allowance of 0.85 m^2.

Key Words: Transport, Welfare, Physiology

531 Gene expression changes in neutrophils of young bulls during transportation stress. K. R. Buckham*[1,2], J. L. Burton[3], B. Earley[2], and M. A. Crowe[1], [1]*University College Dublin*, *Dublin, Co. Dublin, Ireland*, [2]*Teagasc, Grange Beef Research Centre*, *Dunsany, Co. Meath, Ireland*, [3]*Michigan State University*, *East Lansing*.

The inevitable practice of transporting beef cattle results in a stress response that is associated with increased disease susceptibility to opportunistic respiratory pathogens. Other stress models have shown pronounced neutrophilia that correlates with an increase in blood glucocorticoids, implying that these stress steroids may impact innate immunity. The hypothesis of this study was that transport would alter expression of three genes known to be important for neutrophil-mediated immunity, including functions of transendothelial migration (CD62L and MMP-9) and apoptosis (Fas). To test this hypothesis, blood was collected, plasma harvested, and neutrophils isolated from 6 Belgian Blue bulls (231 ± 7.0 kg) at -24, 0, 4.5, 9.75, 14.25, 24, and 48 h relative to commencement of an 8 h transport by truck. Plasma cortisol concentrations, measured by RIA, were elevated at 4.5 and 9.75 h (50.64 ± 4.46 and 37.67 ± 4.15 ng/mL, respectively, ($P < 0.05$) compared to -24 h (22.15 ± 2.43 ng/mL), confirming that the animals were stressed by transport. Blood neutrophil counts were elevated between between 4.5 and 14.25 when compared to -24 h ($1.36 \times 10^6 \pm 5.9 \times 10^4$ cells/mL), reaching a peak of $1.73 \times 10^6 \pm 2.8 \times 10^4$ cells/mL at 9.75 h ($P < 0.01$). A weak positive correlation was observed between cortisol and neutrophil count (r = 0.25; P = 0.11). Neutrophil gene expressions for MMP-9 and Fas were also affected, although no difference in CD62L expression was detectable. Quantitative real-time RT-PCR analyses showed a ≥ 14-fold increase up-regulation of MMP-9 between 4.5 and 14.25 relative to -24 h ($P < 0.01$), while Fas expression was depressed about 2-fold during the same time period ($P < 0.05$). While these gene expression changes require validation at the protein level, our results suggest that transport stress may enhance pro-inflammatory activity of longer-lived circulating neutrophils, potentially compromising immunocompetence with the alteration of these cells' natural protective functions and contributing to disease severity during respiratory tract infections.

Key Words: Transportation stress, Neutrophil, Gene expression

532 Effects of lairage during transport on innate immune function of swine. J. L. Williams*[1,2], S. D. Eicher[1], J. A. Patterson[2], and J. N. Marchant-Forde[1], [1]*USDA-ARS*, *West Lafayette, IN*, [2]*Purdue University*, *West Lafayette, IN*.

Long distance transports may significantly affect the health of pigs; thus, adding a rest stop (lairage) during long journeys may improve their well-being. The objective of this study was to determine whether a mid-journey lairage was beneficial to swine immune variables during a 16-h transport. Four replications were conducted, one in each of four seasons. Eighteen-kg pigs were blocked by weight and assigned to one of two transport treatments. The pigs were housed in 16 pens (13-16 pigs/pen) with 8 pens/treatment. Lairage (La) pigs were transported for 8 h, given a rest with food and water for 8 h, then transported 8 h. Continuous (Co) pigs were continuously transported for 16 h. Jugular blood samples were collected from 16 pigs (8/treatment) on d 1, 3, 7 and 14 post-transport. Hematocrit and white blood cell (WBC) counts were obtained and neutrophil cell functions (phagocytosis and oxidative burst) and phenotypic cell markers (CD14 and CD18) were analyzed using flow cytometry. There were no treatment by block interactions. In Co pigs, total WBC count was higher on d 1 than La pigs ($P < 0.001$). As expected, granulocyte count in Co pigs was higher than in La pigs on d 1 ($P < 0.001$); further, granulocyte count was lowest on d 3 in Co pigs ($P < 0.05$). In both treatments, lymphocyte count was lower on d 14 than on d 1 ($P < 0.05$). There were more cells expressing CD14 in Co pigs than La pigs on d 1 ($P < 0.05$). In addition, Co pigs on d 1 and 14 had the highest percentage of CD14 and CD18 positive cells ($P < 0.05$) and La pigs had the highest percentages of both on d 14 ($P < 0.05$). Percent phagocytosis was highest on d 7 in the Co pigs ($P < 0.05$); however, in both treatments oxidative burst was highest on d 7 ($P < 0.05$). In both treatments, CD18 percentage was lowest on d 0 ($P < 0.05$). This study indicates that extended transport without lairage alters immune functions which may cause greater susceptibility to pathogens. Partial funding of this study was provided by the National Pork Checkoff.

