

**W24 Effect of timing of *Mannheimia haemolytica* challenge following short-term exposure to bovine viral diarrhoea virus type 1b on serum cytokine concentrations and muscle and fat gene expression changes in growing beef steers.** L. Carlos-Valdez\*<sup>1</sup>, L. Burciaga-Robles<sup>1</sup>, D. L. Step<sup>2</sup>, R. W. Fulton<sup>3</sup>, A. W. Confer<sup>3</sup>, U. DeSilva<sup>1</sup>, and C. R. Krehbiel<sup>1</sup>, <sup>1</sup>Oklahoma State University, Department of Animal Science, Stillwater, <sup>2</sup>Oklahoma State University, Department of Veterinary Clinical Sciences, Stillwater, <sup>3</sup>Oklahoma State University, Department of Veterinary Pathobiology, Stillwater.

The objective of this study was to determine the effects of an intratracheal *Mannheimia haemolytica* biotype 1A (MH) challenge following short-term exposure (72 h) to Bovine Viral Diarrhoea Virus (BVDV) type 1b persistently infected calves (PI) on serum concentrations of IL-6, TNF $\alpha$  and IFN $\gamma$  and gene expression changes of TLR4, NF $\kappa$ B, TNF $\alpha$ , and IL6 in subcutaneous fat (SCF) and longissimus dorsi muscle (LDM) of growing beef steers. Eighteen crossbred steers (initial BW = 314  $\pm$  31 kg) were randomly allocated to one of the following treatments: 1) steers

not exposed to steers PI with BVDV or challenged with MH (CON); 2) steers exposed to steers PI with BVDV for 72 h followed by an intratracheal challenge with MH 12 h post BVDV exposure (EarlyCh); and 3) steers exposed to steers PI with BVDV for 72 h followed by an intratracheal challenge with MH 72 h after BVDV exposure (LateCh). Blood samples were collected during the first 336 h for serum cytokine analysis and biopsies were performed for the collection of LDM and SCF at -156, 12, 24, 48 and 72 h relative to MH challenge. Serum concentrations of IL6 (P = 0.001), TNF $\alpha$  (P = 0.04), and IFN $\gamma$  were increased (P < 0.001) in EarlyCh and LateCh steers compared with CON steers. Expression of TLR4, NF $\kappa$ B, TNF $\alpha$  and IL6 in LDM were up-regulated (P < 0.02) for EarlyCh steers compared with LateCh and CON steers. Similarly, TLR4 (P < 0.03), NF $\kappa$ B (P = 0.07), and IL6 (P < 0.03) were up-regulated in SCF for EarlyCh and LateCh steers compared with CON steers. We conclude that muscle and adipose tissue alter expression of cytokines in response to pathogens related to bovine respiratory disease.

**Key Words:** beef cattle, bovine respiratory disease, cytokines, gene expression

## Beef Species: Growth, Concentrate Level, Meat Quality, and Production Traits

**W25 Effect of time of ractopamine feeding on growth, carcass characteristics, and muscle biology of steers.** M. Hill\*<sup>1</sup>, K. Chapalamadugu<sup>1</sup>, C. Schneider<sup>1</sup>, R. A. Hill<sup>1</sup>, G. Gaylord<sup>2</sup>, J. K. Ahola<sup>1</sup>, C. W. Hunt<sup>1</sup>, J. Szasz<sup>1</sup>, and G. K. Murdoch<sup>1</sup>, <sup>1</sup>University of Idaho, Moscow, <sup>2</sup>USDA/ARS/PWA/SGPGRU, Hagerman, ID.

