9 ng/ml) at 17 d of age, (32.4±3.6, 29.4±2.0, 22.7±3.2 ng/ml) at 26 days of age, (156.1±26.4, 50.0±7.4, 88.2±13.9 ng/ml) at 40 d of age, and (403.6±50.3, 198.1±20.6, 392.8±59.1 ng/ml) at 56 d of age for 12–OFF, 12–ON and 21–ON groups, respectively. Mean fecal enterobacteria counts tended to be 5-10 fold lower in 12–OFF versus 21–ON or 12–ON pigs from 17 through 56 d of age. At 56 d of age, total fecal enterobacteria were lower ($P<0.01$) in 12–OFF (2.7×10^5 cfu/g) and 21–ON (2.5×10^7 cfu/g) versus 12–ON (1.1×10^6 cfu/g). Fecal clostridia counts also tended to be lower in 12–OFF pigs and were 3.9×10^8, 5.7×10^8 and 4.3×10^8 cfu/g at 56 d of age in 12–OFF, 12–ON and 21–ON pigs, respectively. Mature neutrophils (PMN), as a percent of total white blood cells, tended to be higher in early weaned pigs (0.39±0.01) from 14 to 26 days of age than in conventionally weaned pigs (0.32±0.01). PMN levels tended to be lowest in 12–OFF pigs (0.26±0.01)compared with 12–ON (0.34±0.02) or 21–ON (0.32±0.02) from 40 to 56 d of age. The results support reduced pathogen load as a factor contributing to improved growth performance in site–segregated early weaned pigs and that the higher growth is associated with higher circulating IGF–I.

135 Skeletal development in weanling horses in response to high dietary energy and exercise. A. Black*, S. L. Ralston, S. A. Shapses, and P. A. Schoknecht, *Rutgers, The State University of New Jersey, New Brunswick.*

High dietary energy intake increases the incidence of orthopedic disease independent of weight gain, suggesting a direct, biochemical effect on skeletal development. The harmful effect of high energy intake may be mitigated by moderate levels of exercise. Two biochemical markers of bone turnover, plasma osteocalcin and urinary deoxypyridinium, were used to assess the effects of high dietary energy and exercise on bone formation and resorption, respectively. Weanling Standardbred fillies were divided into two dietary groups and offered either 100% of NRC recommendations for energy, protein, calcium and phosphorus (n = 8), or 130% NRC for energy + 100% NRC for other nutrients(n = 7). Extra caloric intake was provided by the addition of corn oil. One half of each dietary group was exercised on a treadmill for 30 minutes, 3 times/week. Plasma and urine samples were collected and growth measurements were taken every 2 weeks throughout the 4 month study. Although the 130% group consumed an average of 15% more calories than the 100% group, higher weight gains and faster longitudinal growth rates were not observed. However, within 2 weeks of starting the experimental diets, plasma osteocalcin concentrations in the 130% dietary group were higher ($p \leq .05$) than those of the 100% dietary group and remained so throughout the study. Urinary excretion of deoxypyridinium was not affected by diet,and exercise had no effect on either marker od bone turnover. Although moderate exercise did not alter bone turnover in we, our data do suggest a direct, positive effect of high energy intake on bone formation. The increased rates of bone formation did not, however, translate into increased gains in weight or other growth parameters.

Key Words: Equine, Nutrition, Skeletal Development

136 Dietary fiber sources alter colonic blood flow and epithelial cell proliferation of dogs. M. D. Howard[1]*, M. S. Kerley[1], F. A. Mann[1], G. D. Sunvold[2], and G. A. Reinhart[2], *[1]University of Missouri, Columbia and [2]Iams Research and Development, Lewisburg, OH.*