Key Words: Stress, Immune function, Transport

Beef Species

533 Relationship between residual feed intake and onset of puberty in Brangus heifers. P. A. Lancaster*[1], G. E. Carstens[1], D. W. Forrest[1], R. D. Randel[2], T. H. Welsh, Jr.[1], and T. D. A. Forbes[3], [1]*Texas A&M University*, *College Station*, [2]*Texas A&M University*, *Overton*, [3]*Texas A&M University*, *Uvalde*.

Objectives of this study were to examine relationships between residual feed intake (RFI) and onset of puberty and ultrasound estimates of carcass composition in growing, purebred heifers. Average (± SD) initial ages of Brangus heifers (Camp Cooley Ranch) used in this study were 225 ± 9 and 236 ± 11 d for years 1 (N = 114) and 2 (N = 115). Heifers were individually fed a roughage-based diet (ME = 2.2 Mcal/kg) using Calan-gate feeders, and BW and DMI were measured weekly for 70 d. RFI was calculated as the residual from the linear regression of DMI on mid-test $BW^{0.75}$ (MBW) and ADG. Ultrasound measures of 12th rib fat thickness (BF), longissimus muscle area (LMA), and percent intramuscular fat (IMF) were measured on d 0 and 70. Progesterone analyses of weekly blood samples were used to determine onset of puberty. Heifers exhibiting a progesterone concentration ≥ 2 ng/mL for one wk or ≥ 1 ng/mL for two consecutive wk were considered to be pubertal. Ovarian ultrasound performed on d 63 of each year's study was used to confirm pubertal heifers. Average (± SD) ADG, DMI and RFI were 0.90 ± 0.15 and 1.06 ± 0.16 kg/d, 9.1 ± 1.1 and 9.5 ± 1.0 kg/d, and 0.00 ± 0.75 and 0.00 ± 0.68 kg/d for year 1 and 2, respectively. RFI was phenotypically correlated ($P < 0.01$) with DMI (0.67) and feed conversion ratio (FCR; 0.56), but not ADG

or initial BW. RFI tended to be correlated ($P < 0.10$) with LMA (-0.16) and BF (-0.12) on d 0, but not with LMA or BF on d 70. Heifers with low RFI (< 0.5 SD; n = 73) consumed 17% less ($P < 0.01$) DMI and had 16% lower ($P < 0.01$) FCR than heifers with high (> 0.5 SD; n = 66) RFI, even though final BW and ADG were similar. Across both years, 29% of the heifers were pubertal by d 70. Chi-square analysis revealed that the percentage of heifers that were cycling by d 70 within low (35.6%), medium (27.8%) and high (22.7%) RFI phenotypes were similar ($P > 0.20$). Moreover, of those heifers that were pubertal by 70 d, age at puberty and maximum progesterone concentration were similar between low and high RFI heifers. These data suggest that onset of puberty had a negligible association with phenotypic variation in RFI.

Key Words: Residual feed intake, Reproduction, Carcass traits

534 Variation in number of calves sired/bull in a natural mating multiple sire breeding herd. K. J. Wells*, Q. Xiao, X. Wu, Z. Jiang, and J. J. Reeves, *Washington State University*, *Pullman*.

