

affected than the three-host tick *D. variabilis*. Our results thus suggest that ingestion by herbivores of plants containing compounds such as AzA may reduce external parasites.

Key Words: lamb, tick, azadirachtin

Beef Species: Health, Efficiency and Beef Quality

613 mRNA expression of genes regulating oxidative phosphorylation in the muscle of beef cattle divergently ranked on residual feed intake. A. K. Kelly^{*1}, S. M. Waters², M. McGee², C Carberry^{1,2}, D. H. Crews Jr³, T. M. Boland¹, and D. A. Kenny¹, ¹*School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland,* ²*Animal Bioscience Centre, Teagasc, Grange Beef Research Centre, Dunsany, Co. Meath, Ireland,* ³*Colorado State University, Fort Collins.*

The objective was to evaluate the effects of ranking on phenotypic residual feed intake (RFI) and diet type on the transcription of genes coding for mitochondrial biogenesis in the muscle of beef cattle. Individual dry matter intake and growth was recorded for 90 yearling Limousin × Friesian heifers offered a high energy TMR diet over 120 days. All animals were ranked retrospectively on phenotypic RFI. The 10 highest (inefficient) and 10 lowest (efficient) animals were selected for this study. Animals were then re-allocated to a grass silage diet and feed intake was recorded for a six week period. The experiment was therefore arranged in a 2 (high v low RFI) × 2 (high v low energy diet) factorial design. Biopsies of the *M. longissimus dorsi* were harvested at the end of each dietary period. Total RNA was extracted and real-time PCR was used to quantify mRNA transcripts of genes coding for five enzymes from the respiratory chain complex, two electron carriers, mitochondrial protein and five transcription factors. mRNA expression of the transcription factors PGC1- α and PPAR- γ were 2.0 and 2.8-fold higher ($P < 0.01$) respectively, in inefficient compared with efficient animals. There was a phenotype × diet interaction ($P < 0.05$) for *ant-1* mRNA involved in exchange of ADP and ATP between the mitochondrial matrix and the cytosol. A tendency ($P = 0.09$) for a phenotype × diet interaction was also observed for *atpase*, a critical regulator of the ATP-synthesizing enzyme complex. These data suggest an association between mitochondrial biogenesis and RFI in cattle and could be useful in the development of molecular markers for this trait.

Key Words: residual feed intake, muscle, gene expression

614 Relationship between metabolic hormones, metabolites and energetic efficiency in growing beef heifers. A. K. Kelly^{*1}, M. McGee², D. H. Crews Jr³, T. M. Boland¹, and D. A. Kenny¹, ¹*School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland,* ²*Teagasc, Grange Beef Research Centre, Dunsany, Co. Meath, Ireland,* ³*Colorado State University, Fort Collins.*

Measurement of residual feed intake (RFI) is expensive and thus identification of cost-effective physiological indicators is necessary to facilitate wide-scale adoption. Our objective was to examine the potential of selected metabolic hormones and metabolites as indicators of energetic efficiency in growing beef heifers. Individual dry matter intake and growth was recorded for 90 yearling Limousin × Friesian heifers offered a high energy TMR diet for 120 days. Blood samples (n=4) were collected by jugular venipuncture on a monthly basis for each animal. Concentration of plasma IGF-1 was measured using

RIA, insulin was quantified using fluoro-immunoassay, while selected metabolites were measured using an automated biochemical analyzer. Residual feed intake was computed, for each animal, as the residuals from the regression of DMI on ADG and mid test BW^{0.75} (MWT). Residual feed intake averaged 0.00 kg/d and ranged from -1.25 to 1.87 kg/d. As expected, RFI was not correlated with MWT or ADG, but was correlated ($P < 0.001$) with DMI ($r = 0.48$) and FCR ($r = 0.46$). Plasma IGF-1 was positively correlated ($P < 0.05$) with ADG ($r = 0.25$) but not ($P > 0.10$) with DMI, FCR or RFI. Correlations coefficients between insulin and DMI, ADG, FCR or RFI were not different from zero ($P > 0.10$). Plasma glucose was negatively correlated ($P < 0.05$) with FCR ($r = -0.20$) but not associated with DMI, ADG or RFI. Urea concentrations were related to DMI ($r = 0.33$) and FCR ($r = 0.31$) but not ADG or RFI. Plasma NEFA was negatively associated ($P < 0.05$) with DMI (-0.36), FCR (-0.36) and RFI (-0.23). Positive associations ($P < 0.05$) were observed between BHB and DMI (0.34), FCR (0.25) and RFI (0.39) but an association with ADG was not detected. It is unlikely that the plasma analytes measured here, *per se*, will be useful in the early identification of energetically efficient cattle.

