887 Identification of factors that cause genotype by environment interactions between dairy production systems.

N.R. Zwald* and K.A. Weigel, *University of Wisconsin - Madison.*

The objective of this study was to describe the production systems in countries that participate in international dairy sire evaluations, and to identify factors that cause variation in progeny performance between herds. Test day data from first lactation Holstein cows in Australia, Austria, Belgium, Canada, Czech, Estonia, Finland, Germany, Hungary, Ireland, Israel, Italy, the Netherlands, New Zealand, South Africa, Switzerland, and USA were used. These data included 233,673 herds, 16,403,413 cows, and 131,907,373 test day records from cows calving between 1/1/90 and 12/31/97. Herds were grouped into 5 quintiles for each of 11 management variables and 2 climate variables. Heritability of milk yield was calculated within each quintile of each variable, and genetic correlations between quintiles were computed. Genetic correlations less than unity and significant differences in heritability between quintiles were found for peak yield, average sire PTA milk, temperature, fat to protein ratio, days to peak yield, within-herd standard deviation of milk yield, and percent North American Holstein genes. Currently, differences in production systems between countries are considered in international sire evaluations. However, variation in management or climate within countries is ignored. We have identified some of the factors that cause genotype by environment interactions between individual herds. This research shows that it is more reasonable to define traits based on the production conditions in each herd, as opposed to defining traits based on country borders. Grouping herds on these variables should create international sire evaluations that are more appropriate for genetic selection decisions on individual farms, because each sire will receive a PTA for each unique production system. In addition, the number of unique production systems will likely be less than the number of countries, and this will lead to greater accuracy of parameter estimates and a more efficient international evaluation system.

Key Words: Genotype by Environment, International Evaluations

888 Genotype by environment interaction for milk production traits in Guernsey cattle.

W.F. Fikse*[1], R. Rekaya[2], and K.A. Weigel[2], [1]*Interbull Centre, Uppsala, Sweden,* [2]*University of Wisconsin, Madison.*

International genetic evaluations that use national genetic evaluation results as input need to acknowledge country borders. The current model for international evaluation treats each country as genetically separate trait, and assumes milk production to be similar within country, but different between countries. The use of unprocessed cow performance records does not require such restriction, and allows for other statistical models to consider genotype by environment interaction. First lactation records from 45,000 Guernsey cows in four countries (Australia, Canada, United States and South Africa) were used to detect and describe genotype by environment interaction for milk production traits. Five statistical models were considered: a) single trait across country, b) single trait across country with heterogeneous residual variance, c) multiple trait across country, d) multiple-trait herd cluster model, and e) reaction norm model. For the herd cluster model, herds were clustered into groups based on information on herd management, genetic composition and climate. Reaction norms describe the phenotype expressed by a genotype as a function of the environment, and are modelled by random regression on descriptors of production environment. The same variables to describe production environment were used in the herd cluster and reaction norm model. Gibbs sampling was used to make inferences about the parameters of interest, and models were compared based on Bayes factors and deviance information criterion. Posterior mean and mode for heritability for the single trait model was .33, and ranged from .25 to .40 for models b) and c). Genetic correlations between countries estimated with model c) were generally high (.87 - .92). Heritabilities obtained from the reaction norm model differed substantially depending on descriptive variable, and ranged from .10 to .50 in 'poor' and 'good' environments. Genetic correlations between extreme environments were between .80 and unity depending on environment descriptor. Both Bayes factors and deviance information criterion indicated that country borders do not effectively distinct between production environments.

Key Words: International Genetic Evaluation, Guernsey, Lactation Records

889 Evidence for genotype by environment interacton in production traits of US Holsteins under grazing versus confinement.

J. F. Kearney*[1], M. M. Schutz[1], P. J. Boettcher[2], and K. A. Weigel[3], [1]*Purdue University,* [2]*University of Guelph,* [3]*University of Wisconsin.*