In a large commercial ranch setting it is common practice to run multiple sires with large groups of cows. Little is known about the serving capacity or calf output of bulls in these herds. In this study the calf output of 19 individual, mature Wagyu bulls being utilized as a single multiple sire breeding group was evaluated using DNA parentage verification. Four hundred twenty (420) first calf Angus cross heifers were bred in a 3,000 acre pasture on a western Montana ranch, over a 45 day breeding period. All bulls passed a semen evaluation prior to the breeding season. A total of 392 calves were tested for paternal identity. Of those calves, 364 (92.8%) were assigned a sire with at least an 80% probability of paternity, 24 (6.1%) were unassigned and 4 were unable to be tested. The most probable sire of each calf was determined using a panel of 8 microsatellite markers. A chi-square goodness-of-fit test indicated a significant difference in the number of calves sired per bull ($P < 0.001$). Of the 19 bulls used, 10 (52.6% of bulls) sired 70.6% of the calves to which parentage was assigned. Amongst those bulls, 5 (26.3% of all bulls) sired 42.6% of the assigned calf crop. Alternately, the 5 (26.3%) least prolific bulls sired only 12.4% of the calves, with the two bottom ranking bulls siring only 6 (1.6%) calves each. Scrotal circumference (SC) measurements were available for 15 of 19 bulls; there was no correlation between SC and number of calves sired. The results of this study indicate that there are differences in serving capacity of individual bulls used in multiple sire breeding herds.

Key Words: DNA, Paternity, Cattle

535 Integrating the beef cattle foodchain – A case study of the first organic beef cattle enterprise in Veracruz, Mexico. P. Fajersson*[1] and P. Parada[2], [1]*Colegio de Postgraduados*, *Campus Veracruz, Veracruz, Mexico*, [2]*Carnes Orgánicas La Rumorosa*, *Poza Rica, Veracruz, Mexico*.

After abolishment of agricultural tariffs by NAFTA, the state of Veracruz, Mexico's number one beef cattle producer, is suffering from declining profits in the beef cattle sector. The 3.3 million ha of mostly native pasture utilized for cattle production in extensive grazing systems, with little or no chemical inputs, require innovative use and offer excellent premises for conversion to organic beef production (OBP). A project to develop integrated sustainable OBP systems in the Mexican tropics and market value-added beef began 2002. The hypothesis was that a strategic alliance of researchers, an organic certification agency, and ranchers would enable a pioneer producer to convert to OBP and integrate his enterprise. The methodology used was to offer producers guided implementation of the European norm 2091 for organic livestock production and extension activities on enterprise integration. The pioneer producer used to raise Zebu cattle on 550 ha of native pastures, supplied minerals, applied limited chemical herbicides and tick treatments, and marketed live cattle at 400 kg BW and 27 mo of age with a dressing percentage (DP) of 55%. In 2002, he obtained organic certification of his 565-head integrated OBP with Zebu crosses in a rotational, agroforestry grazing system with mechanical weed and organic parasite control. Finishing cattle are fed 2 kg/d of concentrate with 18% CP during 4 mo and ADG is 830 g until slaughter at 22 mo of age and 450 kg BW with a DP of 58%. In 2003, a butcher shop, packaging and sales of beef were added and the post-harvest chain was certified as organic. Income increased 157% with the enterprise integration, followed by 14.8% in 2004, while variable costs rose 19.6 and 11.1%, respectively. Since 2003, yearly volume of boneless beef sold with 10% added value to the producer grew from 10 to 18 tons in a total of five states. In 2005 income rose 140 and costs 16.6% and a positive balance of USD 51,920 was achieved. In conclusion, the pioneer producer has proven that it is possible to integrate an OBP enterprise in Veracruz. He is now consolidating a group of producers joining him in this effort.

Key Words: Organic, Beef, Enterprise

536 Influence on weaning weights and growth rate of nursing beef calves dewormed 90 days prior to weaning. J. N. Carter*[1], M. J. Hersom[2], R. O. Myer[1], M. M. Brennan[2], M. K. Maddox[1], J. T. Matthews[1], and D. Driver[2], [1]*University of Florida, NFREC*, *Marianna*, [2]*University of Florida*, *Gainesville*.