Key Words: residual feed intake, plasma analytes

615 Predicting body weight in beef heifers using various body measurements. A. G. Fahey^{*}, A. K. Kelly, R. P. McDonnell, and D. A. Kenny, *School of Agriculture, Food Science, and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland.*

Accurate assessment of body weight (BW) is an important management tool in commercial beef enterprises. However, many farmers may not have easy access to weighing facilities. Body measurements (BM) such as wither height or depth of chest require inexpensive equipment. In order to determine the potential of various BM as predictors of BW, back length, wither height, pelvic width, chest depth, and chest girth were measured along with BW. Heifers were divided into two age groups; 6-13 months (mean = 286.8 ± 44.7 d; n = 87 heifers, 176 records), and 17-24 months (mean = 642.3 ± 45.6 d; n=60 heifers, 106 records). Body weight was regressed on BM, and linear, quadratic and cubic effects of the BM variables were considered: $Y = b_0 + \text{age} + b_1X + b_2X^2 + b_3X^3 + \epsilon$. Where Y = body weight, b_0 = the intercept, X = independent variable (i.e. wither height, back length, chest depth, chest girth, or pelvic width). Cubic regression models with and without age were best predictor equations for BW for both age groups. The R² value was used to determine the variation accounted for by the various regression models (Table 1). Overall, the cubic regression models had a better fit for the 6-13 month group for all measurements with the exception of chest girth which was stronger for the 17-24 month heifers. The cubic regression equation for chest depth + age had the best fit for the 6-13 month group, while chest girth + age was the best BW prediction model for the 17-24 month group. These results indicate the potential for the use of BM as indicators of BW, although different BM may have to be used depending on the age of the animal.

Table 1. Cubic regression models with and without age for heifers in both age groups.

Parameter	R ² (6 – 13 months)	R ² (17 - 24 months)
Back Length	0.71	0.31
Back Length + age	0.84	0.31
Pelvic width	0.83	0.26
Pelvic width + age	0.83	0.24
Chest Girth	0.57	0.70
Chest Girth + age	0.79	0.71
Chest Depth	0.91	0.15
Chest Depth + age	0.92	0.25
Wither Height	0.83	0.18
Wither Height + age	0.88	0.29

Key Words: beef cattle, body weight, body measurement

616 Effect of residual feed intake on body composition traits in growing beef heifers. A. K. Kelly^{*1}, M. McGee², T. M. Boland¹, D. H. Crews Jr.³, and D. A. Kenny¹, ¹*School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland,* ²*Teagasc, Grange Beef Research Centre, Dunsany, Co. Meath, Ireland,* ³*Colorado State University, Fort Collins.*

Live animal measurements can be useful predictors of carcass composition and thus may act as early indicators of carcass value. The objective of this study was to assess various ultrasonic and body composition measurements in beef heifers divergently ranked on phenotypic residual feed intake (RFI). Ninety Limousin × Friesian heifers were used in the current study. Individual daily feed intake and bodyweight gain were calculated over a 120 day experimental period. The test diet consisted of *ad libitum* access to a maize silage and pelleted concentrate total mixed ration offered at a ratio of 30:70 respectively. Physical measurements including height at withers, chest girth, pelvic width and length of back as well as ultrasonic fat and muscle depths were recorded on four equally spaced occasions during the experimental period. Residual feed intake was computed, for each animal, as the residuals from a multiple regression model regressing DMI on ADG and mid test BW^{0.75} (MWT). Standard deviations above and below the mean were used to group animals into high (>0.5 SD), medium (± 0.5 SD), and low RFI (<0.5 SD). Gain in body composition traits was computed as the coefficient of the linear regression of body composition measurements on time. Residual feed intake ranged from -1.27 to 1.87 kg/d. representing a mean daily difference of 3.14 kg/DM in feed consumed between the most and least efficient animals. Low RFI animals consumed 15.7 and 7.6% less feed than animals with medium and high RFI, respectively. The high RFI group deposited more ($P < 0.05$) lumbar fat compared to the medium or low RFI groups. There was no difference ($P > 0.10$) in gain of muscle or rump fat or in any other body measurement recorded between RFI groups. The results suggest lower lipid accretion in energetically efficient animals. Attempts should be made to account for this in the estimation of RFI.