The labeled use of the  $\beta$  adrenergic agonist; Optaflexx<sup>TM</sup> in cattle during the last 28-42 days prior to harvest has some practical limitations such as the need to sort cattle. Studies have shown that  $\beta$ -agonists can increase protein accretion and feed efficiency, while potentially decreasing tenderness, marbling, and palatability. An earlier administration of  $\beta$ -agonist (RAC) may enhance the ease of use while maintaining beneficial aspects of late stage RAC supplementation in steers. Eighteen Angus  $\times$  Hereford steers were evaluated for the effects of a 35 d early (BW = 306 kg) administration of RAC versus 35 d late (BW = 508 kg) administration of RAC. Treatments were; no RAC (CON), early RAC (ER), and late RAC (LR) with 6 steer per treatment. Dosage of RAC was based on metabolic body weight (1.15mg RAC kg<sup>-1</sup> BW<sup>0.75</sup>hd<sup>-1</sup>d<sup>-1</sup>). Samples of the biceps femoris of each steer were collected before the trial, during the last 2 d of ER, and post-mortem and were evaluated for fiber type. Urine was collected at the end of each administration period for 1-methylhistidine (1METH) analyses, which serves as an indicator of myofibrillar protein turnover. From the first urine collection, ER showed a decrease in 1METH (P < 0.01) as compared to all other steers, from the second collection both ER and LR showed decreases in 1METH (P = 0.03) from CON. Carcass characteristics and sensory panel analyses were collected and compared among treatments. No significant differences in fiber-types were found between ER and LR. The ER increased ADG during the administration period (P < 0.01) when compared to CON and LR. Over the entire trial ADG was not different among the 3 treatments (P = 0.98). Values from carcass evaluations (HCW, REA, YG, KPH, fat thickness) were not significantly different between ER and LR. Our study suggests that ER performance is not statistically different from LR; therefore it may be more cost effective and practical to administer ractopamine at an earlier growth stage than the final 35 days pre-slaughter.

**Key Words:** muscle, beef, beta-agonist

**W26 Residual feed intake in progeny of Nellore bulls.** Y. B. Farjalla<sup>1</sup>, C. U. Magnabosco<sup>2</sup>, F. Manicardi<sup>3</sup>, F. R. C. Araújo<sup>4</sup>, D. P. D. Lanna\*<sup>1</sup>, and R. D. Sainz<sup>5</sup>, <sup>1</sup>Universidade de São Paulo, Piracicaba, São Paulo, Brazil, <sup>2</sup>Embrapa Cerrados, Planaltina, Distrito Federal, Brazil, <sup>3</sup>Guaporé Pecuária, Pontes e Lacerda, Mato Grosso, Brazil, <sup>4</sup>Aval Serviços Tecnológicos, Uberaba, Minas Gerais, Brazil, <sup>5</sup>University of California, Davis.

Residual feed intake (RFI), defined as the difference between observed intake and that predicted from average weight and daily gain, has been proposed as a criterion for genetic selection. There has been very little work with this trait in *Bos indicus* breeds. The objective of this study was to assess the genetic variability in RFI in Nellore cattle and to determine the relationship between RFI and carcass and performance characteristics. Seventy-five Nellore steers, progeny of eight bulls (minimum five progeny/bull), were fed individually for 85 days. The diet contained 25% sorghum silage and 75% concentrate on a dry matter basis, and was supplied *ad libitum*. The prediction equation was DMI = 0.0766  $\times$  Average BW<sup>0.75</sup> + 1.94  $\times$  ADG (RSD = 0.725). Animals were classed as low or high RFI if their RFI fell 0.5 SD or more below or above the mean (zero). Individual values of RFI ranged from -1.306 to 2.169 kg/d. Mean RFI for the low and high RFI groups were -0.875 and 0.756 kg/d, respectively; by definition, weights and ADG were similar between RFI groups. There was no difference among RFI groups for hip height and carcass traits. However, intakes and feed:gain were greater (P < 0.05) in high as compared to low RFI steers. There was no difference among progeny groups for height, initial and final weight, RFI, carcass weight or marbling score. Progeny groups differed (P < 0.01) in dressing percentage (range 53.6 to 55.8%), backfat (range 4.1 to 6.3 mm), 24-hour pH (range 5.57 to 5.84) and shear force (range 3.92 to 6.42). There were tendencies (P < 0.10) for differences among progeny groups for DMI, ADG, gain:feed, and ribeye area. None of the carcass traits were clearly related to RFI. These results show the genetic variability in RFI and other traits among progeny of Nellore bulls.

