

least two reasons. First because it has been demonstrated that food production models are possible using large herbivores that might actually cause less harm to animals than a vegan food production model. This is because intensive crop production used to produce food for a vegan diet kills (harms) far more animals of the field than extensive agriculture (pasture production). So, a combined food production system that includes crops, and pasture harvested by large herbivores to be used for human food may kill fewer animals than would a vegan/crop model. Second, I say no for pragmatic reasons. It is improbable that all peoples of the world could ever be convinced that they must give up animals. In fact it may be unethical to try to do that because in poor countries these animals are essential to the survival of the human populations. But what about the richer nations? Maybe they will/should be convinced to do without animals because of the moral strength of the animal rights theories. However, I believe that there are far too many obstacles for that to happen. What then are we morally obligated to do about animals? I suggest that animals do have moral standing and that we are morally obligated to recognize their unique species-specific natures, and treat them accordingly. That would mean treating animals according to their physical and behavioral needs or telos. That, I believe is the most likely outcome of the conversation about animal rights.

**Key Words:** Animal Rights, Welfare, Moral Obligations

**210 Ethics and the role of academics, scientists and veterinarians in the formation of public attitudes and societal decisions.** W. R. Stricklin\*, *University of Maryland, College Park.*

Ethics has to do with “doing the right thing,” but reaching a societal-wide consensus on the right thing to do is often difficult. For example in the USA, there is a wide range of opinions regarding the right thing to do about the use and treatment of food animals. On the one-hand, some persons within both academia and the public at large contend that it is wrong for humans to use other sentient beings as simply a means to an end, i.e., food. Further, they contend that eating animal-based food products should be phased out. On the other hand, some persons - including a significant number of animal scientists - contend that providing food for humans is a greater good that justifies the treatment of food animals across basically all current agricultural housing systems and production practices. And there is a middle position that includes the majority of persons who wish to continue to consume animal food products but also want assurance that the welfare of the animals is appropriately considered. In the USA, the viewpoint of the

educated expert or authoritarian figurehead is still generally respected by the public. However, to maintain this credibility, the public must continue to feel that the information they are presented is unbiased. In some instances, animal scientists are becoming viewed as being too closely tied to industry viewpoints and not giving a balanced view of some issues, including animal welfare. Ultimately, both veterinarians and animal scientists have roles to play in helping the public at large gain a greater understanding of the importance of doing the right thing in terms of how animals are to be treated in our society. Thus, it is important that these professionals acknowledge the importance of ethics in their research, teaching, and other professional activities.

**Key Words:** Animal Welfare, Bioethics, Public Attitudes

**211 Production, processing and marketing: an integrated industry’s view of ethical issues.** C. Klippen\*, *Klippen & Associates, LLC, Audubon, PA.*

Decision making is a part of everyday living. In satisfying our basic needs, decisions are made about what to eat, what to wear, how to get where we are going, when to sleep. There is another type of decision that we also make that could be described as ethical. There’s a purity about a decision labeled “ethical”. What’s the basis for that claim of its being “ethical”. Whose values judgment underscore that ethical decision? In making a decision we try to balance an outcome that we perceive as morally right with what is practical and logical from our set of values. We may view the importance of the outcome as justifying the means in making that decision. Is that “ethical”? We may not know or understand all the facts, yet is it better to decide rather than be indecisive? So, we decide, basing our decision on competing moral perspectives. Evaluating complex and sometimes ambiguous scenarios adds to the dilemma in making a decision. When operating in a framework of proven principles that are reliable, our skills for decision-making are more self-assuring. We center on our beliefs about what we perceive to be right or wrong. Is this ethical? As it relates to producing animals for food, processing and marketing meat, milk or eggs, what proven principles aid the decision as to how that animal is raised, processed, or how the animal product is marketed? Is its efficiency in production, processing coupled with profitability in marketing that dictates the “ethical decision”? Or is it a practical decision that is expedient based on the current needs of society? Is there a reasoning approach from history that can help shape our ethical decisions?