Key Words: residual feed intake, body composition

617 The immune response of heifers divergently ranked for residual feed intake. A. G. Fahey^{*1}, B. Earley², A. K. Kelly¹, M. McGee³, and D. A. Kenny¹, ¹*School of Agriculture, Food Science, and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland,* ²*Tea-*

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Feed intake accounts for 70% of the variable costs of beef production. Therefore, the efficiency with which an animal converts feed energy into meat is an economically important trait. An animal's response to stress is characterized by increases in metabolic rate, energy consumption and utilization mediated through alterations in the functioning of the hypothalamic–pituitary–adrenal axis. The objective of this study was to examine the immune response to physiological stress in cattle divergently ranked for residual feed intake (RFI). Limousin × Friesian heifers (n=86) were ranked on phenotypic RFI. The 15 highest and 15 lowest ranking animals were assigned to high and low RFI groupings respectively. All heifers were fitted aseptically with an indwelling jugular catheter for repeated blood sampling. On d 0, two blood samples were taken at -120 and 0 min prior to an intramuscular administration of dexamethasone (20µg/kg). On d 1, blood samples were taken at -40 and 0 min and then animals were intravenously administered bovine corticotrophin releasing hormone (bCRH; 0.3µg/kg). Further blood samples were taken at 60, 120, 240, 350, and 410 min after bCRH. Blood samples were analyzed for lymphocyte, neutrophil and leukocyte (LUC) counts, haemoglobin (HGB) concentration and haematocrit percentage (HCT). A repeated measures ANOVA was conducted with the main effects of bleed time (T), group (G; high or low RFI), T × G, and the average of the two blood samples pre-dexamethasone was used as a covariate. A significant time effect was found for LUC and HGB ($P < 0.01$), and for HCT ($P < 0.05$). There were no significant effects for G or T × G. These data suggest that selection for animals with low RFI will not compromise immune function.

Key Words: residual feed intake, stress, immune response

618 Rubber mats improve finishing beef cattle welfare. M. R. Elmore^{*}, M. F. Elischer, M. C. Claeys, and E. A. Pajor, *Purdue University, West Lafayette, IN.*

Housing beef cattle on concrete can negatively impact welfare, as evidenced by increased lesions and joint swelling. The aim of this study was to compare the effect of rubber mats on the growth, health, hygiene and behavior of finishing beef cattle. Crossbred Angus steers (48, n=4/trt) were housed in pens of 4 and assigned to either slatted concrete (C), slatted rubber mat (S) or solid rubber mat (M) from 36–48 weeks of age. Performance data were collected at 2 week intervals, while frequency of postural changes (indicator of floor traction/comfort) at weeks 0 and 12. Data were analyzed using GLM and post-hoc Tukey tests. There was no effect of flooring on weight ($P=0.429$) or ADG ($P=0.950$). The S steers showed a decrease in lameness (1.69 ± 0.04) compared to M (1.95 ± 0.04) and C (1.98 ± 0.04 ; both $P < 0.001$), M and C did not differ ($P > 0.05$). The S steers showed less joint swelling (knees [K]: 0.17 ± 0.05 , hocks [H]: 0.15 ± 0.07) compared to M (K: 0.41 ± 0.05 , H: 0.51 ± 0.07) and C (K: 0.74 ± 0.05 , H: 0.62 ± 0.07 ; all comparisons $P < 0.001$); while M showed less K swelling compared to C ($P=0.007$), but no effect on H ($P > 0.05$). The M steers showed an increase in lesion score (0.80 ± 0.08) compared to S (0.38 ± 0.08) and C (0.37 ± 0.08 ; $P < 0.001$ and $P=0.003$, respectively), though S and C did not differ ($P > 0.05$). The M (2.88 ± 0.04) and S (1.02 ± 0.04) pens were less clean than C (0.86 ± 0.04 ; $P < 0.001$ and $P=0.023$, respectively) and M was less clean than S ($P < 0.001$). Additionally, M steers were dirtier (3.64 ± 0.05) than S (2.27 ± 0.05) and C (2.19 ± 0.05 ; both $P < 0.001$), S and C did not differ ($P > 0.05$). The S steers changed their posture more frequently (22.50 ± 1.21) than C (17.38 ± 1.21) and M (17.03 ± 1.21 ; $P=0.036$ and $P=0.026$, respectively), M and C did not differ ($P > 0.05$). Compared to C, M

showed a reduction in knee swelling, but an increase in leg lesions and a reduction in cleanliness; while S showed a decrease in joint swelling and lameness and an increase in postural changes. This data suggests that the addition of slatted rubber mats to concrete pens should be considered as a method to improve beef cattle welfare.

