

Breeding and Genetics: Current Issues in Beef Cattle Breeding

622 ASAS Centennial Presentation: Animal breeding and the *Journal of Animal Science*: A century of co-evolution. W. Hohenboken*^{1,2}, ¹Virginia Polytechnic Institute and State University, Blacksburg, ²Oregon State University, Corvallis.

In this paper, I attempt to survey, categorize and characterize papers relevant to animal breeding and genetics that were published in the *Journal of Animal Science* between the initial issue in 1910 and 2008. Graphics and descriptive statistics will be presented that describe allocation of publication effort across species, space and time. I then endeavor to identify and describe the evolution of major themes in research, teaching and extension. When did they begin? How did they expand and contract? Did they mutate or metastasize? Which suffered extinction? Relationships and paths of influence among investigators and among institutions will also be examined. Finally, I will reflect upon changes during the century in the *Journal of Animal Science* and in the manner and style with which animal breeders and geneticists published their findings within its pages.

Key Words: Breeding and Genetics, History, *Journal of Animal Science*

623 Residual feed intake heritability and phenotypic correlations of central tested Simmental bulls. W. C. Rutherford*, L. A. Kriese-Anderson, S. V. Free, M. S. Hittle, and J. K. Grubbs, Auburn University, Auburn, AL.

Feed intake along with weights, hip height, ultrasound carcass traits and scrotal circumference were analyzed for 459 Simmental bulls consigned to the Auburn University BCIA Bull Test from the years 1981 to 2007. All bulls were housed at the Auburn University Beef Evaluation Center for a minimum of 70 days. Bulls were trained to individual Calan Gates® within 21 days of arriving. All bulls were consigned by individual Simmental breeders primarily from Alabama. Bulls were measured for weight and height either biweekly or monthly depending on year. SC and ultrasound measurements for carcass traits were taken at yearling age (330 to 400 days). Residual feed intake (RFI) was determined for each bull by regressing metabolic mid-weight and ADG on intake. Phenotypic correlations among traits were determined using SAS. RFI was positively correlated with total feed intake (Corr=.53211 P<.0001) and has a slight positive correlation with 12th rib fat thickness (Corr=.12117 P=.0125). A mixed model in SAS was used to analyze RFI and determine sire components of variance. Fixed effects included consignor (N=61), and percentage Simmental (7 levels). Sire (n=223) was included as a random effect. Consignor was found to be non-significant (P>.05). Percentage Simmental was found to be significant (P<.0001). LSMEANS separated differences between percentage Simmental for RFI. Bulls that were 37% Simmental had the highest RFI values. The second highest RFI values were with 25% Simmental bulls. The 25% Simmental bulls had greater RFI values than bulls of 50, 62, 75, 87, and 100% Simmental (P<.0105). Heritability of RFI was estimated to be 0.29 ± 0.02.

Key Words: Residual Feed Intake, Heritability, Beef

624 Estimates of genetic variation for feed intake and other characteristics in growing beef cattle. K. M. Rolfe*¹, M. K. Nielsen¹, C. L. Ferrell², and T. G. Jenkins², ¹University of Nebraska, Lincoln, ²US Meat Animal Research Center, Clay Center, NE.

Calves born between 2003 and 2006 at the U.S. Meat Animal Research Center provided data for estimation of genetic and phenotypic parameters for measures of body weight and gain and feed intake during the finishing phase. At average age 278 d, cattle were started on a high energy diet of corn, alfalfa hay, soybean meal, and supplement. They were individually fed for ~138 d in pens of 4 to 8 steers by use of Calan headgates. Cattle were fed to an average optimum end weight, but harvested in four groups per year at a commercial slaughter facility. Steers were produced by randomly mating F1-cross sires to straightbred and F1 females. Nine breeds were represented in various fractions in the steers. These were: Hereford, Angus, Simmental, Charolais, Limousin, Gelbvieh, Red Angus, Pinzgauer, and Red Poll. Fifty-nine sires produced half-sib families. A total of 820 crossbred steers were analyzed with a pedigree file of 4,051 animals. Traits analyzed were ADG, DMI, mid-period body weight (MBW), and residual feed intake (RFI; determined from DMI adjusted for MBW and ADG). Flight time (FT) was collected at least twice (separated by ~60 d) as a possible indicator trait for temperament; two sets of electronic eyes were placed 5.5 m and 10.8 m beyond a scale box where the animals were temporarily detained. REML methods were used in univariate models that accounted for the fixed effects of year, month for only FT, pen size, breed and breed heterozygosity; random effects were animal genetic, pen, permanent environmental for FT only and error. Heritability estimates for ADG, DMI, RFI, MBW, and FT were: 0.21 ± 0.09, 0.21 ± 0.07, 0.40 ± 0.11, 0.45 ± 0.12, and 0.25 ± 0.07, respectively. Repeatability of FT was 0.63. Pen size only had a significant effect on RFI (P<0.001). Month was significant for FT (P<0.001) with flight time increasing as the animal aged.