**Key Words:** beef cattle, carcass, genetic selection

**W27 Effects of breed biotype and concentrate feeding on carcass traits of beef steers.** I. M. Oliveira, P. V. R. Paulino\*, M. I. Marcondes, S. C. Valadares Filho, J. Cavali, L. F. Prados, A. M. Ribeiro, and N. K. P. Souza, *Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

The objective of this trial was to evaluate the influence of breed biotype (Nellore, NE; 1/2 Nellore × 1/2 Angus, NA; or 1/2 Nellore × 1/2 Simmental; NS) and concentrate feeding (1 or 2% of BW as DM) on carcass traits of beef steers. Steers were assigned to one of six treatments in a completely randomized design resulting from the factorial arrangement of breed biotype and concentrate level. Steers were slaughtered at 22 months of age, averaging 413, 496 and 496 kg for NE, NA and NS, respectively. After slaughter, carcasses were sectioned longitudinally and chilled at 4°C for 24 h. After chilling, carcasses were weighed, and had their subcutaneous fat thickness (BFT), ribeye area (REA; at the 12-13th ribs) measured and dressing percentage calculated. The interaction between concentrate allowance level and biotype was not significant ( $P > 0.05$ ) for any variable evaluated. Crossbred steers (NA and NS) had heavier ( $P < 0.05$ ) carcasses with larger ( $P < 0.05$ ) REA (271 kg and 76.4 cm<sup>2</sup>, respectively) than Nellore carcasses (222 kg and 61.6 cm<sup>2</sup>, respectively). Biotype did not ( $P > 0.05$ ) affect dressing percentage (avg. 57.90%). There were differences among biotypes ( $P < 0.05$ ) for BFT. Steers of NA had greater SFT (6.37 mm) than NS (4.62 mm), which was greater than that observed on NE (3.81 mm). Feeding 2% of BW as concentrate led to heavier carcasses and larger dressing percentage (264 kg and 57.6% vs 281 kg and 58.9%, respectively, steers fed 2% vs 1% concentrate as proportion of BW). Concentrate level had no significant ( $P > 0.05$ ) impact on SFT or REA (average 6.56 mm and 75.6 cm<sup>2</sup>, respectively). Under Brazilian feedlot conditions, feeding crossbred cattle or more concentrate in the diet resulted in heavier carcasses with greater yield per carcass.

**Key Words:** carcass, *Bos indicus*, biotype

**W28 Carcass traits of beef heifers of different genetic groups finished with different concentrate allowance levels.** S. F. Reis<sup>1</sup>, P. V. R. Paulino\*<sup>1</sup>, E. J. Souza<sup>3</sup>, J. F. Lage<sup>1</sup>, R. A. A. Torres Júnior<sup>2</sup>, S. C. Valadares Filho<sup>1</sup>, L. F. Costa e Silva<sup>1</sup>, L. F. Prados<sup>1</sup>, and P. B. Benedeti<sup>1</sup>, <sup>1</sup>*Universidade Federal de Viçosa, Viçosa, MG, Brazil*, <sup>2</sup>*EMBRAPA Beef Cattle Research Center, Campo Grande, MS, Brazil*, <sup>3</sup>*Universidade Federal Rural de Pernambuco, Recife, PE, Brazil.*