**Key Words:** Marketing, Processing, Production

## Breeding and Genetics - Livestock and Poultry: Beef Cattle

**212 Identification and characterization of microRNA from the bovine adipose tissue and mammary gland.** Z. Gu\*, S. Eleswarapu, and H. Jiang, *Virginia Polytechnic Institute and State University, Blacksburg.*

MicroRNA (miRNA or miR) are a new class of small RNA molecules (~22 nucleotides) that are processed from precursor sequences that form hairpin secondary structures. miRNA inhibit translation or induce degradation of protein-coding mRNA by base-pairing. Increasing evidence suggests that these small RNA molecules play an important role in many processes of animal development and physiology. We have conducted a study to identify miRNA in cattle. By cloning and

sequencing small RNA from the bovine adipose tissue and mammary gland and by predicting and folding the precursors of these small RNA sequences, we have identified 59 distinct bovine miRNA. Five of them were not homologous to any known mammalian miRNA, hence potentially novel miRNA. Twenty-five of them had 3’ and (or) 5’ end variants, suggesting that miRNA precursors may be alternatively processed. Ribonuclease protection assays (RPA) of 12 selected miRNA confirmed their expression in adipose tissue or the mammary gland, from which they were originally cloned. The RPA also indicated tissue-specific or tissue-enriched expression for several miRNA. For example, miR-122a was only detected in the liver, and miR-133 was detected in the heart, skeletal muscle and rumen but not in ten other

bovine tissues. These results demonstrate that miRNA are expressed and may play an important role in cattle too.

**Key Words:** microRNA, Cattle, Adipose

**213 Feed efficiency of tropically adapted breed and breed cross steers when fed in the southern plains.** S. W. Coleman<sup>\*1</sup>, W. A. Phillips<sup>2</sup>, C. C. Chase, Jr.<sup>1</sup>, and D. G. Riley<sup>1</sup>, <sup>1</sup>USDA ARS Subtropical Agricultural Research Station, Brooksville, FL, <sup>2</sup>USDA ARS Grazinglands Research Laboratory, El Reno, OK.

Beef cows in the subtropical USA require that they be adapted to the stressors of the environment. However, calves produced in the region are usually grown and finished in more temperate regions. The objective of this paper is to determine the feed efficiency of steers from a 3-breed diallel mating of Angus (A), Brahman (B) and tropically adapted Romosinuano (R), a Criollo breed native to Colombia. Calves (n = 261) born over 3 yr from 2002-04 were straightbred AA, BB and RR, or crossbreds (RB, BR, RA, AR, BA, AB; letters indicate breed of sire and dam, respectively). Steer calves were weaned in September and shipped 2025 km to El Reno, OK for growing and finishing. After grazing wheat pasture until May, 2003, they were finished on a conventional feedlot diet using Calan headgates to obtain individual feed intake. Steers were serially harvested at three times each year, ranging from 93 to 168 days on feed. Feed efficiency was calculated as feed per unit gain (FdGn) and as residual feed intake (RFI). The MIXED model included effects of year, stocker treatment, and replicate. Days on feed and calf age at the beginning of the feedlot phase were fit as continuous variables. Sire within breed was the random term. Significance is denoted by + (P < 0.10), \* (P < 0.05) or \*\* (P < 0.01). Direct effects for initial and final weight and daily gain were 43\*\*, 16, and -21+; 19+, 61\*\*, and 0.31\*\*; and -62\*\*, -77\*\* and -.10 kg for A, B, and R, respectively. Direct effects for daily DM intake, FdGn, and RFI were -1, 2.16\*, and 0.48+; -.25, -2.73\*\*, and -.44+; and 1.25+, 0.57, and -.05 for A, B, and R steers. Heterosis (P < 0.01) was noted for all breed combinations for initial and final weights, but not for rate of gain. There was negative heterosis (P < 0.01) for intake by A-B and for B-R crosses. There was no heterosis for feed efficiency. In conclusion, Brahman influenced steers appear to be more efficient than Angus and Romosinuano was intermediate.

**Key Words:** Feed efficiency, Brahman, Romosinuano

**214 Genetic evaluation of growth in a multibreed beef cattle population using random regression linear spline models.** J. P. Sanchez<sup>\*1,2</sup>, I. Misztal<sup>1</sup>, I. Aguilar<sup>1</sup>, and J. K. Bertrand<sup>1</sup>, <sup>1</sup>University of Georgia, Athens, <sup>2</sup>University of Leon, Leon, Spain.