Key Words: Beef Cattle, Feed Intake, Flight Time

625 Analysis of beef cattle growth with a Kalman Filter. S. Forni*, D. Gianola, G. J. M. Rosa, G. de los Campos, and K. A. Weigel, University of Wisconsin, Madison.

A dynamic model known as Kalman Filter (KF) was embedded into a standard linear mixed model, to analyze longitudinal data. Growth data of Nelore cattle were used to compare a standard multiple trait model (MM) with the KF. A data set consisting of body weight records of 6,856 animals was used. Animals were weighed at 90 d intervals from birth to 540 d of age, and six equally-spaced records were used for each individual. Contemporary groups (CG) consisted of: sex, herd, year and season of birth (rain or dry) combinations. A six-variate mixed linear model with CG, additive genetic and maternal effects was employed. KF introduced a time-dependent association between additive genetic, maternal and residual effects, which were assumed to change over time according to a first order autoregressive process. Under KF, covariances between any two time points can be inferred from combinations of variances estimates. Thus, the (co)variance structure can be modeled with fewer parameters than in the MM. The KF and MM models were compared using the Deviance Information Criterion (DIC) and the Bayes

Factor (BF). Models where KF described additive genetic and maternal effects were favored by DIC. However, KF did not describe residual (co)variation adequately. According to the BF, there was not conclusive evidence in favor of a specific model. The KF allowed fitting additive and maternal effects with a meaningful lower number of parameters than the standard procedure. This reduction avoids problems associated with overparameterized models and makes efficient use of the data. Further, fitting KF to growth traits provides estimates of genetic merit for the entire range of time points and captures differences through time between and within individuals.

Key Words: Kalman Filter, Longitudinal Data, Mixed Model

626 Bayesian estimation of the covariance between permanent maternal and temporary environmental effects for weaning weight in beef cattle. R. Cantet^{*1,2}, ¹University of Buenos Aires, Buenos Aires, Argentina, ²CONICET, Aregentina.

The magnitude of the additive covariance between direct and maternal effects (CADM) in the presence of an environment covariance between direct and maternal effects (CEDM) for weaning weight in beef cattle is still an open issue. Inclusion of CEDM presents a challenging problem for fitting the model to data. An animal model with maternal effects is presented that includes random additive direct and maternal effects, as well as random permanent environmental effects (PE) that are correlated to a set of temporary environmental effects (TE) on the individual records through the CEDM parameter. In this model, error terms are independent and identically distributed. Two formulations of the covariance matrix for PE effects are studied. The first one accounts for the environmental influences from grand-dams to all her direct descendant dams. An alternative formulation is presented where the only non-zero covariance is between PE effects of a dam and her daughter dam. The covariance matrix for TE effects is modeled after the time elapsed among progeny records from the same dam. To estimate all dispersion parameters a Bayesian method using conjugate prior densities and Gibbs sampling is used. The inversion of the covariance matrix for the joint distribution of PE and TE is avoided by block sampling of all PE effects by line of dams and all TE of calves out of the same dam. A line of dam involves the records of an ancestor dam, their dam descendants and all their progeny, raised naturally (not by embryo transfer). The TE effects within any line of dam are correlated but are independent with those from the other lines. The number of animals involved in any line of dam is small for beef cattle data (for example, at most 20 in a data set of 80,000 Brangus records, or at most 25 in a 10,000 records from an Angus data set). The resulting means of the marginal conditionals densities for the fixed effects, breeding values, PE and TE effects are linear combinations of some matrices related to the MME and some matrices that are not functions of them.