Twenty-eight adult ovariohysterectomized female dogs were used to determine the effect of dietary fiber on colonic blood flow and epithelial cell proliferation. Fiber treatments were cellulose (C), fructooligosaccharide (FOS), beet pulp (BP), and fiber blend (FB; BP, gum talha, and FOS). Dogs were surgically fitted with ultrasonic blood flow probes placed on the left colic artery. Blood flow measurement were taken at 0600, 1200, 1630, and 2200 on d 19, 21, 26 and 28 of a 35-d experimental period. Blood flow measured as both ml/min and ml/min/100 g of distal colon showed time and time x treatment interactions ($P < .02$). At 0600, dogs fed the FOS diet had greater ($P < .07$) blood flow than C-fed dogs: blood flow of FB- and BP-fed dogs was intermediate ($P > .10$) to FOS- and C-fed dogs. No differences ($P > .10$) among treatments were found at the three other time points. Measurement of epithelial cell proliferation was determined by intravenous injection of 5-bromo-2'-deoxyuridine and subsequent immunocytochemistry procedures to identify proliferating cells. In the proximal colon, dogs consuming the FOS diet had the shortest ($P < .07$) leading edge (distance between base of the crypt and highest labled cell), and smallest ($P < .01$) proliferation zone (ratio of leading edge to crypt depth). Crypt depth, unlabeled, and labeled cells were not different among treatments. Indices of cell proliferation in the distal colon were not different ($P > .10$) among diets. These data suggest that epithelial cell response to dietary fiber source will vary between regions of the large intestine. Shorter leading edge and smaller proliferation zone in the proximal colon with FOS consumption, combined with similar values for other morphological measurements is suggestive of decreased cell proliferation and increased cell differentiation. Results of this experiment indicate that consumption of fermentable fiber can increase colonic blood flow, and FOS consumption may reduce the incidence of colonic neoplastic growth.

Key Words: Dietary fiber, Colonic mucosa, Colonic blood flow

137 Anabolics and breed types effects on growth, serum hormone concentrations and live animal traits of young bulls. O. E. Moron-Fuenmayor, S. Pietrosemoli*, J. A. Aranguren, and M. A. Navarro, *Universidad del Zulia, Facultad de Agronomia, Venezuela.*

The objective of this study was determine the effects of different anabolics implants and breed types on growth, serum hormone concentration and live animal traits of young bulls. Fourty six young bulls grazing tropical grasses were grouped as Bos *indicus* predominance or Bos *taurus* predominance and were randomly assigned a treatments: non implanted (NI), zeranol implanted (ZI), ATB+17β-estradiol implanted (AI) and zeranol plus ATB+17β-estradiol implanted (ZAI). The experimental design was a completely randomized. The trial lasted 328 d. Analysis of covariance was performed using GLM procedure to evaluate average daily gain (ADG), thoraxic circumference (TC), scrotal circumference (SC), body type, frame size, serum testosterone (T), cortisol (C), insulin (Y), triiodothyronine (T_3) and thyroxine (T_4) concentrations were determined. Implants did not influence ($P>0.05$) ADG, TC, body type, I and T_4. SC and T concentrations differed ($P<0.001$) between NI and ZI, AI, ZAI (10.56 vs 2.21, 3.58, 2.43 cm of increase) and (1.07 vs 0.27, 0.08, 0.19 ng/ml)respectively. AI and ZI had lower values of C (9.29, 11.0 ng/ml) but NI and ZI had higher values (20.63, 20.91 ng/ml). AI had lower values T_3 (0.76 ng/ml) compared with NI, ZI and ZAI (1.00, 1.02 and 1.00 ng/ml) respectively. NI was different ($P<0.05$) compared with AI and ZAI for frame size. There were not differences between breed types. Treatments × breed types interactions affected ($P<0.05$) C concentrations, SC, and frame size. AI and ZAI for Bos *indicus* predominance and ZI, AI and ZAI for Bos *taurus* predominance had lower ($P<0.001$) C concentrations. NI Bos *indicus* predominance and Bos *taurus* predominance had higher SC. In conclusion, the use anabolics implants in prepuberal animals are not recommended.