The objective of this study was to examine the feasibility of using random regression, spline models (RR-s) for fitting growth traits in a multibreed beef cattle population. The evaluation results from this model were compared to those obtained using a multi-trait model (MT) when both were used to fit the US Gelbvieh data set (1.8 million records and 1.1 million animals). Both models included direct and maternal additive genetic, contemporary group, age of the animal, direct and maternal heterosis, and direct and maternal additive genetic mean of the breed effects. Additionally, the RR-s model included a direct permanent environmental effect. The effect of prior information for heterosis and breed effects on the EBV of sires was

also investigated. When both MT and RR-s models were fitted to the data set containing records for weaning weight (WWT) and yearling weight (YWT) within specified age ranges and medium weight was posed on prior information, the rankings of bulls direct EBV (as measured via Pearson correlations) provided by both models were comparable ( $\geq .99$ ). For maternal effects, these correlations were also high, being the lower case YWT ( $= .92$ ). The inclusion of prior information had negligible effect in the overall ranking for bulls with greater than 20 BWT progeny records, the correlations between EBV obtained in the situations of weak and strong prior information were  $\geq .98$  for direct effect and  $\geq .87$  for maternal effects. However, the effect of prior information for breeds or groups poorly represented in the data, i.e. Zebu, was very important. By using the random regression approach, to discard records outside the usual age ranges of measurement can be avoided and higher accuracies are achieved (2.5% WWT and 2.9% YWT). However the overall rankings after adding this extra information remains nearly unchanged, correlations between them were  $\geq .96$  ( $\geq .95$ ) for direct effects (maternal effects). RR-s model requested three times more rounds to convergence (5.0e-13) than the MT model.

**Key Words:** Beef Cattle, Growth, Linear Splines

**215 Growth and carcass characteristics of lot-fed Wagyu beef cattle and the estimation of homozygosity from band sharing patterns of random amplified polymorphic DNA markers.** A. E. O. Malau-Aduli<sup>\*1</sup>, S. Inoue<sup>2</sup>, T. Richards<sup>2</sup>, A. Howard<sup>2</sup>, and A. Thompson<sup>2</sup>, <sup>1</sup>University of Tasmania, Hobart, Tasmania, Australia, <sup>2</sup>Tasmania Feedlot Pty Ltd, Perth, TAS, Australia.

The Wagyu breed of beef cattle is renowned for its ability to deposit high levels of intramuscular fat resulting in highly marbled beef that meets consumer demands in some niche export markets. We evaluated the post-weaning growth performance and carcass characteristics at slaughter of purebred Wagyu steers raised in the feedlot after an initial backgrounding on grass and silage. Our main aim was to study the average daily gains (ADG), body condition scores (BCS) and liveweight (LWT) changes from weaning to slaughter and to estimate homozygosity and inbreeding coefficients through band sharing patterns using random amplified polymorphic DNA (RAPD) markers. LWT, ADG and BCS were monitored monthly from 2005-2006. Genomic DNA was extracted from blood samples, amplified using RAPD primers, fragments resolved by gel electrophoresis and banding patterns elucidated under UV light. A linear increase in liveweight as age increased was observed and the typical fluctuation due to seasonal variations observed under grazing conditions was unnoticeable. Average LWT ranged from an initial 110kg to 660kg, ADG ranged from 0.7-2.0kg/day and BCS reached the maximum of 5 at the end of the experiment. Average LWT at slaughter was 574kg with a hot carcass weight of 329kg and a dressing percentage of 57%. Mean eye muscle area was 94cm<sup>2</sup>, eye muscle width 8cm and eye muscle length 16cm. Marbling score was 3, subcutaneous fat depth of 17cm and total trimmed fat weight was 34kg. Average saleable meat yield based on the 4 most valuable hind muscles were: Round (11.7kg), Topside (19.3kg), Rump (13.6kg) and Silverside (15.8kg). Average band sharing frequencies ranged from 0.60 to 0.96 with estimated inbreeding coefficients ranging from 0.5% to 7%, respectively. It was concluded that the inbreeding level was low, negligible and not in any way detrimental to meat yield and carcass quality destined for the Japanese market. Finally, RAPD markers were not versatile enough to

clearly differentiate between the fastest and slowest growing animals within the Wagyu breed.