Winter and spring born beef calves (n=568; 177.7 kg ± 34.0) at three different locations in Florida (MAR, BRU, SFE) were used to determine the effectiveness of deworming prior to weaning in order to achieve heavier weaning weights. At least three breed types were available at each location and included Angus, Brangus, Brahman, and Romosinuano. Calves were individually weighed unshrunk on d 0 and randomly assigned to treatment groups. Unshrunk BW were also obtained at a mid-point and on d 90. Treatments included no deworming (CON) or deworming (DW; doramectin injectable, 1 mL / 50 kg BW). Bahiagrass (*Paspalum notatum*) pastures were grazed at all locations; within a location, cow-calf pairs from both treatment groups were managed identically and forage allowances were monitored to minimize any potential bias due to variations in pasture conditions. Data were analyzed using Proc GLM and Proc Mixed of SAS. In the GLM procedure, data were blocked by location and treatment differences were tested using location x treatment as the error term. In Mixed, an analysis of covariance was performed with d 0 BW as the covariate; the Mixed model contained treatment as a fixed effect and the random effect was location. Within location, total gain and ADG was not different. Across all locations, DW calves gained more total weight ($P < 0.001$; 59.5 kg vs 55.0 kg) and ADG was greater ($P < 0.001$; 0.66 kg/d vs 0.62 kg/d) compared with CON. Although weight gain was greater ($P = 0.002$; 38.3 kg vs 35.5 kg) for DW calves during period 1, the difference was not as great during period 2 ($P = 0.06$; 21.1 kg vs 19.9 kg). Deworming costs averaged $1.57/hd. DW calves returned $1.94/hd more net revenue than CON calves when considering only the deworming product costs. Under these experimental conditions, our data indicated both an animal performance advantage and a positive ROI from deworming early. This management practice may improve the value of calves beyond that of simply more weight at

weaning. Providing a healthier calf to the stocker or feedlot with process verification of this practice may garner additional premiums.

Key Words: Beef calves, Deworming, Preweaning

537 Effect of number of feeding places per pen on performance, blood metabolites and haptoglobin during the first month of adaptation to the feedlot. L. A. González*[1], A. Ferret[1], X. Manteca[1], J. L. Ruiz-de-la-Torre[1], S. Calsamiglia[1], M. Devant[2], and A. Bach[2,3], [1]*Universitat Autonòma de Barcelona*, *Bellaterra, Spain*, [2]*Unitat de Remugants-IRTA*, *Barcelona, Spain*, [3]*ICREA*, *Spain*.

Seventy two Holstein female calves (104.7 ± 1.25 d of age; initial BW 110.36 ± 2.54 kg) were randomly assigned to a 3 × 3 complete block design to study the effect of the number of feeding places per pen on performance and blood profile during the first month after arrival at the feedlot. Calves were blocked by BW and treatments consisted of 1 (T1), 2 (T2) or 4 (T4) feeding places/pen (8 calves/pen). Concentrate (3 Mcal/kg ME, 16.4% CP, 20.3% NDF, DM basis) and barley straw, both fed once a day, and water were offered ad libitum and in different containers. The DMI and ADG were recorded, and blood samples were taken weekly during the first 4 weeks after arrival at the feedlot. Data were analyzed with a mixed model considering the fixed main effects, and their possible interactions, of treatment, block and week, which was the repeated measure subjected to pen nested within block by treatment interaction. Treatments affected total DMI ($P < 0.01$) and ADG ($P = 0.03$). The T1 calves ate less DM and gained less ($P < 0.05$) than T2 and T4 (3.72, 4.05 and 4.00 ± 0.07 kg DMI/d; 0.86, 1.05 and 1.05 ± 0.05 kg ADG/d, respectively). However, the gain to feed ratio was similar among treatments (0.25 ± 0.07 kg/kg). Blood haptoglobin (0.30 ± 0.08 mg/mL) and β-hydroxybutyrate (0.180 ± 0.004 m*M*) were not affected by the number of feeding places per pen. Non-esterified fatty acids (m*M*) were affected (P = 0.006), being lowest for T4 (0.176) compared to T2 (0.226) and T1 (0.233, SEM ± 0.01). Total blood leucocytes (10.00 ± 0.17 × 10^3 cells/mL) and the neutrophile to lymphocyte ratio (0.58 ± 0.02) were not affected by treatments. The lowest number of feeding places (T1) resulted in a lower performance compared with T2 and T4. However, immune status and haptoglobin levels were not affected by increases in the number of feeding places.

Key Words: Calves, Feeding places, Performance

538 Effect of number of feeding places per pen on performance, blood metabolites and haptoglobin of Holstein heifers on high-concentrate diets. L. A. González*[1], A. Ferret[1], X. Manteca[1], J. L. Ruiz-de-la-Torre[1], S. Calsamiglia[1], M. Devant[2], and A. Bach[2,3], [1]*Universitat Autonòma de Barcelona*, *Bellaterra, Spain*, [2]*Unitat de Remugants-IRTA*, *Spain*, [3]*ICREA*, *Spain*.