This trial aimed to evaluate carcass traits of heifers of various genetic groups (Nellore n=12, 1/2 Nellore 1/2 Red Angus n=12 and 1/2 Nellore 1/2 Simmental n=12) finished on one of two concentrate levels (0.8% and 1.2% of body weight). The experiment was a completely randomized design with a factorial arrangement of treatments (two concentrate levels × three genetic groups). Diets were isonitrogenous and formulated to meet requirements for maintenance and gain according to Brazilian recommendations. After 84 days on feed, heifers were slaughtered and carcasses cooled for 24 hours at 0°C. Backfat thickness, ribeye area (REA) and cold carcass weight (CCW) were measured. Measurements of carcass temperature and pH were taken immediately after slaughter, and 24 h after cooling. Data were analyzed using the GLM procedure of SAS; effects of treatments were considered significant at  $P < 0.05$ . Concentrate levels had no effect on carcass traits ( $P > 0.05$ ). The interaction between genetic group and concentrate level was not significant ( $P > 0.05$ ) for any trait evaluated. Differences were detected ( $P < 0.05$ ) in carcass traits among genetic groups: 1/2 Nellore 1/2 Angus heifers had higher mean values for backfat thickness (6.71 mm), REA (68.85cm<sup>2</sup>), HCW (251.8 kg) and CCW (247.0 kg), than the 1/2 Nellore 1/2 Simmental, (4.49 mm; 62.86 cm<sup>2</sup>; 212.2 kg; 207.5 kg) and Nellore heifers

(4.83 mm; 56.82 cm<sup>2</sup>; 205.8 kg; 201.8 kg). The REA/HCW ratio was higher ( $P < 0.05$ ) for the 1/2 Nellore 1/2 Simmental heifers (0.60±0.02) than that observed in the Nellore (0.57±0.02) and 1/2 Nellore 1/2 Angus (0.54±0.01) heifers. No differences were detected ( $P > 0.05$ ) for carcass pH and temperature, after 24 h of cooling, with mean values of 5.69 and 2.24°C, respectively. As carcass traits were not altered by the concentrate levels assessed (0.8% and 1.2% of BW), costs of feeding concentrate in Brazilian feedlots can be reduced, without compromising carcass quality of beef heifers.

**Key Words:** Nellore, crossbred, concentrate

**W29 Feedlot performance of cull cows fed using three systems.** C. L. Wright\*<sup>1</sup> and R. J. Maddock<sup>2</sup>, <sup>1</sup>*South Dakota State University, Brookings, SD, USA*, <sup>2</sup>*North Dakota State University, Fargo.*

An experiment was conducted to determine the effect of 3 feeding systems on the performance of cull cows. Seventy-two cull cows (initial BW = 551.3 ± 35.9 kg; initial BCS = 5.1) were randomly allotted to 12 pens. Pens were then randomly assigned to 1 of 3 treatments: 1) traditional, dry rolled corn (DRC)-based finishing diet (TRAD; 81.5% DRC, 11.3% grass hay, and 7.2% supplement), 2) DRC and dried distillers grains (DDGS)-based diet (LOCAL; 54.4% DRC, 29.9% DDGS; 14.3% grass hay, and 1.5% supplement), or 3) a commercial, self-fed product (SELF). Cows on the TRAD and LOCAL treatments were fed a single finishing diet; however, DMI was limited during the first 5 wk of the experiment. Feed was delivered once daily as a totally mixed ration. Cows on the SELF treatment were provided with 3 different blends of the commercial product. On d 0, cows were provided with 75.7 kg/head of a blend containing 60% supplement and 40% DRC in a self feeder. On d 13, 111.4 kg/head of a blend containing 30% supplement and 70% DRC was added to the self feeders. While consuming the first 2 blends, cows were provided grass hay daily at approximately *ad libitum* intake. On d 38, the final blend containing 10% supplement and 90% DRC was added to the self feeder. Grass hay was provided for an additional 7 d once the final blend was added to the self feeder. After 7 d, no forage was provided to cows on the SELF treatment. Treatments were fed for 95 d. Final BW was greater ( $P < 0.02$ ) in cows fed TRAD or LOCAL treatments than those fed the SELF treatment (701.2, 702.6, and 667.8 kg, respectively; SEM = 8.3). Cows fed the TRAD or LOCAL treatments gained faster ( $P < 0.04$ ) than those fed the SELF treatment (1.60, 1.55, 1.28 kg/d, respectively; SEM = 0.08). Dry matter intake (13.1, 13.1, 12.9 kg/d for TRAD, LOCAL, and SELF, respectively; SEM = 0.36) and gain:feed (0.12, 0.12, 0.10 for TRAD, LOCAL, and SELF, respectively; SEM = 0.08) were not affected by treatment. Cull cows fed using traditional feeding systems gain faster than those fed using a commercial self-fed system.