**Key Words:** RAPD Markers, Wagyu, Carcass Traits

**216 Examination of residual feed intake with post-weaning growth and carcass traits in central test bulls.** G. S. Hecht\* and L. A. Kriese-Anderson, *Auburn University, Auburn, AL.*

Since 1978, individual feed intake has been measured on bulls (n = 2,180) consigned to the Auburn University Bull Test along with weights, heights, scrotal circumference and ultrasound carcass traits. Test length since 1977 was reduced from 140 d to 112 d to 84 d. Eight breeds were used in MTDFREML analyses to estimate heritabilities of and genetic correlations between residual feed intake (RFI) and average daily gain (ADG), scrotal circumference (SC), 12th rib fat thickness (FT), *longissimus dorsi* area (REA) and percent intramuscular fat (IMF). Breeds included were Angus (n = 857), Brangus (n = 41), Charolais (n = 380), Gelbvieh (n = 103), Hereford (n = 192), Limousin (n = 106), Santa Gertrudis (n = 106) and Simmental (n = 395). Traits were analyzed using three trait analyses and a sire-maternal grandsire model with either age or weight as covariates. Fixed effects included length of test, breed and year. Covariance estimates were averaged across analyses. Estimates of genetic correlations between RFI and ADG, SC, FT, REA, IMF and FE were 0.00, -0.03, -0.03, -0.44, 0.62, and 0.51, respectively with age as covariate. Estimates of genetic correlations between RFI and ADG, SC, FT, REA, IMF and FE were 0.12, 0.19, -0.02, -0.70, 0.64, and 0.44, respectively with weight as covariate. Heritability and genetic correlation estimates of all traits were on the lower end of reported literature estimates. These results may be due to consignment of elite bulls to a central test station and suggest that selection of animals with a lower residual feed intake should not increase individual size and should improve feed efficiency.

**Table 1. Means and Heritability Estimates of Traits Across Breeds**

| Covariate | RFI       | ADG       | SC       | FT      | REA       | IMF    | FE        |
|-----------|-----------|-----------|----------|---------|-----------|--------|-----------|
| Age       | 0.08      | 0.17      | 0.14     | 0.17    | 0.07      | 0.16   | 0.12      |
| Weight    | 0.09      | 0.16      | 0.17     | 0.15    | 0.12      | 0.12   | 0.12      |
| Means     | 1.04 kg/d | 1.73 kg/d | 36.32 cm | 0.80 cm | 100 sq cm | 3.20 % | 3.42 kg/d |

**Key Words:** Residual Feed Intake, Bulls, Post-Weaning Growth and Carcass

**217 Genotype by environment interactions estimated by using reaction norms in Brazilian Nellore cattle.** E. A. Maricle\*<sup>1</sup>, J. C. Souza<sup>2,3</sup>, L. O. Campos de Silva<sup>3</sup>, A. Gondo<sup>3</sup>, R. L. Weaber<sup>1</sup>, and W. R. Lamberson<sup>1</sup>, <sup>1</sup>University of Missouri, Columbia, <sup>2</sup>Parana Federal University, Palotina, PR, Brazil, <sup>3</sup>Embrapa, Campo Grande, MS, Brazil.

The influence of genotype by environment interactions (GxE) on animal performance complicates selection decisions. Reaction norms are a statistical technique used to characterize GxE. The objective of this study was to evaluate GxE by comparing reaction norms among Brazilian Nellore bulls. Dependent variables were birth, 205 d weaning, 365 d yearling, and 540 d weights. Weights were adjusted for known fixed effects based on Beef Improvement Federation Guidelines.

Environments were defined as progeny groups with a common herd, birth year and season (wet or dry). For data to be included, the following criteria had to be met: all four weights had to be recorded on each progeny, a minimum of four progeny were present in each environment, progeny were present in five different environments, and each environment contained three bulls (n = 4,280 progeny, n = 57 bulls, and n = 161 environments). Reaction norms for each bull were calculated by regressing progeny means within an environment, weighted by number of progeny, on environment means (SAS PROC GLM). To create pseudoreplication, bulls with progeny in ten or more environments had separate regressions determined for each set of five environments. Regression coefficients were fitted to an ANOVA model including bull and environment. Regression coefficients differed among bulls for all traits (P<0.0001). Proportion of variation accounted for by bull and environment, respectively, were for birth weight 0.05 and 0.58; for weaning weight 0.08 and 0.43; for yearling weight 0.08 and 0.49; and for 540 d weight 0.07 and 0.44. These results suggest that bulls differ in the consistency of their progeny's performance across environments. Estimates of genetic merit of regressions from reaction norms may be a useful selection tool for ranking bulls to be used across diverse environments.