Seventy two Holstein heifers (initial BW 138.0 ± 2.4 kg) were randomly assigned to a 3 × 3 complete block design to study the effect of the number of feeding places per pen on performance, blood metabolites and haptoglobin. Heifers were blocked by BW and treatments consisted of 1 (T1), 2 (T2) or 4 (T4) feeding places/pen (8 heifers/pen). Pelleted concentrate (3 Mcal/kg ME, 16.4% CP, 20.3% NDF, DM basis) and barley straw, both fed daily at 0800, and water were offered ad libitum and in different containers. After five weeks of adaptation, DMI and ADG were recorded at 28-d intervals during 6 periods. Blood samples were taken at 1600 of d 23, 24 and 25 of each period, for high, medium and low block of BW, respectively. Data were analyzed with a mixed model considering the fixed main effects, and their possible interactions, of treatment, block and week, which was the repeated measure subjected to pen nested within the block by treatment interaction. Total DMI (6.76 ± 1.15 kg/d), ADG (1.24 ± 0.10 kg/d), gain to feed ratio (0.188 ± 0.031 kg/kg) and final BW (389.47 ± 3.85 kg) were not affected by treatments. Blood haptoglobin was affected by treatments (P = 0.02; 0.178, 0.170 and 0.157 ± 0.005 mg/mL for T1, T2 and T4, respectively). Plasma non-esterified fatty acid concentrations (0.097 ± 0.002 m*M*) were not affected by treatments, whereas β-hydroxybutyrate ($P = 0.05$; m*M*) was greater for T1 (0.281) than T4 (0.251) but similar to T2 (0.276 ± 0.009). Low feeding places per pen did not affect performance, but blood haptoglobin and β-hydroxybutyrate levels were increased.

Key Words: Heifers, Feeding places, Blood

539 Effects of ractopamine and days on feed on performance and carcass traits of calf-fed steers. C. D. Reinhardt[1], G. L. Parsons*[1], B. J. Johnson[1], J. P. Hutcheson[2], and W. T. Nichols[2], [1]*Kansas State University*, *Manhattan*, [2]*Intervet, Inc.*, *Millsboro, DE*.

Two-thousand sixty English × Continental steer calves (avg. 252 kg) were used in a randomized complete block study to evaluate the effects of ractopamine and DOF on performance and carcass traits. Steers were blocked by arrival time at the research facility. On each arrival d cattle were processed and randomly allotted to 6 pens of 75 to 125 head each. All steers received Revalor-IS (16 mg estradiol-17β (E_2) and 80 mg trenbolone acetate (TBA)) upon arrival and were reimplanted with Revalor-S (24 mg E_2 and 120 mg TBA) on d 75. Within each block, three pens were randomly selected to receive ractopamine at the rate of 200 mg/hd daily for the final 28 d on feed (RAC) and the remaining three were fed no ractopamine (CON). Within each treatment and block combination, pens were randomly assigned to be fed for either 181, 202, or 223 d. There were 4 reps per treatment × DOF combination for a total of 24 pens. When measured over the entire feeding period, feeding RAC increased ADG 2.7% and increased final weight 6.8 kg. There was an interaction between DOF and treatment for feed conversion ($P < 0.10$), as RAC improved G:F ($P < 0.05$) in steers fed 202 d but had no effect on steers fed either 181 or 223 d. Feeding RAC also increased HCW 4.6 kg, increased the percentage of Yield Grade 1 carcasses by 6% units and decreased the percent grading Choice by 8% units ($P < 0.05$). All other carcass measurements were similar. Additional DOF resulted in linear increases in final wt and DMI and linear decreases in ADG and G:F ($P < 0.05$). There were no interactions between treatment and DOF for carcass traits. Increasing DOF caused linear increases in dressing percentage, HCW, fat thickness, marbling score, percentage Prime combined with Choice, and Yield Grade ($P < 0.05$). Increasing DOF decreased performance and increased carcass fatness but increased carcass quality and carcass weight. Feeding RAC improved performance regardless of DOF; however, RAC had a less pronounced effect on growth in this study with calves than has been reported elsewhere using yearling steers.