**Key Words:** cull cows, self-fed, distillers

**W30 Impact of castration and weaning age on yearling carcass and meat quality.** R. Berthiaume\*<sup>1</sup>, L. Faucitano<sup>1</sup>, I. Mandell<sup>2</sup>, S. Miller<sup>2</sup>, and C. Lafrenière<sup>3</sup>, <sup>1</sup>*Agriculture and Agri-Food Canada, Sherbrooke, Quebec, Canada*, <sup>2</sup>*University of Guelph, Guelph, Ontario, Canada*, <sup>3</sup>*Agriculture and Agri-Food Canada, Kapuskasing, Ontario, Canada.*

Our objective was to determine the effect of castration and weaning age on carcass and meat quality of forage-fed yearlings. Spring calving crossbred cows (48 in 2004; 48 in 2005) with male calves were blocked based on parity, breed and calving date. Cow-calf pairs were randomly

assigned to one of six weaning [early (100 d), normal (200 d), late (300 d)] by castration (bull, steer) groups. Weaned calves were fed a grass silage (GS), oats and treated soybean meal (50: 40: 10) diet in confinement. Nursing calves went on pasture with their dams. From d 200 to 300 lactating cows and nursing calves were fed GS ad libitum. All calves were slaughtered at 300 d of age with carcass and meat quality evaluated. Data were analyzed as a randomized complete block design experiment using the MIXED procedure of SAS. Castration decreased carcass weights (197 vs. 213 ± 4.4 kg;  $P < 0.01$ ) whereas carcass weights and carcass yields increased linearly with weaning age (188 vs. 204 vs. 225 ± 5.1 kg and 52.6 vs. 53.2 vs. 54.6 ± 0.38%, respectively;  $P < 0.01$ ). Castration increased subcutaneous (3.7 vs. 2.7 ± 0.36 mm;  $P < 0.01$ ) and renal fat (3.54 vs. 2.68 ± 0.304 kg;  $P < 0.01$ ), and decreased saleable meat yield (61.5 vs. 62.1 ± 2.0%;  $P < 0.01$ ). Weaning age had no effect on carcass fatness. Conversely, castration decreased loin eye area (LEA; 64.4 vs. 69.2 ± 2.50 cm<sup>2</sup>;  $P = 0.01$ ) whereas LEA increased linearly with weaning age (63.7 vs. 65.5 vs. 71.2 ± 2.50 cm<sup>2</sup>;  $P < 0.01$ ). A castration by weaning age interaction was present for ultimate pH ( $P < 0.01$ ) of the *Longissimus* muscle (LM). Ultimate pH of LM decreased with weaning age in bulls (6.06 vs. 5.62 vs. 5.61 ± 0.045) resulting in a lower incidence of dark cutters in late versus early weaned bulls (0 vs. 25%). Ultimate pH did not vary in steers (5.69 vs. 5.65 vs. 5.71 ± 0.045). Our results suggest that, in a forage based production system, late weaning may enhance carcass yield and may reduce the incidence of dark cutters in bulls.