**Key Words:** Beef Cattle, Genotype x Environment Interaction, Reaction Norm

**218 Genetic parameter estimates for two measures of disposition.** F. E. Creason\* and R. L. Weaber, *University of Missouri, Columbia.*

Two measures of disposition were collected on Angus and Red Angus cross steers (n=315) with known pedigree from four sources during the initial weighing of steers on a feedlot trial. Steers were weighed and disposition scores recorded through two facilities on the same farm. Disposition was measured as pen score (PS; 1=gentle, 5=aggressive) and exit velocity (EV; m/sec). Exit velocity was measured using infrared electronic triggers to start and stop an electronic recording device to time a steer as it traveled a fixed distance upon exiting a squeeze chute. Exit velocities were recorded when animals were weighed on two consecutive days. The weights and EV were averaged to produce AVGWT and AVGEV. Pen scores were recorded during the feeding trial. At the start of the trial steers in each facility weighed 342.6 ± 25.3 kg and 305.4 ± 32.0 kg, EV averaged 2.50 ± 0.68 m/sec and 2.68 ± 0.99, while PS averaged 1.95 ± 0.70 and 1.86 ± 0.81 respectively. Previous work has shown that EV and PS are positively correlated. EV and PS are negatively correlated with weight gain during the 55d post-weaning growing period and with feedlot placement weights. Sire was included in these models as a random effect and found to be a significant source of variation suggesting a heritable component of disposition. The data described above was included in a sire genetic model to estimate (co)variance components and heritabilities for EV and PS. A two-trait model was fit that included contemporary group (source, collection location, GrowSAFE group) as a fixed effect. Linear and quadratic covariates for each trait included age (d) and AVGWT. A six generation sequential pedigree of 661 animals including 315 progeny and 26 sires was generated. Genetic parameters and expected progeny differences (EPD) were calculated using MTDFREML software. Estimates of heritability (standard error) for EV and PS were 0.35 (0.078) and 0.15 (0.058) with a genetic correlation of 0.28 (0.825). Average, min. and max. EPD for EV and PS were -0.02, -0.33, 0.27 and 0.01, -0.10, 0.10, respectively.

**Key Words:** Temperament, Heritability, Genetic Parameters

**219 Segregation of polymorphisms at Calpain and Calpastatin in beef cattle grown in the tropics.** J. H. Bosques-Méndez<sup>\*1</sup>, M. Pagan<sup>1</sup>, and E. Casas<sup>2</sup>, <sup>1</sup>University of Puerto Rico, Mayagüez, Puerto Rico, <sup>2</sup>Roman L. Hruska USDA MARC, Clay Center, Nebraska.

The distribution of single nucleotide polymorphisms (SNP) in two regions of Calpain (CAPN1-316 and CAPN1-530) and a SNP in Calpastatin (CAST) was determined in beef cattle grown in the tropics (n = 372). Genotypic and allelic frequencies were determined for each SNP in Senepol (n=60), Charolais (n=62), Angus (n=39), Charbray (n=43), Brahman (n=19), Zebu (n=17) and crossbred bulls (n=132). For CAPN1-316, genotypic frequencies were 0.05/AA, 0.63/AG and 0.32/GG with allele frequencies of 0.21/A and 0.79/G. The AA genotype was absent in Charbray, Charolais, Angus, Zebu and Brahman breeds. In Charolais and Senepol GG was greater than AG and the inverse was observed for Zebu, Brahman and Crossbred bulls. In Angus bulls, the AG and GG genotypes were evenly distributed. The A allele was more frequent in Charolais, Angus, Zebu and Brahman, whereas the G allele predominated in Charbray and crossbred animals. Genotypic frequencies for the SNP in CAPN1-530 region were 0.17/CC, 0.40/CT and 0.43/TT. Allelic frequencies were 0.39/C and 0.61/T. Animals of CT genotype were more frequent in Charolais, Senepol, Angus and crossbred, whereas TT was more common in Charbray, Zebu and Brahman bulls. Greater allelic frequencies for C were observed in Senepol and Brahman. The inverse was observed in the other breeds. For CAST, genotypic frequencies were 0.03/CC (n=10), 0.26/CT (n=79), and 0.71/TT (n=79), respectively. Global allele frequencies were 0.46/A and 0.54/C. The allelic frequency of C was greater in Charolais and Angus bulls. Animals having CC genotype were absent in Charolais, Angus and Brahman animals genotyped. The TT animals were more frequent in Charbray, Charolais, Senepol, Angus Brahman, Zebu and crossbred animals. The segregation of the polymorphisms in CAPN1 and CAST could be implicated in differences observed in economically important traits in beef cattle grown in tropical environments.