Key Words: beef cattle, rubber mats, welfare

619 Feedlot growth performance and carcass characteristics of heifers treated for clinical signs of bovine respiratory disease during preconditioning. B. P. Holland*, L. O. Burciaga-Robles, C. J. Richards, D. L. Step, and C. R. Krehbiel, *Oklahoma State University, Stillwater.*

Heifers (n = 337; initial BW = 241.3 ± 16.6 kg) were assembled by a western Kentucky order buyer and shipped to Stillwater, OK. During a 63-d preconditioning period, morbidity and mortality attributed to Bovine Respiratory Disease (BRD) was 57.6% and 8.6%, respectively. At the end of preconditioning, 193 heifers were selected and allotted to finishing pens (5 to 7 heifers/pen) based on the number BRD treatments received. Heifers were never treated for BRD (0X; n = 9 pens), treated one time (1X; n = 9 pens), two times (2X; n = 6 pens), 3 times (3X; n=6 pens), or designated as chronically ill (C; 2 pens). Arrival BW were not different ($P = 0.21$) among treatment categories. However, disease incidence during preconditioning decreased ($P < 0.01$) performance, resulting in BW of 318, 305, 294, 273, and 242 kg for 0X, 1X, 2X, 3X, and C, respectively, at the start of the finishing period. On d 65 and 122, LM measurements were made by ultrasound to estimate average end point within category and block. On average, heifers were slaughtered on d 163 for 0X, 1X, and 2X, d 182 for 3X, and 189 for C ($P < 0.01$). Final BW was similar for heifers treated 0, 1, 2, or 3 times, but was lower ($P = 0.05$) for heifers deemed chronically ill. Overall ADG was not different among BRD treatment categories, but DMI was lower ($P < 0.01$) for chronically ill animals. Therefore, G:F was greatest ($P < 0.01$) for C, intermediate for heifers that received either 2 or 3 BRD treatments, and least for heifers never treated or treated 1 time. Similar to BW, HCW was lower ($P = 0.03$) for C than other categories. Marbling score tended ($P < 0.10$) to be lower for 3X and C than 0X, 1X, and 2X, but other differences in carcass characteristics were not detected ($P \geq 0.12$). Less than 20 additional days on feed were required for heifers treated 3 times to have similar weights and carcass characteristics to heifers never treated for BRD. Segregating and re-starting animals during finishing may be a viable alternative to realizing chronically ill animals.

Key Words: bovine respiratory disease, cattle, feedlot

620 Effects of growing phase diet on fatty acid profile of beef steers. K. E. Hudelson*, C. R. Krehbiel, G. W. Horn, J. W. Dillwith, M. P. McCurdy, R. D. Madden, and R. G. Mateescu, *Oklahoma State University, Stillwater.*

Fatty acid composition of intramuscular (IM) beef fat depots is influenced by diet. Previous research indicates that the benefits of grass-feeding beef cattle include decreased omega-6/omega-3 fatty acid ratio and atherogenic index and increased concentration of conjugated linoleic acid (CLA), all healthfulness traits that are becoming increasingly important to consumers. However, the effects of growing phase diet on the fatty acid profile of IM fat after the finishing phase are unclear. The purpose of this study was to investigate the effects of feeding regimen during the growing phase on fatty acid profile pre- and post-finishing.