Key Words: Ractopamine, Feedlot, Steers

540 Effects of ractopamine and days on feed on performance and carcass traits of yearling heifers. C. D. Reinhardt[1], J. P. Hutcheson*[2], W. T. Nichols[2], R. S. Swingle[3], and K. J. Karr[3], [1]*Kansas State University*, *Manhattan*, [2]*Intervet, Inc.*, *Millsboro, DE*, [3]*Cactus Research, LTD*, *Amarillo, TX*.

English × Continental yearling heifers (n=2,252, avg. 286 kg) were used in a randomized complete block study to evaluate the effects of

ractopamine and DOF on performance and carcass traits. Heifers were blocked by arrival time at the research facility. On each arrival d cattle were processed and randomly allotted to 6 pens of 91 to 97 hd each. Within each block, three pens were randomly selected to receive ractopamine at the rate of 200 mg•hd^{-1}•d^{-1} for the final 28 d on feed (RAC) and the remaining three were fed no ractopamine (CON). Within each block and treatment combination pens were randomly assigned to be fed for either 129, 150, or 171 d. All heifers were implanted with Revalor-IH (8 mg estradiol-17β (E_2) and 80 mg Trenbolone acetate (TBA)) on arrival and re-implanted with Revalor-200 (20 mg E_2 and 200 mg TBA) on d 75. There were 4 reps per treatment × DOF combination for a total of 24 pens. When measured over the entire feeding period, feeding RAC increased final BW 8.5 kg and G:F 2.0%. Feeding RAC tended ($P < 0.15$) to increase HCW and REA. All other carcass measurements were similar. Additional DOF had a significant ($P < 0.05$) effect on final BW, ADG, G:F, dressing percentage, HCW, Yield Grade distribution, and marbling score. There were interactions ($P < 0.10$) between treatment and DOF for ADG and dressing percentage. Feeding RAC improved some performance parameters regardless of DOF. Increasing DOF decreased performance but resulted in increased carcass weight and marbling score.

Key Words: Ractopamine, Feedlot, Heifers

541 Effect of Optaflexx and days on feed on muscle gene expression in calf-fed steers. G. L. Parsons*[1], S. J. Winterholler[1], C. D. Reinhardt[1], J. P. Hutcheson[2], D. A. Yates[2], W. T. Nichols[2], and B. J. Johnson[1], [1]*Kansas State University*, *Manhattan*, [2]*Intervet Inc.*, *Millsboro, DE*.

Calf-fed steers (n=2060, 252 kg) were used to determine the effects of Optaflexx and days on feed on finishing performance and carcass characteristics. Treatment consisted of serial harvest dates 181, 202, or 223 d. Within each harvest group, steers received either (200 mg/hd daily of ractopamine-HC1) for the final 28 days, or a control diet consisting of no Optaflexx. All steers were implanted with Revalor-IS (80 mg trenbolone acetate 16 mg estradiol) at processing (d 0), and Revalor-S (120 mg trenbolone acetate and 24 mg estradiol) at 75 days on feed (DOF). At harvest, samples were taken from the inside round for analysis of IGF-I and the β-adrenergic receptors (AR) mRNA abundance. Four samples per treatment per DOF group totaling twenty-four samples were analyzed. Days on feed did not increase abundance of β1-AR ($P \geq 0.38$), β2-AR ($P \geq 0.89$), β3-AR (P≥0.90) mRNA, but numerically increased the abundance of IGF-I levels ($P = 0.21$). Addition of Optaflexx had no effect on expression of IGF-I and β-adrenergic receptors (βAR). The data obtained from these calf-fed steers contradict results obtained from older yearling steers in which expression of β2-AR mRNA increased with advanced DOF. Increased understanding of receptor abundance related to DOF and age may explain some response differences in calf-feds vs. yearlings.

Key Words: Skeletal muscle, β-Adrenergic receptors, Steers

542 Effect of optaflexx™ and days on feed on feedlot performance, carcass characteristics, and skeletal muscle gene expression in yearling steers. S. J. Winterholler*[1], G. L. Parsons[1], J. P. Hutcheson[2], D. A. Yates[2], W. T. Nichols[2], R. S. Swingle[3], and B. J. Johnson[1], [1]*Kansas State University*, *Manhattan*, [2]*Intervet, Inc.*, *Millsboro, DE*, [3]*Cactus Research, LTD*, *Amarillo, TX*.