**Key Words:** CAPN1, CAST, SNP

**220 Genetic analysis of rebreeding to produce a calf at three years of age in beef cows.** J. M. Rumph<sup>\*1</sup>, D. D. Kress<sup>1</sup>, K. C. Davis<sup>1</sup>, D. C. Anderson<sup>1,2</sup>, R. M. Enns<sup>3</sup>, C. M. McAllister<sup>1</sup>, and D. L. Boss<sup>2</sup>, <sup>1</sup>Montana State University, Bozeman, <sup>2</sup>Montana State University, Havre, <sup>3</sup>Colorado State University, Fort Collins.

Rebreeding a first calf heifer to produce her second calf at 3 yr of age can be challenging for beef producers. Heifers generally require more recovery time following their first calf which may delay the onset of estrus to a point beyond the normal breeding season. In an effort to improve heifer rebreeding, data on beef cows at 2, 3, and 4 yr of age were analyzed to determine if rebreeding of first calf heifers is under any degree of genetic control. Records on 417 females born from 1976 – 1994 were analyzed to determine genetic parameters and the percentage of females in each breed group that produced a calf as a 3-yr-old after having their first calf as a 2-yr-old. Animals included in the analysis consisted of Hereford and Tarentaise purebred cows as well as F1, F2, and 3/4 blood females created from these two breeds. Young cows in this herd were not culled unless they were open for two consecutive years. To be included in the data set, cows were required to produce a calf as 4-yr-olds to avoid bias due to culling for reasons other than ability to breed back at 2 years of age. Overall, 72% of females were successful in breeding back to produce a calf at 3 yr of

age. Individual groups were 73%, 79%, 64%, and 62% successful for purebreds, F1, F2, and 3/4 blood cows, respectively. To estimate the genetic parameters associated with this trait, data was analyzed using MTDFREML with breed type, heterosis percentage, and year of birth as fixed effects. Based on the observed trait, heritability was estimated to be 0.08. Converting the observed trait to the underlying scale produced a heritability for rebreeding of 0.14. Although this is a lowly heritable trait, there does appear to be a genetic component and selection against females who fail to rebreed should result in a positive genetic response.

**Key Words:** Genetic Parameters, Reproduction, Beef Cattle

**221 Evaluation of the relationship between scrotal circumference and ultrasound intramuscular fat measurements in Angus cattle.** A. M. Arnett<sup>\*</sup>, J. M. Bormann, M. E. Dikeman, and D. W. Moser, Kansas State University, Manhattan.

Recently, cattle breeders have questioned whether scrotal circumference has an impact on ultrasound predictions of intramuscular fat (IMF). The objective of this study was to investigate the relationship between ultrasound intramuscular fat (IMF), carcass marbling score (MS), and yearling scrotal circumference (SC) in Angus cattle. The American Angus Association provided pedigrees and expected progeny differences (EPD) for 290 Angus sires. All sires in the dataset had an accuracy of at least 0.50 for IMF EPD and MS EPD. Accuracies ranged from 0.50 to 0.97 (mean 0.75) for IMF EPD, 0.50 to 0.89 (mean 0.62) for MS EPD, and 0.05 to 0.96 (mean 0.73) for SC EPD. Individual performance records from 332,162 progeny of these sires and their contemporaries were also provided. These data were age-adjusted to 365 d for growth and ultrasound traits, and to 480 d for carcass traits. Correlations of SC EPD with IMF EPD and MS EPD were not significant ( $P > 0.10$ ). Correlations existed ( $P < 0.05$ ) between SC EPD and birth weight EPD (0.12), weaning weight EPD (0.13), yearling weight EPD (0.14), yearling height EPD (0.25), mature height EPD (0.17) and ultrasound scan weight EPD (0.22). IMF EPD was regressed on Marbling score EPD alone and with SC EPD. Intramuscular fat EPD was highly significant ( $P < 0.01$ ) in predicting MS EPD. Scrotal circumference EPD was also a significant ( $P < 0.05$ ) predictor of MS EPD, but only explained an additional 1% of the variation. Linear and quadratic regressions of IMF on SC were estimated from the performance data. Regression coefficients for SC were small but significant (-0.086, linear and 0.001, quadratic;  $P < 0.05$ ). Correlations of high-accuracy sire EPD indicate that selection for SC should not significantly influence carcass traits.