**Key Words:** weaning, castration, beef

**W31 Fatty acid profile of back fat and intramuscular fat from yak and Chinese Yellow Cattle.** Y. S. Peng<sup>\*1</sup>, M. A. Brown<sup>2</sup>, and J. P. Wu<sup>1</sup>, <sup>1</sup>*Gansu Agricultural University, Lanzhou, Gansu, PRC*, <sup>2</sup>*USDA-ARS, Grazinglands Research Laboratory, El Reno, OK*.

Meat from yak (*Bos grunniens*) and Chinese Yellow Cattle (*Bos taurus*) are important human dietary components in Northwest China and throughout the world. Fatty acid (FA) composition is an important factor in the definition of meat quality due to its association with meat odor, flavor, and nutritional value of fat for human consumption. Qinghai yak bulls (3-yr-old; n=6) and Chinese Yellow Cattle bulls (3-yr-old; n=5) were used to evaluate the effects of species on FA profile of longissimus dorsi intramuscular fat (LD) and back fat over the longissimus dorsi (BF). Animals were randomly picked from herds grazing summer pasture in alpine meadow regions of the Qilian mountains in Qinghai Province in China. Fatty acid analyses were done using a GC-MS; which resulted in profiles of 50 FA. Statistical analyses were conducted using mixed model procedures using a linear model that included the fixed effects of species, tissue (LD,BF) and species × tissue and random effects of animal in species and tissue × animal in species. Yak BF, but not LD fat, contained less ( $P < 0.05$ ) palmitic and oleic acid. Yak BF and LD fat contained more vaccenic acid ( $P < 0.01$ ), and tended ( $P < 0.10$ ) to contain more conjugated linoleic acid (CLA<sub>c9,t11</sub>). Yak LD fat contained greater ( $P < 0.05$ ) concentrations of polyunsaturated FA (PUFA) and ratio of PUFA to saturated FA ratio. Yak BF and LD contained a smaller ( $P < 0.05$ ) ratio of n6 to n3 FA, and more ( $P < 0.05$ ) linolenic acid. Results suggest that the FA profile in yak BF and LD is more consistent FA profile thought to be beneficial to human health; yet, it is dependent on adipose tissue depot.

**Key Words:** yak, beef cattle, fatty acids

**W32 Differences in hair coat shedding, calf weaning weight and BCS among Angus dams.** K. A. Gray\*, J. P. Cassidy, and C. Maltecca, *North Carolina State University, Raleigh*.

The objective of the study was to assess possible variation in coat shedding of Angus cows, and its effect on kg of calf weaned (KGW) and cow's body condition score (BCS). Data were available from 304 registered Angus cows sired by 41 bulls, from NC State University. Cows were grazed on pastures which were predominantly endophyte infected fescue, known to cause increased heat stress in cattle. Over 2 years, beginning at March and for 5 months at 30 day intervals, trained technicians scored cows on a scale from 1 to 5, with 1 representing slick coats and 5 winter coats. For each cow the first month with a score of 3 or less (MS, 5 levels) was considered the beginning of winter coat shedding and used in the analyses. Association between MS and KGW or BCS, was investigated using the mixed procedure of SAS. Each year was at first analyzed separately. Models for KGW and BCS included fixed effects of age of cow and MS, covariate of age of calf at weaning d and random effect of cow's sire. No significant association was found between MS and KGW or BCS. Data were further analyzed by dividing cows into two groups, cows that began shedding by May and those that began after May (MS1, 2 levels). In this analysis different years were pooled and a fixed effect of year was added to the model. Calves from dams that began shedding by May were 8.2 ± 3.9 kg heavier at weaning ( $P < 0.04$ ) than calves from later shedding cows. No significant differences were found among different levels of MS1 and BCS. This data was also analyzed to determine if there were differences in MS among cow's sires using the GLM procedure in SAS adjusting for age of cow. Differences in sire were significant ( $P < 0.01$ ). In this study evidence of increased calf weaning weights amongst cows that shed earlier in the year was found. Differences among sires suggest that Angus cattle may differ genetically in their ability to shed their winter coat. Further collection of hair shedding data will be needed to confirm these results.

