

fed to postpartum beef cows, and may serve as a tool to improve young cow productivity.

Key Words: Insulin, Glucose, Supplementation

191 Effects of delayed implant protocols on performance, carcass characteristics and meat tenderness in Holstein steers. J.L. Beckett*¹ and J. Algeo², ¹Cal Poly State University, ²Algeo Nutrition Consulting.

One hundred eighty-six Holstein steers (156 kg) randomly assigned to one of five treatment groups (n = 38) were used to investigate the effects of delaying the onset of implant treatment during the early and intermediate feeding phases on growth and carcass characteristics. Implants contained Zeranone (Z), trenbolone acetate (TBA) or estradiol (E₂). Treatment descriptions are listed in the following table. Animals were weighed at 30-d intervals and weight gain, average daily gain (ADG), and feed efficiency were calculated. Steers were harvested after 288 d on feed and carcass measurements were collected. All implanted groups had heavier (P<0.05) average final live weights and improved ADG (P<0.05) than non-implanted controls, but did not differ (P>0.05) within implanted treatments. Average REA were greater (P<0.05) for all implanted groups compared with the control group, but did not differ (P>0.05) by implant. The percents of carcasses with USDA quality

grade of Choice or better were significantly lower (P<0.05) for treatments B and C (27.0 and 31.6%, respectively) compared with treatment E (57.9%). Treatments A and C (40.5 and 52.8%, respectively) were intermediate and were not different (P>0.05) from other treatments. Warner-Bratzler shear force values did not differ (P>0.05) between treatments. However, sensory evaluation indicated less desirable tenderness in delayed implant groups compared with the control treatment (P<0.05). Based on these data, delayed initiation of implants during the early growth phase of Holstein steers does not adversely affect growth and improves quality grade compared with early implants, but may decrease tenderness in the resulting meat.

Treatment	Day 0	Day 60	Day 120	Day 180
A	Z(36)	TBA (80) +E ₂ (16)	None	TBA (120) +E ₂ (24)
B	None	TBA (80) +E ₂ (16)	None	TBA (120) +E ₂ (24)
C	None	Z(36)	Z(36)	TBA (120) +E ₂ (24)
D	None	None	Z(36)	TBA (120) +E ₂ (24)
E	None	None	None	None

Key Words: Holstein steers, Implants, Tenderness

Breeding and Genetics

Applications of Random Regression Models in Animal Breeding

192 Random regression models in animal breeding. L. R. Schaeffer*¹, ¹CGIL, Dept. Animal & Poultry Sci, Guelph, Ontario, Canada N1G 2W1.

Random regression models (RRM) have become common for the analysis of longitudinal data or repeated records on animals over time. The best known application of RRM has been to genetic evaluation of dairy cattle using test day production records. Other applications include growth traits in all species, feed intake, body condition scores, and conformation traits. A general description of a RRM is given with a simple example. Some unique applications of RRM have been to the analysis of survival data and to the study of genotype by environment interactions. Examples of these applications are provided and discussed. RRM allow the researcher to study changes in genetic variability with time and allow selection of animals to alter the general patterns of response over time.

Key Words: random regressions, applications, dairy cattle

193 Implementation issues for Markov Chain Monte Carlo methods in random regression test-day models. J. Jamrozik*, University of Guelph, Guelph, ON, Canada.

Markov Chain Monte Carlo (MCMC) methods make it possible to estimate parameters for complex random regression (RR) test-day models. Models evolved from single-trait with one set of random regressions to multiple-trait applications with several random effects described by regressions. Gibbs sampling (GS) is used for models with linear (with respect to coefficients) regressions and normality assumptions for random effects. Efficient, model-specific algorithms based on iteration on data and block sampling have been applied for problems with up to 4 million levels in the mixed model equations and more than 3000 dispersion parameters. General-purpose software is currently also available. Difficulties associated with implementations of MCMC schemes include lack of good practical methods to assess convergence, slow mixing caused by high posterior correlations of parameters and long running time to generate enough posterior samples. Those are illustrated through comparison of GS schemes for single-trait RR test-day models with different model parameterisations, different functions used for regressions and posterior chains of different sizes. Orthogonal polynomials showed better mixing properties in comparison with 'lactation curve' functions of the same number of parameters. Increasing the order of polynomials resulted in a smaller number of independent samples for covariance components. GS under hierarchical model parameterization had a lower level of autocorrelation and required less time for computation. Posterior means and

standard deviations of genetic parameters were very similar for chains of different size (20,000 - 1,000,000) after convergence. Minimal length of the chain for a specific parameter and a given level of Monte Carlo error can be determined using estimates of the posterior standard deviation and the number of independent samples from a shorter chain after burn-in. Single-trait RR models with large data sets can be analysed by MCMC methods in relatively short time. Multiple-trait (lactation) models are computationally more demanding and better algorithms are still required.