**Key Words:** Beef Cattle, Intramuscular Fat, Scrotal Circumference

**222 Phenotypic relationships among measures of feed utilization, ADG, and ultrasonic measures.** K. A. Gray<sup>\*</sup>, G. B. Huntington, M. H. Poore, C. S. Whisnant, and J. P. Cassady, North Carolina State University, Raleigh.

The objective of this research is to estimate phenotypic relationships among measures of feed utilization and economically important traits in beef cattle. Data were available from 124 registered Angus bulls ( $262 \pm 3.4$  Kg BW,  $266 \pm 1.76$  d of age) from the NC State University Historic Angus Herd which is maintained at the Upper Piedmont Research Station in Reidsville, NC. Bulls were blocked based on BW

and sire into groups of 12, adapted to a corn silage-based diet (140g CP, 1.73 Mcal NEM and 1.22 Mcal Neg per kg DM), and trained to use calen gates. Feed offered was recorded on a daily basis and used to calculate average daily feed intake. Bulls were weighed every 14 d and growth (ADG) was determined by linear regression of weight against time. Mean ADG and DMI were  $1.52 \pm .23$  DM/day and  $7.25 \pm 1.12$  kg. Three measures of feed utilization were calculated and compared. Feed to gain ratio (FGR) was calculated by taking the average DMI of each bull divided by ADG. Residual feed intake (RFI) was calculated using two different methods. Method 1 was based on the NRC equations (NRFI) and for method 2 phenotypic regression using ADG and DMI adjusted to a common 42 day mid weight (RRFI) was used. Partial correlations with sire nested within year, year, and

pen as fixed effects were calculated. Correlations between NRFI with RRFI, FGR and ADG were 0.965, 0.794 and -0.217, respectfully. Correlations between RRFI with FGR and ADG were 0.819 and -0.005. There were no relationships found to be significant between feed utilization calculations and ultrasonic measurements of intramuscular fat, rib eye area, rump fat and rib fat. As expected NRFI and RRFI were highly correlated indicating that they are the same trait. Both NRFI and RRFI were highly correlated with FGR. It was concluded that FGR is a good predictor of RFI. Alternative methods of calculating RFI were found to be nearly identical and independent of ultrasonic measures of body composition.

**Key Words:** Beef Cattle, Residual Beef Intake, Efficiency

## Breeding and Genetics - Livestock and Poultry: Dairy Cattle I

**223 Dry matter feed intakes for first lactation Holstein, Jersey and their reciprocal crosses in the Virginia Polytechnic Institute and State University crossbreeding project.** K. M. Olson\*, B. G. Cassell, and M. D. Hanigan, *Virginia Polytechnic Institute and State University, Blacksburg.*

The crossbreeding project at Virginia Polytechnic Institute and State University began in the fall of 2002. Holstein and Jersey foundation females were mated to four Holstein bulls and four Jersey bulls to create JJ, HH, JH and HJ breed groups (sire breed listed first). Collection of individual feed intakes on first lactation project cows began in September 2005 and continues through 2007. Individual feed intakes are measured in two week trials during every six week period (two weeks on, four weeks off) on first lactation cows less than 305 days in milk. All cows were fed the herd total mixed ration before and during the trial. Forages, grains and concentrates were submitted for nutrient analyses at least once during each trial period. An 'as-fed' intake and dry matter intake were calculated daily for the project cows during the feed intake cycle and averaged across week of production. A mixed model using repeated records was used to analyze dry matter intakes. Effects included trial, breed group [(HH (n=25), HJ (n=17), JH (n=15), JJ (n=11)], age at calving, week in milk and breed by week in milk interaction. Significant effects ( $P < 0.05$ ) for dry matter intake included breed group and week in milk however, the interaction between week in milk and breed and differences between trials were not significant. LSM for dry matter intakes across all weeks were  $22.2 \pm 0.3$ ,  $21.2 \pm 0.3$ ,  $20.8 \pm 0.4$ , and  $17.5 \pm 0.4$  kg for HH, HJ, JH and JJ respectively. In general, dry matter intake reached a plateau at 13 weeks. All breed groups were significantly different from one another except the HJ and JH. Visual inspection of breed group means by week in milk suggests a positive heterosis for dry matter intake (untested).