Grazing, as a form of low input dairying, has increased in popularity. However grazing herds tend to forego conventional US Artificial Insemination (AI) sires, in favor of sires proven in other grazing countries or novel breeds. The objective of this study was to investigate possible genotype by environment interaction in grazing versus confinement herds in the US. Grazing herds (GH) were defined as utilizing grazing for at least 6 months each year and were enrolled in Dairy Herd Improvement. A total of 414 GH in 14 states contributed 101,872 records of 24,451AI-sired Holstein cows, calving from 1990 to 1999. Control herds (CH) were confinement herds of similar size in the same states. The CH had 144,863 records from 61,273 AI-sired Holstein cows. The performance of daughters in GH and CH was examined using linear regression of mature equivalent milk (MEM), fat (MEF) and, protein (MEP) yield on the 11-00 USDA Predicted Transmitting Abilities (PTA) of their sires for those traits. The model also included the fixed effects of herd, year-season, and age-parity. For GH or CH, regression coefficients were estimated for all records, for four random subsets, and for four subsets based on quartiles of herd average MEM. Average MEM was greater for CH (10,008 kg) versus GH (8602 kg). For GH, the coefficients of regression of MEM, MEF, and MEP on PTA were significantly less ($P<0.01$) than 1 (the expected value), except for MEM and MEP in the highest quartile ($P>0.2$) and MEP in one of the random subsets. In CH, MEF, and MEP were significantly less ($P < 0.01$) than 1, only for the lowest quartile. MEM was less ($P < 0.05$) than 1 in two of the random subsets and in the lowest and second highest quartiles. MEM, MEF, and MEP were all greater ($P < 0.01$) than 1 for the highest quartile. Results suggest that performance of cows in GH may not be predicted adequately by current US recording and genetic evaluation systems, but relationships may be due to both production level and management system.

Key Words: Genetics, Grazing, Genotype by environment interaction

890 Effects of genotype-by-environment interactions in conventional versus pasture-based dairies.

P. J. Boettcher*[1,2], J. Fatehi[1], and M. M. Schutz[3], [1]*University of Guelph, Canada,* [2]*ANAFI, Cremona, Italy,* [3]*Purdue University, West Lafayette, IN.*

The objective of this study was to evaluate effects of genotype-by-environmental interaction (GxE) on dairy traits among herds in Canada that practice intensive rotational grazing versus conventional methods that rely on stored feeds. The basic approach taken was to estimate the genetic correlation between phenotypes for a given trait expressed under the two different environmental conditions. Based on responses to questionnaires, 22 herds were selected for the grazing group. These herds were required to intensively graze their cattle for at least six months per year, during which pasture provided at least 70% of the forage in the cows' diets. In addition, herds were required to be enrolled in DHI and to record pedigree data. All herds were in either Nova Scotia or Ontario. The control (conventional) group consisted of 34 large free-stall operations. Data were DHI records from 1990 and later and consisted of 6749 lactations from 2817 cows in the grazing herds and 29,371 lactations from 12,774 cows in the control herds. Per cow production was greater in the conventionally managed herds (9947 kg milk) than in the grazing herds (9300 kg). Genetic corelations were estimated by multiple trait REML and a model that included fixed effects of age-parity and herd-year-season-parity classes and random effects of animal, permanent environment, and residual. Effects of GxE were minor, with genetic correlations of near 0.90 or greater. Genetic correlation was lowest for fat yield (0.88 with SE = 0.04). Genetic correlations for milk and protein

were 0.93 and 0.94, respectively. Heritabilities were greater for the yield traits in the conventionally managed herds, averaging about 0.37 versus 0.32 in the grazing herds. An equivalent analysis was performed for the conformation traits Frame and Capacity, Mammary System, and Feet and Legs, using data from approximately 12,000 cows. Genetic correlations for Mammary System (1.00) and Feet and legs (0.97) were near unity. The estimate for Frame and Capacity was slightly lower (0.90). These results demonstrate that effects of GxE are small between the two types of management systems analyzed and that sires will rank similarly when progeny tested in the two environments.

Key Words: Genotype-by-Environmental Interaction, Intensive Grazing

891 Method to establish average relationships among Holstein bull populations over time.

B. Auvray*[1], G.R. Wiggans[2], F. Miglior[3], and N. Gengler[1,4], [1]*Gembloux Agricultural University, Belgium*, [2]*Agricultural Research Service, USDA, Beltsville, MD*, [3]*Canadian Dairy Network, Guelph, Canada*, [4]*National Fund for Scientific Research, Brussels, Belgium*.