Yearling steers (n=2,252; avg. 314 kg) were used to evaluate the effects of Optaflexx™ and d on feed on finishing steer performance and carcass characteristics. This study utilized a randomized complete block with a 3×2 factorial arrangement. Treatment groups included serial harvest dates of 150, 171, or 192 d. Within harvest date, steers either received Optaflexx (200 mg/steer daily of ractopamine-HCl) for the final 28 d, or did not receive Optaflexx. All steers were initially implanted with Revalor-IS and were re-implanted with Revalor-S after 75 d on feed. At harvest, muscle samples from the inside round were obtained for analysis of β-adrenergic receptor (AR) mRNA levels. Optaflexx increased daily gains, hot carcass weight, ribeye area, and G:F ($P \leq 0.05$). Optaflexx did not affect dressing percent, USDA yield grade, or quality grade ($P > 0.3$). There was no change in overall feed intake across the entire feeding period; however, feed intake was increased during the 28-d period that steers were fed Optaflexx ($P \leq 0.05$). As expected, greater d on feed decreased daily gains, overall feed intake, the number of yield grade 1 and 2 carcasses, and G:F ($P \leq 0.05$). Also, greater d on feed increased hot carcass weight, dressing percent, and the number of prime and choice carcasses, as well as the number of yield grade 4 and 5 carcasses($P \leq 0.05$). Increasing d on feed decreased the abundance of mRNA for β_1-AR and β_3-AR, and increased the abundance of β_2-AR mRNA ($P \leq 0.05$). Optaflexx had no effect on abundance of mRNA for β_1-AR, or β_3-AR, but it increased the abundance of mRNA for β_2-AR ($P = 0.09$). Further studies with primary muscle cell cultures revealed that advancing time in culture increased the β_2-AR mRNA ($P \leq 0.01$) but had no effect ($P > 0.10$) on β_1-AR or β_3-AR mRNA. These data suggest that d on feed and Optaflexx are affecting βAR mRNA levels which could in turn impact the response to Optaflexx feeding in cattle.

Key Words: β-adrenergic receptors, Ractopamine, Steers

543 Evaluation of a single Revalor-200 compared to Revalor-IH and Finaplix-H in a reimplant program for finishing heifers. C. D. Reinhardt*[1], J. P. Hutcheson[2], and W. T. Nichols[2], [1]*Kansas State University*, *Manhattan*, [2]*Intervet, Inc.*, *Millsboro, DE*.

Data from 3 studies utilizing 2,417 head of feedlot heifers (avg. BW=273, 248, and 283 kg for studies 1, 2, and 3) and 17 pen replicates per treatment were pooled to evaluate the use of Revalor-200 (20 mg estradiol 17-β (E_2) and 200 mg trenbolone acetate (TBA); R200) in a single implant program and Revalor-IH (8 mg E_2 and 80 mg TBA) followed by Finaplix-H (200 mg TBA) in a reimplant program (IHFH). All studies were conducted at a common research facility feeding similar diets using heifers of similar background. Heifers were randomized to treatments within each study. For studies 1, 2, and 3 heifers were fed for 171, 193, and 182 d and IHFH-treated heifers were reimplanted on d 68, 47, and 58, respectively. There were no differences in performance or Yield Grade between implant treatments, but compared to heifers receiving IHFH, those receiving R200 did have lower marbling score and percentage grading Choice ($P < 0.10$). These studies indicate that although implanting heifers with Revalor-200 initially provided similar growth performance compared to using 2 lower dosage implants sequentially in a reimplant program, these data also provide evidence that use of a higher dosage implant on arrival

in lightweight heifers may adversely affect the relationship between marbling and external fatness.

Table 1. Effects Rev200 vs IHFH on Performance and Carcass Traits

Trt	ADG, kg	G:F	HCW, kg	YG	MarbScore[1]	%Ch
IHFH	1.36	0.187	330	2.85	417[a]	48[a]
R200	1.39	0.187	333	2.87	407[b]	40[b]

[1] 400=Small[0]; 500=Modest[0]; [a,b] Columns without common superscripts differ ($P = 0.07$).

Key Words: Anabolic implants, Trenbolone acetate, Feedlot

Breeding and Genetics: Phylogenetics and Genetic Diversity

544 An overview of phylogenetics. M. Cronin*, *University of Alaska, School of Natural Resources and Agricultural Sciences*, *Fairbanks*.