**Key Words:** Crossbreeding, Dry Matter Intake, Feed Intake

**224 Comparison of Holstein–Friesian, Norwegian Red and Holstein–Friesian×Norwegian Red cows on Irish dairy farms: Milk production and udder health.** N. Begley\*<sup>1,2</sup>, M. Rath<sup>2</sup>, and F. Buckley<sup>1</sup>, <sup>1</sup>*Teagasc, Moorepark, Fermoy, Co. Cork, Ireland*, <sup>2</sup>*School of Life Sciences, UCD, Belfield, Dublin, Ireland.*

The objective of this study was to compare the milk production performance and udder health of Holstein–Friesian (HF), Norwegian

Red (NRF) and Holstein–Friesian×Norwegian Red (F1) cows in first lactation. This study forms part of a 3–year on–farm crossbreeding study comprising 46 dairy herds. Milk production data was available for 1327 first lactation cows: 710 HF, 325 NRF and 292 F1. Predicted 305 d yields were obtained from the Irish Cattle Breeding Federation. These were derived using the SLAC method which adjusts for calving month, age at calving, parity and season of calving. Production data were analyzed in SAS using proc GLM and udder health data were analyzed using proc LOGISTIC. Herd, breed and calving date (udder health only) were included in the model. The 305 d milk yields of the HF and F1 were similar at 5,353 kg and 5345 kg, respectively. The NRF produced slightly less milk at 5149 kg ( $P < 0.001$ ). Fat content was highest for the HF at 4.00%, intermediate for the F1 at 3.96%, and lowest for the NRF at 3.94% ( $P < 0.05$ ). Protein content was similar for all breeds; 3.46%, 3.45% and 3.45% for the HF, NRF and F1, respectively. The NRF and F1 showed superior udder health during lactation. Compared to the HF (2.04), the F1 and NRF cows had lower somatic cell score at 1.97 ( $P < 0.01$ ) and 1.92 ( $P < 0.001$ ), respectively. The proportion of NRF cows (5.8%) with somatic cell counts averaging greater than 400,000 during lactation was lower than the HF (9.9%;  $P < 0.05$ ). That of the F1 (6.7%) tended to be lower ( $P = 0.097$ ) than the HF. The incidence of mastitis was available for 42 of the 46 herds. Fourteen percent of the HF cows had mastitis at least once during lactation, compared to 9.5% for both the F1 ( $P = 0.063$ ) and the NRF ( $P < 0.05$ ). In conclusion, based on data from year one, the F1 cows produced similar levels of milk production to the HF. Both the NRF and F1 exhibited superior udder health compared to the HF.

**Key Words:** Norwegian Red, Udder Health, Milk Production

**225 Heritability of electronically recorded daily body weight across lactation using random regression models.** J. K. Toshniwal\*<sup>1</sup>, C. D. Dechow<sup>1</sup>, J. A. D. R. N. Appuhamy<sup>2</sup>, and B. G. Cassell<sup>2</sup>, <sup>1</sup>*The Pennsylvania State University, State College*, <sup>2</sup>*Virginia Polytechnic Institute and State University, Blacksburg.*

The objectives of this study were to estimate heritability for daily body weight (BW) and genetic correlations among BW at different days in milk (DIM). The Afiweigh cow body weighing system records BW of every cow exiting the milking parlor. The Afiweigh system was installed at the The Pennsylvania State University dairy herd in August of 2001 and in July of 2004 at the Virginia Polytechnic Institute and State University dairy herd. BW recorded after 365 DIM were