Average relationship coefficients between groups of animals were calculated by repeating three calculation steps until convergence was reached. The first step was a stratified sampling of pedigrees. Second, relationships between animals in the sample were calculated, using the group relationships computed in a previous round for unknown parent relationships. Third, results were accumulated by group. Average relationship coefficients calculated in this way can be used for such purposes as to better understand the structure of a population, to more accurately calculate inbreeding coefficients, and to assign unknown parent groups using clustering methods. This method was applied to the pedigree data for the worldwide Holstein sire population. The data was derived from Interbull and North American pedigree databases. Groups were defined by year of birth, sex, and country. Average relationships between US and Canadian bulls increased across time from 0.02 in 1960 to 0.12 in 1999. The increase was continuous except for a plateau in 1992, followed by a slight decrease until 1995 when the trend to increase resumed. Average relationships across time comparing Canadian with European bulls and US with European bulls are quite similar. They increased from about 0 in 1963 to 0.10 in 1999. After a peak of 0.05 in 1966, the relationships dropped to 0.03 in 1976 before starting to increase again. For bulls born in 1996 in the US, Canada, and Germany (representing a typical European country), the average relationships were: 0.116 (Canada-Canada), 0.112 (Canada-USA), 0.1 (Canada-Germany), 0.101 (USA-USA), 0.101 (USA-Germany) and 0.084 (Germany-Germany). These results demonstrate the recent dramatic increase in relationships and inbreeding in the worldwide Holstein population, and show the power of this method of calculating relationship coefficients.

Key Words: Relationship, Holstein, Bull population

892 Possible global scale for ranking dairy bulls by blending national rankings.

R.L. Powell* and P.M. VanRaden, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*.

International genetic evaluations are computed routinely for dairy bulls using multi-trait across country evaluation methods. Separate rankings are provided on the scales of member countries, but a global scale also could be useful in marketing across countries and for use by nonmember countries. National units of expression were removed by dividing the evaluation on each scale by the country's standard deviation. These standardized evaluations were weighted by each country's fraction of global cow numbers and blended into a global evaluation. That approach is predicated on interest in breeding for a world market, but other weights may be considered. Fractions of global cow numbers were estimated by the proportions from each country of all daughters of evaluated bulls in the international evaluation. For the Holstein evaluation, countries with the largest cow numbers included the United States (18%), Germany (15%), France (13%), New Zealand (10%), and the Netherlands (9%). Twenty one other countries accounted for 35%. Standard deviation of the global scale can be set to a constant and a fixed genetic base can be imposed simply by setting the mean of evaluations equal to the previous mean. Conversion formulas for the global scale to and from each country scale may be needed. Correlations of bull evaluations on the separate country scales for protein averaged .976 within birth year. Correlations of the country scales with the global scale ranged from .955 to .995 with a mean of .988. Even with high correlations, there was reranking. The use of a global scale could ease the transition to an evaluation of data grouped and modeled by herd management and climate variables instead of national borders. Separate regional, country, or cluster rankings would still be needed to provide selection tools adapted to local conditions. Global evaluations would allow both participants and non-participants to select for a global market.

Key Words: genetic evaluation, international rankings, dairy cattle

893 Estimation of genetic correlations between countries and prediction of sire breeding values using individual animal performance records.

K. A. Weigel*[1], R. Rekaya[1], N. R. Zwald[1], and W. F. Fikse[2], [1]*University of Wisconsin, Madison*, [2]*Interbull Centre, Uppsala, Sweden*.

Our objective was to estimate genetic correlations between milk production in different countries and to predict international sire breeding values using individual animal performance records. Data included first lactation records of 16,403,413 Holstein cows that calved between January 1, 1990 and December 31, 1997 in 233,673 herds in Australia, Austria, Belgium, Canada, Czech Republic, Estonia, Finland, Germany, Hungary, Ireland, Israel, Italy, Netherlands, New Zealand, South Africa, Switzerland, and USA. Milk yield in each country was considered as a different trait. Genetic parameters and sire breeding values were estimated using a multiple-trait sire model that included the effects of sire, herd-year-season of calving, age at calving, milking frequency, and heterosis class. Heritabilities ranged from 0.25 in Finland to 0.34 in Israel. Genetic correlations between countries ranged from 0.77 between Estonia and both Ireland and Israel to 0.96 between Belgium and Netherlands and between New Zealand and both Australia and Ireland. Some correlations differed markedly from values that are now used in international sire evaluations. In particular, correlations of 0.94 or greater were found between Australia, Ireland, and New Zealand, all countries that rely heavily on rotational grazing. Correlations of 0.92 or greater were found between Belgium, Canada, Italy, Netherlands, and USA. Correlations between the intensively managed countries and the rotational grazing countries ranged from 0.82 to 0.88. Examination of the top 1% of bulls (N=665) on each country scale revealed that 556 bulls were selected in one country only, 861 were selected in at least five countries, 461 in at least 10 countries, and 107 in all 17 countries.