Key Words: Anabolics, Growth, Hormones

138 Predicting bull performance from growth hormone response to growth hormone-releasing hormone. E. E. Connor*, S. M. Barao, L. W. Douglass, and G. E. Dahl, *University of Maryland, College Park.*

The traditional "bull test" in the beef industry to evaluate potential sires is time-consuming and costly to producers. Methods that provide an earlier indication of a bull's merit would benefit the beef industry greatly. We evaluated the potential for predicting bull growth performance characteristics from growth hormone (GH) response to growth hormone-releasing hormone (GHRH). Fifty-six Angus bulls averaging 228 (SD=27) days of age received 3 doses (0, 1.5 and 4.5 μg/100 kg BW) of human GHRH (1-29) analog in a randomized block design and evaluated for GH response. Area under the GH response curve (AUC) exhibited a significant ($P<0.001$) GHRH dose response. Regression analysis was used to study the relationship between AUC and percentage change in hip height (%DHH) and body weight (%DBW) from a 140-day bull test. Preliminary results indicated no significant relationships between growth characteristics and AUC from the 1.5 μg/100 kg BW dose of GHRH; however, a relationship was found between AUC from the 4.5 μg/100 kg BW dose and %DBW at day 28 ($P=0.03$), day 56 ($P=0.02$), day 84 ($P=0.07$) and day 112 ($P=0.06$). The relationship between AUC and %DHH was significant ($P=0.02$) at day 28 of the bull test, but not at day 56, day 84 or day 112. Growth hormone response to GHRH in young bulls is associated with subsequent growth and may be a useful sire selection criterion in beef production.

Key Words: Beef cattle, Growth hormone-releasing hormone, Selection

139 Relationships between serum isoenzymes of feeder cattle and carcass characteristics: I. lactate dehydrogenase. B. C. Paria, C. F. Rosenkrans, Jr.*, C. Y. Tarn, K. P. Coffey, and Z. B. Johnson, *University of Arkansas, Fayetteville.*

Genetic markers specific for cattle carcass traits could be used in feeding and marketing strategies. Our objective was to determine if serum isoenzymic patterns of lactate dehydrogenase (LDH) were related to carcass traits of cattle. Blood samples were drawn from crossbred calves (n = 181) as they entered a feedlot period. Isoenzymic profiles of LDH were separated using PAGE. Relative area percentage of each isoenzyme was determined for each calf using a laser densitometer. In addition, isoenzymes for each calf were categorized as high (greater than 1 SD above the mean), medium (within 1 SD of the mean), low (less than 1 SD below the mean), or none (band did not exist for that calf). Calves were fed typical feedlot rations for approximately 150 d prior to slaughter. Approximately 24 h after slaughter longissimus muscle area (REA), and backfat (BF) thickness were measured, and USDA quality grades assigned. Serum LDH isoenzymes were not related (P > .1) to REA except when expressed as a function of body weight. Most calves had five LDH isoenzymes (L1 - L5) present in their serum. Isoenzyme L1 (homologous heart type) was present for all animals and was related (P < .05) to BF and percentage of animals grading USDA Choice (1.24, 1.01, and .76 cm; and 58, 46, and 22 % for high, medium, and low, respectively). In addition, L3 (50 % heart type and 50% muscle type) was related (P < .05) to BF and the percentage of animals grading USDA Choice; however, L5 (homologous muscle type) was not related to the traits determined. Therefore, an index was developed weighting each isoenzyme for its content of heart type LDH. The index was not related to REA. However, BF and percent USDA Choice were related (P < .05) to the index (1.2, .99, and .58 cm; and 63, 36, and 0 % for high, medium, and low, respectively). Serum LDH isoenzyme content may be useful in predicting, prior to entering a feedlot, whether an animal will grade USDA Choice.