Thus, 36 British crossbred steers were randomly assigned to one of four treatment diets: high-concentrate ad libitum (CF); wheat pasture (WP); sorghum silage-based (SF); or high-concentrate program (PF). Steers in the WP, SF, and PF treatments were managed such that rate of gain was approximately equal across groups. Four steers from the WP, SF, and PF groups were harvested at the end of the 112 day treatment; the remaining 24 steers were finished on a concentrate diet until they reached a 12th rib fat thickness of 1.26 cm. Rib eyes were collected from the left side of each steer for analysis of fatty acid content. Rib eyes were trimmed of subcutaneous fat and powdered in liquid nitrogen prior to total lipid extraction in triplicate from approximately 40 mg tissue using a 2:1 chloroform: methanol method. Acid and base catalyzed derivitizations were performed. Extracts were analyzed using an Agilent 6890 GC with FID and a DB-23 column. Percent composition of each fatty acid was calculated and fatty acids were grouped by class prior to assessment of variation between treatments using the GLM of SAS followed by orthogonal contrasts with 1 degree of freedom. Significant differences in saturated ($P=0.029$) and monounsaturated ($P=0.035$) fatty acids, atherogenic index ($P=0.039$), and omega-6/3 ratio ($P=0.001$) were detected between treatments prior to finishing. Except for the omega-6/3 ratio ($P=0.010$), no significant differences were detected post-finishing suggesting that finishing diet is the determining factor of fatty acid profile at harvest.

Key Words: lipids, grass-fed, marbling

621 Comparison of fatty acid profiles of longissimus muscle from Angus and Charolais finishing steers. A. K. Lunsford*, J. W. Dillwith, C. R. Krehbiel, and R. G. Mateescu, *Oklahoma State University, Stillwater.*

Beef is a rich source of protein and micronutrients, however beef is perceived as having high fat content with undesirable composition: high percentage of saturated fatty acids. Genetic variability in beef fatty acid composition consists of differences between breeds and between animals within breed. The effect of breed on fatty acid profile in beef was evaluated in longissimus muscle from Angus (n=19) and Charolais (n=14) feedlot finished steers. Steers were fed a total of 140 d before slaughter. Longissimus muscles were biopsied on d 127 of the finishing period between the 10th and 13th ribs and fatty acid composition was determined. Lipids were extracted in triplicate with a 2:1 (v,v) methanol:chloroform solution then acid and base derivitized before separation by gas chromatography on an Agilent 5890 gas chromatograph with 7673 autosampler. Percent composition of each fatty acid was calculated and the effect of breed was analyzed using the general linear model of SAS. Hot carcass weights did not differ, however, Angus steers had higher marbling scores ($P=0.01$) and more backfat ($P=0.01$) than Charolais steers. Although percent of saturated fatty acids did not differ between Angus (44.9%) and Charolais (44.0%) steers, Angus steers LM had a higher percent of monounsaturated fatty acids (43.7 vs. 39.4%; $P=0.01$) and a lower percent of polyunsaturated fatty acids (11.1 vs. 16.3%; $P=0.03$), omega-3 fatty acids (0.58 vs 0.82%; $P=0.04$) and omega-6 fatty acids (10.5 vs. 15.5%; $P=0.03$). Specifically, Angus had a higher ($P<0.04$) percentage of palmitic (16:0), palmitoleic (16:1), heptadecenoic (17:1), and oleic (18:1) acids in LM than Charolais steers. Angus steers had a lower ($P<0.03$) percentage of behenic (22:0), lignoceric (24:0), linoleic (18:2), linolenic (18:3), eicosadienoic (20:2), arachidonic (24:0), and docosahexaenoic (22:6) acids in LM than Charolais steers. The challenge for the beef industry is to develop and implement a program aimed at improving healthfulness of beef utilizing existing natural genetic variation in fat composition. These

results indicate the possibility of manipulating beef fat composition through breed selection.

Key Words: beef, fatty acid, longissimus

622 Fatty acid profile in beef meat and baby food based on beef meat. A. Nudda^{*1}, G. Battacone¹, R. Boe¹, M. G. Manca¹, M. Mele², A. Serra², and G. Pulina^{1,3}, ¹*Dipartimento di Scienze Zootecniche, University of Sassari, Italy*, ²*Dipartimento di Agronomia e Gestione dell'Agroecosistema, University of Pisa, Italy*, ³*Agricultural Research Agency of Sardinia - AGRIS Sardegna, Sassari, Italy*.