**Key Words:** beef cattle, hair coat shedding, calf performance

**W33 Age at first calving and longevity of Charolais cows.** F. Szabó\* and Z. Zsuppán, *University of Pannonia, Keszthely, Hungary*.

The length of productive life of beef cows is a trait of great importance with a significant impact on the profitability of beef cattle farming. The objective of the study was to evaluate the age at first calving (AFC), age at culling (ACU) and the longevity (LONG) of Charolais beef cows in Hungary. Longevity was defined, as a length of productive life; the period between first calving and culling. A database of 2766 cows, born between 1982 and 1993 was evaluated using multivariate analysis considering breeding region, birth year, birth season, genotype and sire of cows. Excel (MS 2002) and SPSS for Windows (1998) were used for data processing. The overall mean value and standard error of AFC, ACU and LONG were: 2.76±0.02 years, 8.41±0.18 years and 5.65±0.18 years, respectively. Breeding region, birth year, season, and cow sire had significant influence ( $P < 0.05$ ) on each of the three evaluated traits, while genotype influenced only the AFC. Age at culling and LONG showed a decreasing trend for the birth years of cows from 1982 to 1993. Longer lifespan (ACU) and productive life (LONG) were reached by crossbred than purebred cows. Heritability values of AFC, ACU and LONG were 0.46; 0.21; 0.25, respectively.

**Key Words:** length of productive life, environmental and genetic effects, heritability

**W34 Weaning performance of Charolais calves.** F. Szabó<sup>1</sup>, A. Fördös<sup>1</sup>, Z. Domokos<sup>2</sup>, and S. Bene<sup>1</sup>, <sup>1</sup>*University of Pannonia, Keszthely, Hungary*, <sup>2</sup>*National Association of Hungarian Charolais Breeders, Miskolc, Hungary*.

Weaning weight (WW), preweaning daily gain (PWDG) and 205-day weight (205DW) of 23010 Charolais calves (10696 male and 12314 female) born between 1990 and 2005 from 10098 cows mated with 149 sires were analyzed. Breeding region, year and season of birth, age of dam, and sex of calves were fixed effects, and sire was random effect. Data were analyzed with Harvey (1990) Least Square Maximum Likelihood Computer Program, and two animal models were used for breeding value estimation. Variance, covariance components, heritability, correlation coefficients and the effect of the maternal environment on genetic parameters and breeding values were examined. The overall mean value and standard error of WW, PWD and 205DW were 219±7.60 kg, 939±40.63 g/day and 227±8.58 kg, respectively. Significant ( $P<0.005$ ) region, year, season, sire and dam age effects, and sire × herd interaction were found. Weaning performance increased with increasing dam age up to six years of age. The direct heritability ( $h^2_d$ ) of the evaluated traits was between 0.54 and 0.59. The maternal heritability ( $h^2_m$ ) of these traits was 0.32 and 0.38. The direct-maternal correlations ( $r_{dm}$ ) were strong and negative (-0.84). Contribution of maternal heritability and maternal environment to phenotype was smaller than that of direct heritability ( $h^2_m + c^2 < h^2_d$ ). The proportion of the variance of maternal permanent environment in the phenotypic variance ( $c^2$ ) changed from 0.02 to 0.03. The rank of animals based on breeding value for weaning traits was not changed whether the maternal environmental effect was modeled. The genetic value for weaning results of Charolais population has increased since 1993.

**Key Words:** weaning weight, environmental effects, heritability

**W35 Improving the profitability of beef from pastures: A case study of Tasmania's Circular Head Beef Business Group.** A. E. O. Malau-Aduli<sup>1</sup>, I. D. Bruce<sup>1</sup>, B. Doonan<sup>2</sup>, and P. A. Lane<sup>1</sup>, <sup>1</sup>*School of Agricultural Science, University of Tasmania, Hobart, Tasmania 7001, Australia*, <sup>2</sup>*Davey & Maynard Consultants, Davenport, Tasmania 7310, Australia*.