Key Words: Beef Cattle, Carcass, Genetic Markers

140 Relationships between serum isoenzymes of feeder cattle and carcass characteristics: II. glucose 6-phosphate dehydrogenase. B. C. Paria, C. F. Rosenkrans, Jr., C. Y. Tarn, K. P. Coffey, and Z. B. Johnson*, *University of Arkansas, Fayetteville.*

Metabolic enzymes with multiple forms have been related to carcass traits of sheep. Our objective was to determine if serum isoenzymic patterns of glucose 6-phosphate dehydrogenase (G6PDH) were related to carcass traits of cattle. Crossbred feeder calves (n = 181) had sera harvested prior to a feedlot period. Separation of G6PDH isoenzymes was accomplished using PAGE, and laser densitometry was used to determine the relative area percentage of each isoenzyme for each calf. In addition, isoenzymes for each calf were categorized as high (greater than 1 SD above the mean), medium (within 1 SD of the mean), low (less than 1 SD below the mean), or none (band did not exist for that calf). Calves were fed typical feedlot rations for approximately 150 d prior to slaughter. Approximately 24 h after slaughter, longissimus muscle area (REA) and backfat (BF) thickness were measured, and USDA quality grades assigned. Most calves had four G6PDH isoenzymes (G1 - G4) present in their serum. Serum G6PDH isoenzymes were not related (P > .1) to REA. Animals grouped by isoenzyme G1 (from none to high groups) had increasing (P < .05) quantities of BF (from .48 to 1.26 cm) which also impacted the percentage of calves grading USDA Choice (0 to 44 %). Isoenzyme G2 was related (P < .01), but inconsistently to BF and percent USDA Choice. When animals were categorized by isoenzyme G3, BF decreased (P < .01) from the none to high isoenzyme groups, resulting in percent grading USDA Choice of 30, 31, 40, and 80 for high, medium, low, and none, respectively. Isoenzyme G4 was not related (P > .25) to BF, but the percentage of animals that graded USDA Choice was related (P < .05) to G4 (27, 41, 13, and 71 % for high, medium, low, and none, respectively). Serum G6PDH isoenzyme content may be useful in identifying those rare animals that will have both desirable USDA quality grades and yield grades.

Key Words: Beef Cattle, Carcass, Genetic Markers

141 Growth curve analysis of Guzera and Guzera crossbreds cows and steers fed under grazing with or without concentrate supplementation. L. O. Tedeschi[1], C. Boin[2], R. F. Nardon[3], and P. R. Leme[3], *[1]ESALQ/USP, Piracicaba-SP, [2]EMBRAPA-CNPGC, Campo Grande-MS, and [3]IZ, Nova Odessa-SP, Brazil.*

This study evaluated seven nonlinear equations to describe Guzera (GU) and GU crossbreds (Brown Swiss - BS; Nellore - NE; Chianina - CH; and Caracu - CA) cows and steers. The following genotypes born in two consecutive years (trials) were used: GU; ¾GU¼BS; ½NE¼BS¼GU; ½BS½GU; ½CH¼BS¼GU; ½CA½GU; and ½CA¼BS¼GU. In the first trial animals were not supplemented, or were only during the first dry season (steers) or during every dry season (cows) with 0.5 kg of soybean meal (54% CP, DM). In the second trial, animals were not supplemented, or were during two dry seasons (steers), or every dry season (cows), or during the whole period (GU; ¾GU¼BS; ½NE¼BS¼GU) with 1.5 kg of a concentrate based on corn, wheat bran and urea (21% CP, DM). The parameters used to select the nonlinear equation were: regression deviation, residual sum of squares, determination coefficient, parameters variation among animals and convergence. The Gompertz function showed the best results. Richards equation presented the worst convergence probably due to its hard adjustment. Brody equations tended to estimate larger mature weights while the modified Gompertz and the Logistic equations tended to estimate lower one. The interactions, trial × supplementation × genotype and genotype × sex, were significant (P<.05) for mature weight and maturing rate, while the supplementation × sex interaction was significant for maturing rate and integration parameter (P<.05). Genotypes differed for the integration parameter (P<.05). Mature weight was not affected by dry season supplementation (P>.05). Supplementation during the whole year decreased estimated mature weight and increased maturing rate (P<.05). Cows which calved consecutively as 3 and as 4-year old had lower mature weight and higher maturing rate than cows that calved only as 3 and cows that did not calve (P<.05). An allometric relationship (r = –.82) between mature weight and maturing rate was found.