Key Words: genetic evaluation, dairy sires, international

894 Simultaneous estimation of genetic correlations for milk yield among a large number of Holstein populations.

H Jorjani*, *Interbull, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences*.

Estimation of genetic correlations among all 26 Holstein populations participating in Interbull#s international genetic evaluation of AI bulls is hampered by the large number of country combinations (325), the large number of bulls in the correlation estimation (>110000) and the low number of common bulls with estimated breeding values (proofs) in more than one country (about 110 country combinations had less than 20 common bulls). These problems have led to the current practice of estimating genetic correlations among smaller well-connected groups of countries rather than among all 26 countries in one single evaluation, which in its turn leads to the prolongation of the turn around cycle, multiple estimates of some country combinations, and more importantly the need for bending the resulting covariance matrix. Therefore, to find a subset of data that facilitates a simultaneous and speedy estimation process for all 26 populations without introducing bias is desirable. To achieve this, new methods of selecting well-connected subsets of data have been examined. These involved selection of data based on the bulls' number of proofs and two different measures of connectedness, namely, weighted and effective number of proofs, which are based on number and distribution of bulls' daughters across countries. These alternatives were used in combination with time edits, that is selecting the subset from all available bulls or only bulls born in the last 17 years, i.e. as is the current practice for estimation of breeding values. Results indicated that the estimated genetic correlations are very sensitive to even small changes in the number of common bulls, probably because few bulls can potentially provide a significant amount of genetic links. Subsets selected based on different measures of connectedness resulted in higher average genetic correlations and larger number of correlations that are biologically sensible (>0.75). Time edit resulted in increased estimates among countries that share young bulls and decreased estimates among countries that rely heavily on the importation of old proven bulls.

Key Words: Connectedness, data subset, time edit

895 Alternative strategies for estimation of country sire variance in international evaluations of dairy bulls.

F. Miglior*[1], P. G. Sullivan[2], and B. J. VanDoormaal[1], [1]*Canadian Dairy Network*, [2]*CGIL, University of Guelph, Guelph, ON, Canada.*

Three alternatives were compared to estimate sire variances in Interbull evaluations. Sire variance estimates are used in international evaluations of dairy bulls to account for different scales of proof expression in each country. Currently these variances are estimated in MACE using all bulls that have daughters in at least 10 herds by country. This group includes locally sampled bulls and imported bulls first sampled abroad. Sire variances are estimated using approximate Mendelian sampling terms (MS), which have an assumed expected value of 0 for all bulls. While average MS of bulls sampled locally may be close to zero, MS of imported bulls tends to be positive, as only top proven bulls are imported in any country. A total of 59,657 Holstein bulls from ten major dairy countries were evaluated with MACE, based on genetic evaluation files and genetic correlation estimates used by Interbull in the November 2000 routine run. Sire variances were estimated for each country using MS of either: a) all bulls (the current Interbull procedure); b) only bulls sampled locally; or c) only bulls born in the last five years (1992-96). The last group included mostly first crop locally sampled bulls. Variances were estimated by birth year and across all years for each of the three data sets for milk, fat and protein yield. For protein yield, sire variances estimated using only locally sampled bulls ranged from -1% to -12% lower than variance estimated using all bulls. Sire variances estimated using bulls born in the last 5 years ranged from -8% to +9% of the variance estimated using all bulls. In order to quantify the impact of different estimates of sire variability on international evaluations, changes in bull rankings and bull proofs were also compared. A simulation study is required to identify the most accurate strategy to estimate sire variance in a MACE evaluation.