This case study on improving grazing management skills was conducted over a 12-month period in 2007 utilizing 1200 beef cattle on two properties of 60 hectares each, subdivided into 24 paddocks. The objectives were to evaluate pasture utilisation, liveweight gains and profitability using a multi-faceted economic model. Leaf emergence rate, average pasture cover, pasture growth rate, pre-grazing pasture mass, post-grazing residual and cattle liveweight gain data were collected monthly. Data were analysed using mixed (PROC MIXED) and general linear (PROC GLM) models in SAS to test for the fixed effects of property, date of sampling, cattle type and their second order interactions, while age of cattle and paddocks were fitted as random effects. Relationships between livestock and pasture variables were tested in correlation analyses using PROC CORR and significance established using Bonferroni probabilities. Results demonstrated that significant improvement in grazing management led to an increase in total pasture utilisation per hectare of over 40%, significantly greater than the set target of 7000kgDM/Ha on both properties. Pasture utilised directly for liveweight gain was positively correlated with total pasture utilised ( $r = 0.8686$ ,  $p<0.0001$ ). Energy partitioning for animal maintenance was found to be negatively correlated with total pasture utilised ( $r = -0.5927$ ,  $p<0.05$ ), and pasture utilised for liveweight gain ( $r = -0.8112$ ,  $p<0.0001$ ) and related to the nutritive value and species composition of the pastures. Average daily liveweight gain was found to be positively correlated with total pasture utilisation ( $r = 0.7302$ ,  $p<0.0001$ ) and pasture utilised for liveweight gain ( $r = 0.9181$ ,  $p<0.0001$ ) and negatively correlated with energy partitioned for animal maintenance ( $r = -0.9263$ ,  $p<0.0001$ ). It was concluded that increased pasture utilisation per hectare allowed for stocking rate increases across each property resulting in significant increases of approximately 73% in beef produced per hectare, thus increasing profitability by an overwhelming average of 250% across both properties.

**Key Words:** beef, pasture grazing, profitability

## Breeding and Genetics: Genomic Evaluation, Molecular Genetics, Statistical Methods, Sheep Breeding, and Swine Breeding

**W36 Value of genome-wide selection in Japanese dairy population.** H. Ohmiya\* and M. Suzuki, *Obihiro University of Agriculture & Veterinary Medicine, Obihiro, Hokkaido, Japan*.

Little research has been done on the genomic breeding program for the Japanese dairy cattle population. Therefore, we examined the rate of genetic gain, the rate of inbreeding increase, and the reduction of economic costs associated with the implementation of genome-wide selection in the Japanese dairy cattle population. The simulation data, which mimics the Japanese dairy population, were used to evaluate progeny testing by BLUP with an animal model and genome-wide selection scheme by improved BayesB (Meuwissen et al. 2001). These simulations were replicated 20 times with 30 chromosomes and having 100 QTLs and 101 biallelic SNP markers per chromosome. The candidate bulls in the progeny testing scheme were raised for 5 years until their semen could be used, however in the genome selection scheme candidate

bulls were selected at birth and put into service in one year. All records and pedigree information were used for calculating breeding values by BLUP, whereas only records and genotyping information of each generation were used in the BayesB scheme because of recombinant locus. The results showed that the accuracy of estimated breeding value for bulls by BayesB was a little lower than BLUP (0.82 vs 0.89), however, the reduction of generation interval and larger selection differential per generation in the genome-wide selection led to more genetic gain than BLUP. The rate of inbreeding increased 0.44 during the 10-year period in the progeny testing scheme, but the genome-wide selection scheme was 0.28. Furthermore, the economic costs in genome-wide selection scheme were reduced by 63% compared with the traditional progeny testing strategy. This suggests that genome-wide selection is effective genetically and economically.

**Key Words:** genome-wide selection, BayesB