Phylogeny generally refers to the genealogy of a group of organisms. For example, the phylogeny of the ruminants would include all of the ancestors, including the common ancestor, of the extant species of cattle, sheep, goats, deer, etc. In this paper, I present basic concepts of phylogenetics, and give examples of phylogenies of domestic and wild species above and below the species level. Taxonomic classifications are based on phylogenetic relationships, which can be inferred from paleontology, morphology, or genetics. Phylogeny can also be inferred for genes, as the genealogy of genes derived from a common ancestral gene. Gene phylogenies and species phylogenies are not always concordant for a variety of reasons. It is also important to recognize that phylogenetics is an historical science, and phylogenetic relationships can only be inferred. Nevertheless, phylogenetic inference has become a rigorous science, with important empirical and theoretical advances in the last few decades. The phylogeny of the horse, including ancestors with progressively decreasing numbers of toes over time, is an example of classical phylogenetic inference from fossils and morphology. The advances of molecular genetics have greatly enhanced and expanded phylogenetic inference from DNA sequences. In general, DNA sequences are assumed to evolve as a function of time, and similarity of sequences indicates recent common ancestry. However, is important to understand the factors affecting molecular sequences that may invalidate this assumption, including linkage, selection, modes of inheritance, lineage sorting of ancestral alleles, and gene duplication. The importance of distinguishing molecular sequence data from gene frequency data is also discussed. Examples are given of mitochondrial DNA (mtDNA) and nuclear DNA sequences that have been used to infer relationships of taxa at the levels of family, genus, species, and intra-species. At the level of higher taxa, the phylogeny of artiodactyls (even toed ungulates) has been inferred from molecular sequences for several genes. This includes the relationships among artiodactyls including non-ruminants (e.g. pig), ruminants (e.g., cattle sheep, deer), and more distantly related groups (e.g. whales). At the level of species, subspecies, and breeds, examples of cattle, bison, and several deer species are described. This includes groups in which molecular phylogenies are discordant with classical understanding of relationships from morphology, distribution, and natural history. The phylogenies of some domestic and wild ruminants are compared, and the concepts of wild subspecies and domestic breeds are discussed.

Key Words: Phylogenetics, Genealogy

545 Measuring diversity among breeds and populations. P. W. Hedrick*, *Arizona State University*.

There are a number of new genetic markers and approaches that can be used to measure and evaluate genetic diversity among different breeds and among populations of a breed. I will first evaluate the relative merits of different types of markers for these purposes, including microsatellite loci, mtDNA variants, SNPs, and QTLs. I will then discuss various approaches to measure the pattern of diversity among and within breeds, including FST, genetic distance, assignment, and clustering. The comments about these markers and approaches will be illustrated with data from recent studies in various cattle breeds.

Key Words: Microsatellite loci, FST, Clustering

546 Applications of phylogenetic inference to livestock science. A. R. Freeman*, *Smurfit Institute, Trinity College Dublin*, *Dublin, Ireland*.

The phylogenetics of domestic animals are profoundly influenced by domestication. The gene pools which these species possess today are the result of episodes of capture and taming of the wild progenitors which were restricted both spatially and temporally. In this presentation I will outline some of the wide-ranging applications of phylogenetics with reference to livestock science. More specifically, I will show how well-constructed phylogenies can be use to test varying hypotheses about the history of a population. Firstly, livestock species are not genetically homogenous, but rather are usually the result of two or several separate episodes of domestication. These scenarios have been confirmed by mitochondrial DNA phylogenetic analysis in many species. Secondly, phylogenies describe patterns of diversity which reflect both the history and biology of a species. In the case of a domesticated species, the number of original wild founders that created the population, the diversity levels in the wild ancestral populations, continual introgression from wild relatives and hybridization can affect the diversity levels in the modern population. Thirdly, the relationship between different breeds within a species may be clarified with careful interpretation of phylogenetic data. Finally, and perhaps most interestingly, different selection pressures acting in the two populations can also result in divergence at particular genetic loci which can be detected using phylogenetics. These loci are likely to relate to traits that have been selected in particular breeds, but also to the historical disease challenge that a species has faced. Thus, identification of these loci that show signatures of natural selection