Key Words: International evaluations, sire variance estimation

896 Variance of effects of lactation stage within herd by herd yield.

N. Gengler*[1,2] and G.R. Wiggans[3], [1]*Gembloux Agricultural University, Belgium*, [2]*National Fund for Scientific Research, Brussels, Belgium*, [3]*Agricultural Research Service, USDA, Beltsville, MD.*

First-lactation test-day yields from New York, Wisconsin, and California herds with low (<7257 kg), medium (9072 to 9525 kg), and high (>11,340 kg) annual milk yields were adjusted additively for age and lactation stage. Two random regression models with third-order Legendre polynomials for permanent environmental and genetic effects were used. The second model also included a random effect with the same polynomial regressions for 2-yr intervals within herd (herd-stage effect). Mean adjusted test-day milk yields were 35.4 kg (75,838 test days in 9108 lactations) for high-yield herds, 28.8 kg (74,845 test days in 8887 lactations) for medium-yield herds, and 25.6 kg (71,996 test days in 8490 lactations) for low-yield herds. Although estimated phenotypic variances also declined with herd yield, those variances were surprisingly similar for medium- and low-yield herds. Herd-stage effect on phenotypic variance was negligible. Heritabilities for high- and medium-yield herds initially decreased and then gradually increased across lactation stages. Maximum heritability (0.33, high-yield herds; 0.30, medium-yield herds) was reached from 200 to 300 d in milk. Heritabilities were lower for low-yield herds but increased rapidly (maximum of 0.22 at lactation end). Introduction of a herd-stage effect eliminated the heritability decrease in early lactation for high- and medium-yield herds and reduced the increase in late lactation for low-yield herds. Heritabilities generally were lower with inclusion of a herd-stage effect, which indicated that variances for this effect were partly considered genetic in the less complete model. Herd-stage variances relative to phenotypic variance were highest at the beginning (12%) and end of lactation (7%) for medium-yield herds. Herd yield and stage had a large effect on variance size and change across lactation stages during first lactation and should be considered when accounting for heterogeneous variances in genetic evaluations.

Key Words: Heterogeneous variance, Test-day model

897 Lactation curves of milk production traits of Italian Water Buffaloes estimated by a mixed linear model.

N.P.P. Macciotta*[1], G. Catillo[2], G. Pulina[1], A. Carretta[2], and A. Cappio-Borlino[1], [1]*Dipartimento di Scienze Zootecniche, universit di Sassari, Italia*, [2]*Istituto Sperimentale per la Zootecnia, Roma.*

Aim of the work is the estimation of lactation curves of milk production traits of Italian water Buffaloes pertaining to different age classes and seasons of calving. Data were 4064 Test Day records of milk production traits (milk yield, fat and protein percentages) recorded on 534 Italian buffalo cows during the years 1986-1999 in a farm of the Istituto Sperimentale per la Zootecnia. Animals were grouped according to 6 level of age at calving and to 4 levels of season of calving. Data were analysed with a mixed linear model that included test date, age at calving, season of calving and stage of lactation as fixed effects plus a random animal effect associated with each lactation. Average lactation curves were estimated by solving for the effects of stage of lactation nested within age at calving and season of calving. Milk yield lactation curves of animals of different ages resulted clearly separated till 20 weeks from parturition, with buffaloes of 4-5 years having the highest curve. Peak yield occurred at around the 6th week of lactation in all age classes; buffalo cows of 2-3 years of age showed the highest persistency which, however, is markedly lower than in dairy cattle. No effect of age at calving could be observed for fat and protein percentages. Season of calving affected milk yield only in the first phase of lactation, with the lowest production levels for summer calvings; no effect could be observed on fat and protein contents. Actually, the inclusion of a TD effect accounted for much of the seasonal variation normally observed among buffalo cows calving in different seasons, in agreement with previous results obtained in dairy cattle. Average correlations among TD measures within animal or repeatabilities, calculated on the basis of the variance component associated to the random animal effect and of the residual variance, were 0.59, 0.31 and 0.36 for milk yield, fat and protein percentages respectively.

Key Words: Buffalo, Milk Production Traits, Lactation Curves

898 Heritability estimates for birth weight of exotic dairy breeds in Nigeria.

O.T.F. Abanikannda*[1], O. Olutogun[2], A.O. Leigh[1], M. Orunmuyi[3], and O.Y. Apena[1], [1]*Department of Zoology, Lagos State University, Nigeria*, [2]*Department of Animal Science, University of Ibadan, Nigeria*, [3]*Department of Animal Science, Ahmadu Bello University, Zaria, Nigeria.*