The aim of this study was to compare fatty acid (FA) profile of fresh beef meat with that of baby foods based on beef meat. For this purpose, 20 samples of homogenized beef–meat baby food (80–g jars; HO) and 18 samples of lyophilized (freeze–dried) beef–meat baby food (30–g jars; LIO), produced by various infant–food companies, and 10 samples of fresh beef meat (FM) were collected and analyzed by gas chromatography. The content of each fatty acid methyl ester (FAME) was expressed

as a percentage of total FAME. Data were analyzed with one–way ANOVA using type of product as the main effect. All fatty acids, except for α -linolenic acid (C18:3 ω 3) and c9,t11 conjugated linoleic acid (CLA), differed among the three products tested. The sum of ω 6 FA was higher in HO (21.2%) compared to FM (12.5%) and LIO (4.0%) samples, due to its higher content of linolenic acid. Therefore, ratio ω 6/ ω 3 FA was markedly higher in HO (32.1) compared to FM (9.0) and LIO (8.4) samples. On the other hand, the content of arachidonic acid (C20:4 ω 6) was more than 9–fold higher in FM compared to LIO and HO. The content of total PUFA ω 3 was highest in FM (1.5%), because of greater content of EPA, DPA and DHA compared to HO (0.8%) and LIO (0.6%) baby foods. Fatty acid composition was more similar between LIO and FM samples than between HO and FM samples, probably as a consequence of the high level of vegetable oil added to HO products. This study suggests the possibility of enhancing the FA profile of commercial baby food based on beef meat by using meat with a healthier FA profile. *Acknowledgements: Research supported by the Fondo di Ateneo per la Ricerca Scientifica (FAR, ex 60%).*

Key Words: beef meat, fatty acid, baby food

Breeding and Genetics: Breeding & Genetics Workshop

623 Solving a dilemma in graduate education: Animal Breeding and Genetics Online. R. M. Lewis^{*1}, B. B. Lockee¹, M. S. Ames¹, G. C. Márquez¹, R. M. Enns², J. M. Rumph³, T. W. Wilkinson¹, and E. J. Pollak⁴, ¹*Virginia Tech, Blacksburg*, ²*Colorado State University, Fort Collins*, ³*Michigan State University, Lake City*, ⁴*Cornell University, Ithaca, NY*.

Diminishing faculty numbers has reduced opportunities for coursework tailored to the needs of future scholars in quantitative aspects of genetics. Existing faculty must focus on basic content, limiting their ability to offer advanced instruction. A potential solution to this dilemma is utilizing distance learning technologies within a collaborative framework. Distance delivery programs have advantages: more students can access expertise within a technology-enriched learning environment. However, challenges exist. There is risk of a “psychological distance” separating students and faculty. Furthermore, distance education increases demands on faculty time, particularly with course design and implementation across institutions. A consortium of four universities has combined efforts to develop eight graduate-level online courses in animal breeding and genetics. The instructional design adopted embraces both the advantages and challenges of distance delivery. Discussion boards and virtual office hours have been used to encourage communications. A game-based genetic simulation was developed, with across-institutional teams competing through a common web-based interface. An annual face-to-face event has been held to allow social and academic interactions. Thus far, students from 19 universities have participated, with each course enjoying an enrollment of 10 to 30 students. Originally, seven courses were planned. However, based on student feedback and performance, it became clear that pre-requisite knowledge varied widely among participants. Therefore, an eighth course was added to provide foundational knowledge. Consistency in course design and implementation remains a challenge. Joint working sessions will be held to define common instructional and assessment strategies. With such a concerted effort, the Animal Breeding and Genetics Online curriculum offers promise for solving a dilemma in graduate education.

Key Words: graduate education, distance learning, quantitative genetics

624 Recent developments in genetic evaluation tools. D. Garrick^{*}, *Iowa State University, Ames.*

The principal tool for genetic evaluation is a sound and practical statistical basis to determine linear functions for combining recorded performance on an individual, its relatives and contemporaries in order to minimize the prediction error variance of the estimated genetic merit of each animal. Hazel and Lush’s methodology, known as best linear prediction or selection index, was limited to circumstances where observed performance had been corrected, prior to analysis, with the true or parametric adjustment factors for non-genetic effects such as herd-year. In practice, their method was applied using estimated adjustments for non-genetic effects and ignoring the contributions of all animals except a few close relatives. Henderson extended the method. First, to account for the estimation of fixed effects from the data, by restricting analysis to certain linear combinations of observations that resulted in translation invariant prediction, known as best linear unbiased prediction. Those evaluations had larger prediction error variance, but lacked the bias from errors in estimation of non-genetic effects. Second, a computing algorithm was developed to include information from all relatives. It used expected or average relationships between animals. A recent extension exploits the availability of genetic markers to characterize the realized rather than expected inheritance of chromosome fragments among close and distantly related animals. The combined use of genomic and phenotypic data is known as genomic prediction. It can provide genetic evaluations of animals without individual or progeny records that are more accurate than was the case using expected relationships.

Key Words: genomic prediction