Key Words: Maternal Effects, Environmental Covariance, Gibbs Sampling

627 ASAS Centennial Presentation: Future needs in animal breeding. R. D. Green*, Pfizer Animal Genetics, Sutton, NE.

The past century has seen animal breeding and genetics evolve and expand from definition and validation of basic population genetics

theory to development of selection index theory to today's relatively sophisticated genetic prediction systems enabling industry genetic improvement. The end of the first century of the ASAS also coincides with the rapid movement of the field into the era of genome-enabled genetic improvement and precision management systems. Led by recent research infrastructure investments by the US and international partners to develop chicken, bovine, swine, ovine, and equine "genome toolboxes", the animal breeding community is poised to play a crucial role in the century to come. These genome toolboxes provide the needed platforms for developing whole genome selection programs based on linkage disequilibrium for a wide spectrum of traits; allow the opportunity to re-define genetic prediction based on allele sharing as opposed to traditional pedigree relationships; and provide for the first time simultaneous information upon which to practice genetic selection and plan precision management of specific genotypes --all early in the life of the animal. An area of major focus will be mining of the genomes through systems biology approaches to better understand gene and metabolic networks --what has previously been lumped into poorly understood GxE, and GxG interactions. Perhaps the greatest obstacle to the successful merger of genomic and quantitative approaches will be the lack of necessary animal resource populations to appropriately define and measure phenotypes, i.e. the so-called "phenomic gap", for difficult to measure traits (e.g. resistance to disease and stress, adaptability, longevity, efficiency of nutrient utilization). Additionally, due to de-emphasis of quantitative genetics and animal breeding programs in academia over the past quarter century, a dearth of qualified young scientists to effectively mine the genomes must immediately be addressed. Whilst the motivating factors may have changed, the need for high quality animal breeding and genetics research and education has never been higher.

Key Words: Animal Breeding, Genomes

628 Genetic trends for production traits of the Montana Line 4 Hereford herd. J. M. Rumph^{*1}, D. D. Kress², K. C. Davis², D. C. Anderson^{2,3}, H. C. Van Wagoner³, and D. L. Boss³, ¹Michigan State University, Lake City, ²Montana State University, Bozeman, ³Montana State University, Havre.

To commemorate the centennial of the ASAS, the researchers thought it was fitting to analyze the genetic trends of the Montana Line 4 Hereford herd, a closed herd descended from the Miles City Line 1 which has also been maintained as a closed population for 74 years. The Line 4 herd has been managed at Montana State University's Northern Agricultural Research Center (NARC) in Havre, Montana since 1963 and has undergone various selection programs since its introduction to NARC. The herd is currently managed at approximately 100 females with an average inbreeding of 37.2% for the 2006 calf crop with individual animals ranging in inbreeding coefficient from 34.0 to 46.6%. The average inbreeding of the herd is increasing at a rate of 0.5% per year. Genetic parameters were analyzed for production traits routinely measured on this herd. All traits were analyzed using a univariate model. Estimates of direct heritability (and associated s.e.) were 0.52 (0.09), 0.24 (0.08), 0.32 (0.12), and 0.23 (0.09) for birth weight, weaning weight, weaning wither height, and weaning condition score, respectively. Estimates of maternal heritability were 0.08 (0.04), 0.09 (0.06), 0.12 (0.07), and 0.09 (0.07), respectively. The estimate of the direct-maternal genetic correlation was non-significant for most traits with estimates of 0.19 (0.27), -0.13 (0.34), 0.53 (0.22), and -0.41 (0.31), respectively. The proportion of variance due to maternal permanent environmental effects

was only significant for weaning weight and weaning condition score with estimates of 0.28 (0.04) and 0.12 (0.04), respectively. Birth weight direct breeding value (DBV), maternal breeding value (MBV), and phenotypic trends were estimated to be +0.008, 0.003, and -0.034 kg/yr, respectively. Weaning weight trends were estimated to be +0.346, +0.051, and +0.276 kg/yr, respectively. Weaning wither height trends were +0.033, +0.006, and -0.130 cm/yr, respectively. Weaning condition score trends were +0.0068, -0.0004, and +0.0040 score/yr. Trends for these traits are relatively flat for the period of time studied.