Genetic parameter estimates for traits are specific for a particular breed in a specified environment. Weight of calves at birth has been established to be the first and quickest index of some of the performance traits of cattle. The correlation of birth weight to other performance traits as weaning weight, milk yield and survivability has been well documented. This research aim at computing the heritability of birth weight of Holstein and Jersey breeds, calved and bred in the medium to high trypanosomiasis-risk zone of Southern Nigeria. The 475 Holstein calves used in this analysis are from 13 sires and the 39 Jersey calves are from 4 sires. Factors studied included year of birth, season of birth, sex of calf, parity of calf as fixed effects and the sire effect was used as random effect. The SPSS (1996) software was used for both the analysis of variance and the variance component estimation. The General Linear Model (GLM) for variance component estimation using the ANOVA method was used to estimate the variance components. The paternal half sib method of Henderson ($h^2 = 4\sigma_s{}^2 \ / \ \sigma_s{}^2 + \sigma_w{}^2$) was used to compute heritability for both breeds. In the Holstein calves, all factors except the parity were highly significant ($P<0.01$), while only the sire effect was significant ($P<0.05$) in the Jersey calves. The mean birth weight for the Holstein and Jersey calves are 32.59 ± 0.24kg and 21.15 ± 0.44kg respectively. In the Holstein breed, the males were 1.67kg heavier than females and the highest birth weight was recorded in the late wet season. This seasonal variation in birth weight was due to the amount of precipitation recorded in those seasons as reflected in the availability of forage for the pregnant dams, which are rarely given supplemental feeds. and the h^2 for Holstein and Jersey was 0.49 ± 0.26 and 0.54 ± 0.35 respectively. The moderate to high heritability estimate obtained in these analyses implies that these breeds of animal could be maintained as purebred, despite the prevailing inimical environmental conditions.

Source	DF (Holstein)	MS (Holstein)	DF (Jersey)	MS (Jersey)
Year of birth	15	90.87**	6	8.27ns
Season of birth	3	163.02**	3	10.82ns
Sex of Calf	1	213.87**	1	1.42ns
Parity of dam	7	24.66ns	5	11.42ns
Sire of calf	12	67.99**	3	22.55*
Error	436	23.36	19	7.10

**=P<0.01; *=P<0.05; ^{ns}=P>0.05

Key Words: Heritability, Birthweight, Trypanosomiasis

ASAS/ADSA Extension Education: Beef

899 Performance comparisons between mature cows categorized by weight and frame score combinations that are enrolled in a cow herd performance testing program.

S.R. McPeake*, W.T. Wallace, and L. Keaton, *University of Arkansas Cooperative Extension Service.*

Data from (n = 164) cows and their calves were analyzed to compare differences in performance levels between cows categorized by weight and frame score combinations. General linear model procedures were used to generate least squares means for dependent variables. Weight categories (WT) for the cows were small (< 500 kg), moderate (500 to 544 kg), large (545 to 590 kg) and extra large (> 590 kg). Frame scores (FS) represented included 4, 5, 6, and 7. Cow size (CS) included all possible combinations of WT and FS that were available in the data set. WT was significant (P < 0.05) for adjusted 205 day weight (WWT), cow efficiency (CE) and FS. CS was significant (P < 0.05) for WWT, CE, and body condition score of cows (BC). No significant differences were found between CS for muscle score (MS) of calves. As WT increased, WWT increased but CE decreased. Within WT, cows with larger frame scores generally had higher WWT with the exception of extra large cows. Within each WT, CE increased with FS with the exception of the extra large cows. Cow frame size and weight may need to be considered when matching cows to production environments.

Key Words: Beef cattle, Cow size, Efficiency

900 Designing and implementing a quality assured, source-verified feeder calf sale program.

T. Nennich[a], C. R. Dahlen[b], C. M. Zehnder[b], L. R. Miller[b], G. C. Lamb[c], D. Kampmeier[d], and A. DiCostanzo*[b], [a]*Clearwater County Extension, Bagley, MN,* [b]*University of Minnesota, St. Paul,* [c]*North Central Research and Outreach Center, Grand Rapids,* [d]*Central Livestock Association, South St. Paul.*