Key Words: Beef cattle, Growth curves, Nonlinear equations

142 Effects of winter and whole year concentrate supplementation on gain up to slaughter weight of Guzera and Guzera crossbreds steers grazing P. maximum Jacq. L. O. Tedeschi[1], C. Boin[2], R. F. Nardon[3], and P. R. Leme[3], *[1]ESALQ/USP, Piracicaba-SP, [2]EMBRAPA-CNPGC, Campo Grande-MS, and [3]IZ, Nova Odessa-SP, Brazil.*

This study deals with winter (dry season) and whole year supplementation of grazing steers of the Guzera (GU) breed and their crossbreds with Brown Swiss (BS), Nellore (NE), Chianina (CH), and Caracu (CA). Genotypes born in two consecutive years (two trials, first and second respectively) were used. The genetic composition of the 63 animals used in the first trial and of the 91 animals used in the second one were: first - GU; ½BS½GU; ½NE¼BS¼GU; ¾GU¼BS; and ½CH¼BS¼GU; second - GU; ½BS½GU; ½NE¼BS¼GU; ¾GU¼BS; ½CH¼BS¼GU; ½CA½GU; and ½CA¼BS¼GU. The animals entered the trials after weaning at the end of the wet season, and were slaughtered after about two years at the end of the second wet season. In the first trial animals were not supplemented, or were only during the first dry season with 0.5 kg of soybean meal (54% CP, DM). In the second trial, animals were not supplemented, or were during the two dry seasons, or during the whole period (only genotypes GU; ½NE¼BS¼GU; and ¾GU¼BS) with 1.5 kg of a concentrate based on corn, wheat bran and urea (21% CP, DM). The statistical analysis was carried out using repeated measures with polynomial adjustment. Linear relationship between weight and age was the best regression (P<.01). Guzera breed showed the lowest weight (P<.05). In the first trial, the interaction genotype × supplementation was significant (P<.05). The ¾GU¼BS steers presented better performance (P<.05) due to dry season supplementation (71 kg in slaughter weight) compared to the other genetic groups (range from 12 to 37 kg). In the second trial, the effect of dry season supplementation was smaller than in the first one and no statistical differences were observed among genotypes. Whole year supplementation increased gain over dry season supplementation significantly (P<.05) for the crossbreds compared to the straightbred GU steers. The behavior of the growth curve between trials were not identical.

Key Words: Beef cattle, Growth, Supplementation

143 Value of ultrasound scans and neural net models to estimate gain and carcass yield grade of cattle. A. Trenkle* and J. C. Iiams, *Iowa State University, Ames.*

An experiment was conducted with ninety six 382 kg yearling steers to determine if initial measurements of the cattle could be used to predict gain and final carcass yield grade. The steers were weighed, height at the hips measured and scanned with ultrasound between the 12th and 13th ribs transverse to the *Longissimus dorsi* to measure subcutaneous fat thickness and muscle crossectional area. Half of the steers were implanted with Revalor S. All steers were fed a diet containing 1.39 Mcal NEg/kg for 158 days and then processed at a commercial beef plant. The initial measurements at the beginning of the experiment were correlated (P<.01) with final daily gain (R=.52) and calculated yield grade (R=.57) using multiple linear regression. These same measurements were related to final daily gain (R=.70) and yield grade (R=.60) using a neural net model (Neural Works predict). Adding ratios of muscle area/fat cover, fat thickness/body weight or muscle area/body weight did not improve the estimates of gain or yield grade with either model. Sorting the steers into control and implant groups did not improve the R values for estimating gain or yield grade. These results indicate that building prediction models with neural networking using measurements that can be obtained under practical conditions may have potential to estimate performance and carcass parameters of feedlot cattle.