Key Words: Genetic Trends, Inbreeding, Weaning Weight

629 Clustering of herds to account for heterogeneous variance of docility scores in Limousin cattle. D. W. Beckman* and D. J. Garrick, *Iowa State University, Ames.*

Analyses of docility in Limousin cattle have shown the significance of random maternal and sire by herd interaction effects as artifacts of the data, resulting from heterogeneous variation. The objective of this study was to determine whether heterogeneous variance by herd stems from the subjective method used to allocate docility scores. Animals were assigned to a low (L) or high (H) variance cluster according to phenotypic variation estimated within-herd. Two univariate analyses examined clusters L and H as separate traits using ASReml. Animal models encompassed combinations of random factors: direct genetic, maternal genetic and sire by herd interaction effects. Models ranged from the most basic, containing direct genetic and residual effects (model D), to a model including all random factors. Likelihood ratio tests indicated model D best fit the data for both L and H. A bivariate model D further examined the genetic relationship between clusters. Direct heritability estimates from univariate analyses were 0.24 ± 0.05 and 0.38 ± 0.05 , and estimates of residual variance were 0.2 ± 0.01 and 0.35 ± 0.02 , for L and H, respectively. Similar estimates of direct heritability (0.22 ± 0.05 and 0.38 ± 0.05) and residual variance (0.21 ± 0.01 and 0.35 ± 0.02) were observed in the bivariate analysis for L and H, respectively. The genetic correlation between clusters was 0.8 ± 0.14 . Residual variance and heritability estimates were greatest in H, indicating herds that utilize a greater range of scores are a preferred environment for sire selection, as the accuracy of evaluation is greater. Results indicate variance of

docility scores between herds is not homogeneous, and is due to the subjective nature of scoring.

Key Words: Beef Cattle, Heterogeneous Variance, Temperament

630 Estimation of breed and heterosis effects for growth and carcass traits in cattle using published crossbreeding studies. J. L. Williams*, R. Rekaya, and J. K. Bertrand, *University of Georgia, Athens.*

Current genetic evaluations are performed separately for each breed. Multiple breed genetic evaluations, however, assume a common base among breeds enabling producers to compare cattle of different breed makeup. Breed and heterosis effects are needed in a multi-breed evaluation because databases maintained by breed associations include few crossbred animals which may not be enough to accurately estimate these effects. The objective of this study was to infer breed effects (BE), maternal effects (ME), direct heterosis effects, and maternal heterosis effects for growth and carcass traits using least square means estimates from crossbreeding studies published in the literature from 1976 to 1996. The data set was formed by recording each least square mean along with the breed composition, maternal breed composition, and direct and maternal heterozygosity. A Bayesian approach was implemented to analyze each trait with a fixed linear model which included study as a fixed effect and breed composition as a covariate. Breed solutions for each trait were expressed relative to the Angus breed. Direct BE for weaning weight ranged from -7.0 ± 0.67 kg (British Dairy) to 29.3 ± 0.74 kg (Simmental) and ME ranged from -11.7 ± 0.24 kg (Hereford) to 31.1 ± 2.22 kg (Gelbvieh). Direct BE for birth weight ranged from -0.6 ± 0.14 kg (British Dairy) to 10.1 ± 0.46 kg (Continental Beef) and ME ranged from -7.1 ± 0.13 kg (Brahman) to 5.8 ± 1.07 kg (Continental Beef). Direct BE ranged from -17.9 ± 1.59 kg (Brahman) to 21.7 ± 1.96 kg (Charolais), from -6.1 ± 1.29 kg (Brahman) to 55.1 ± 1.49 kg (Charolais), from -8.1 ± 0.47 cm² (Shorthorn) to 20.9 ± 0.48 cm² (Continental Beef), and from -1.1 ± 0.02 cm (Continental Beef) to -0.02 ± 0.03 cm (Shorthorn) for post weaning gain, carcass weight, rib eye area, and fat thickness, respectively. The use of literature estimates to predict breed and heterosis effects may be an alternative to their direct prediction in a multi-breed evaluation.

Key Words: Breed Effects, Multi-Breed Evaluation, Heterosis