A producer-driven quality assured, source verified feeder calf sale program was initiated to enhance marketing options for producers, to create a repeat-buyer feeder calf outlet, and to increase profitability and growth of the Minnesota beef industry. Several marketing agencies were interviewed according to marketing criteria producers wished to follow. A marketing agency was chosen and charged to set and promote sale dates, provide transportation, facilities and personnel to form outcome groups of cattle of similar color, frame and muscling, and to sell outcome lots within a regular sale date. Producers agreed to follow specific beef quality assurance (MBQA) procedures, and to background and process calves for disease prevention. Cattle were immunized against viral and bacterial diseases at weaning time and boostered against viral diseases 15 d before the sale. On the sale date, an experienced sale observer gathered cattle description, weight and price data on all lots sold. A regression equation was fitted to determine factors that had a significant (P < .05) effect on sale price. Color, muscling, sex, and health status were factors that influenced sale price in addition to weight and lot size. Steer MBQA lots sold better than other vaccinated steers or steers under no vaccination protocol 56% or 75% of the time for a total advantage of $3 or $13/head, respectively. Heifer MBQA lots sold better than other vaccinated heifers or heifers under no vaccination protocol 41% or 76% of the time for a total advantage of $1.86 or $12.21/head, respectively. Compared to single source lots, when a producer contributed up to 12 steers or heifers to a larger lot, the advantage of selling in larger lots was $.068/kg. Producers and the marketing agency were satisfied with the experience and have made a commitment to continue this endeavor.

Key Words: Quality Assurance, Cattle, Sales

901 Mississippi farm to feedlot program: carcass performance.

W.B. McKinley, A.R. Williams*, J.N. Myers, A.G. Gardner, and E. Ward, *Mississippi State University, Starkville, MS.*

The objectives of the Mississippi Farm to Feedlot program are to evaluate production and carcass information of steers produced in Mississippi, and to provide educational information regarding retained ownership as a marketing alternative. Seven years (1993-1998) of data were collected and the effects of year of feeding (YR) and sire breed (SB) on carcass performance were evaluated. Sire breeds were classified into three breed groups, British Breeds (BB), European breeds (EB), and American breeds (AB). Carcass performance response variables included steer hot carcass weight (HCWT), back fat thickness (BF), ribeye area (REA), marbling score (MS), quality grade (QG), and yield grade (YG). Both YR and SB significantly influenced carcass performance. HCWT was greatest (p<.05) for steers in YR 5 and 6 (352 and 344 kg, respectively) compared to all other years. Steers in YR 1 had greater (p<.01) BF (1.52 cm) than steers in all other years. REA was larger for steers in YR 3 and 7 (87.09 and 87.07 cm^2) and least for steers in YR 1 (79.04 cm^2, p<.01). MS was the highest in YR 5 at 396 and the lowest in YR 1 at 362 (p<.01). QG mirrored MS with steers in YR 5 having the highest QG and those in YR 1 the lowest QG (17.89 and 17.24, respectively, p<.01). YG was greatest in YR 7 at 2.86 and the lowest in YR 4 at 2.57 (p<.01). SB did not influence (p>.05) HCWT. However, SB did significantly influence all other carcass traits. BB and AB sired steers had greater (p<.01) BF (1.34 and 1.31 cm, respectively) than EB sired steers (0.97 cm). EB sired steers had larger REA (88.14 cm^2, p<.05) than BB and AB sired steers (83.39 and 82.16 cm^2, respectively). MS and QG were greater (p<.01) for BB sired steers (403 and 18.07, respectively). YG was lowest (p<.01) for EB sired steers at 2.4 compared to 2.76 and 2.89 for AB and BB sired steers, respectively. Overall, QG improved as the program progressed. BB sired steers exhibited the highest QG, while EB sired steers had the lowest YG.

Key Words: Cattle, Feedlot, Carcass

902 On farm/ranch HACCP - Is it time?

W.J. Means*, *University of Wyoming, Laramie, WY/USA.*

Based on review of available literature, the objective was to determine if HACCP (Hazard Analysis Critical Control Points) could be efficaciously applied to livestock production systems to reduce the prevalence of *Escherichia coli* O157:H7 in beef products. HACCP involves prevention of hazards affecting food safety from production to consumption. Currently, HACCP application in relation to control of pathogenic foodborne bacteria extends to processing plants, retail outlets, and restaurants - not to the farm or ranch. Steps necessary for food borne illness (FBI) to occur include pathogen contamination of the food, abuse of the food, improper cooking, and consumption of the food in question by a susceptible individual. Measures that break the sequence of events, thus deterring FBI, may be considered critical control points (CCP's). Reducing the number of pathogens entering a food/meat processing facility in/on livestock could further decrease the pathogen load of finished raw or cooked product. However, prevalence of *E. coli* O157:H7 in individual animals/herds as well as factors affecting shedding of the organism