Key Words: Cattle, Ultrasound, Neural net

144 Potential value of ultrasound to sort feeder cattle into more uniform groups for finishing and marketing. A. Trenkle and J. C. Iiams*, *Iowa State University, Ames.*

Data were summarized from three cattle feeding trials to determine the value of using initial ultrasound measurements of fat cover and ribeye area to sort feeder cattle. All the cattle were scanned initially between the 12th and 13th ribs transverse to the *Longissimus dorsi* to measure fat thickness and ribeye area. Trial 1 included 156 yearling heifers weighing 358 kg, Trials 2 and 3 both included 96 yearling steers weighing 381 kg and 426 kg, respectively. For the purpose of this analysis, the cattle within each experiment were divided into four groups based on the initial ultrasound scan: small ribeye area and low fat cover (SmLo), small ribeye area and high fat cover (SmHi), large ribeye area and low fat cover (LgLo), and large ribeye area and high fat cover (LgHi). In Trial 1 the heifers in these groups were scattered among the pens. In Trials 2 and 3, steers were allotted to pens based on this grouping. Cattle with greater fat cover at the beginning of the feeding period were heavier, seemed to be more mature and had less muscle growth during the finishing period. There were no effects on carcass quality grades related to sorting of the cattle. There were no significant differences in gain among the groups, but cattle with more fat cover had poorer feed efficiency. The results of this analysis indicated that scanning feeder cattle with ultrasound to measure ribeye area and fat thickness can be used to sort cattle into groups with more potential to have high yielding carcasses. Sorting cattle based on initial fat thickness was of somewhat more value than initial measurements of ribeye area. Using both measurements was most effective in sorting cattle into potentially high yielding carcasses. Carcass data were:

	SmLo	SmHi	LgLo	LgHi
n	87	84	85	86
Fat cover, cm	.81[a]	1.19[b]	.76[a]	1.19[b]
REA, cm^2	87.1[a]	84.5[a]	95.5 [b]	91.6[c]
YG 1	33	8	47	16
YG 2	42	43	30	52
YG 3	11	29	6	16
YG 4	1	4	2	3

[a,b,c]Means in a row with different superscripts are different ($P < .01$).

Key Words: Ultrasound, Feedlot, Carcass

145 Stimulated growth in rainbow trout administered bovine somatotropin. G. T. Schelling[1]*, R. A. Roeder[1], E. L. Brannon[1], and J. C. Byatt[2], *[1]University of Idaho, Moscow and [2]Monsanto Agricultural Company, St. Louis.*

Two 9-wk growth studies with rainbow trout administered bovine somatotropin (bST) were conducted to determine the effect on growth performance and body composition. In trial I each treatment consisted of 3 replicates of 10 fish having an initial weight of 190 g. The fish were grown in 15° C water and were daily hand-fed to satiety. A commercial high-fishmeal trout diet which contained 57% protein and met the recognized nutrient requirements was used. The somatotropin treatment consisted of the intraperitoneal injection of 20 μg bST/g of body weight from a sustained-release commercial source every 3 weeks. The conditions were the same in trial II except that larger fish were used. All fish in trial II were the same age but the bST treated fish (initial weight 390 g)had previously received bST for 9 wks, and were therefore larger than the control fish (initial weight 290 g) which did not have previous exposure to bST. In trial I the administration of bST increased (P<0.01) growth rate by 68.7% with the 9-wk gain/fish being 115 g for the controls and 194 g for the bST-treated fish. Feed efficiency was improved (P<0.01) by 67.3%, with gain/feed being 0.715 for the controls and 1.196 for the bST-treated fish. The bST treatment altered carcass (heads on)composition by the following percentages (all P<0.05): –9.5 dry matter, –23.7 ether extract, 16.4 protein and 20.9 ash. Comparable values for fillets were (all P<0.05): –14.5 dry matter, –36.0 ether extract, 15.4 protein and 22.0 ash. In trial II with the larger fish bST increased (P<0.01) growth rate by 81.8% with the 9-wk gain/fish being 170 g for the controls and 309 g for the bST-treated fish, and improved (P<0.01) feed efficiency by 54.8%. This work demonstrates that the administration of bST to rainbow trout over a wide size range drastically increases growth rate, considerably improves feed efficiency, and results in a leaner carcass with leaner fillets.

Key Words: Fish growth, Bovine somatotropin, Growth improvement, Leaner carcass