Key Words: Gibbs sampling, Random regression models, Test-day data

194 Accuracy of genetic evaluation of beef cattle for growth fitting a random regression model. K. Meyer*¹, ¹Animal Genetics and Breeding Unit, University of New England.

A simulation study was carried out to assess the potential improvement in accuracy of genetic evaluation of beef cattle for growth by replacing the current multi-trait (MT) analysis comprising birth, weaning, yearling and final weights with a random regression model (RRM) analysis. Data were simulated assuming a cubic regression on Legendre polynomials of age for direct and maternal, genetic and environmental effects and heterogeneous error variances for ages from birth to 730 days, maintaining the original data and pedigree structure for three data sets. Set I comprised records from an experimental herd with monthly weight recording. Data sets II and III were field data, selecting a subset of herds with ≥ 55% animals with at least four weights recorded, and all herds for a breed. Each data set was analysed fitting a RRM using all records available (RR), a MT model using up to four records per animal, and a RRM (RR*) using the same subset of records as the MT analysis. Accuracy of evaluation (ρ) was calculated as correlation between true and estimated breeding values at target ages and averaged over replicates. Across all animals, ρ for RR* was consistently larger than for MT due to more appropriate modelling of variances. For data sets II and III, RR yielded little additional gain. For data set I, the overall ρ increased by 0.026 to 0.037 equivalent to 4.2 to 6.3% for 200, 400 and 600-day breeding values (RR vs. MT), and 0.024 or 4.1% for 200-day maternal genetic effects. Gains were largest for bulls with few progeny, ranging up to 9.3%.

Key Words: Random regression model, Genetic evaluation, Beef cattle

195 Differences in genetic parameters for production traits and somatic cell scores estimated using a multiple trait random regression test day model in the Italian Holstein population. A.B. Samore*^{1,2}, F. Canavesi¹, S. Biffani¹, P. Boettcher³, and J. Jamrozik⁴, ¹ANAFI, Italy, ²Wageningen University, The Netherlands, ³IDGVA-CNR, Italy, ⁴CGL, University of Guelph, Canada.

Genetic parameters for a multiple test day random regression model, that Italy is planning to implement for routine genetic evaluation in the future, need to be estimated for production and somatic cell scores. The lactation model now used in Italy accounts for heterogeneity of genetic variance across herds. A similar adjustment could be still necessary when using a test day model. A first data set was randomly sampled by herd number including 82,368 test day (TD) records from 5,675 cows without regards to production level. Low (52,527 TD) and high (71,986 TD) production data sets were created by randomly sampling herds differing for milk production by more than two standard deviations. Genetic parameters were estimated using an animal model and including the fixed effect of herd-test day, and the random effects for permanent environment, animal, and residual. The shape of lactation was modelled using the function of Wilmink (1987) as: $W(t) = w_0 + w_1 t + w_2 \exp(-0.05t)$. The residual covariances differed across 4 stages in each lactation. In total the model estimated 666 genetic, 666 permanent environmental, and 120 residual (co)variances for each data set. A Bayesian approach, as described in Jamrozik et al. (1998), was used to obtain the means of the posterior distributions for all parameters of the model. Heritabilities ranged from .15 to .38 depending on trait and parity. A wide range of values was found for correlations between traits and parities. Interesting null or slightly favourable correlations were reported between somatic cell scores and production traits (on average -.10), also in first lactation (from -.02 to -.04), in the first data sets. Differences in parameters were found for different levels of milk production and will be considered to define the adjustment for heterogeneity of variances across herds in the official test day model evaluation procedure.

Key Words: Genetic parameters, Italian Holstein, Test day model

196 Nonparametric Bayesian Analysis Of Test Day Milk Yield Data. R. Rekaya*¹, ¹Dept. of Animal and Dairy Science, University of Georgia.

The practice of hierarchical modeling has increased in the last decade both in applied statistics and in animal breeding, in part, as a result of development in Markov Chain Monte Carlo methods (MCMC) to overcome the computational complexity. In hierarchical models, as with all parametric models, specification of distributions for parameters and often hyper-parameters is required. Usually a considerable uncertainty is associated with those distributions leading to inevitable concerns about the sensitivity of the resulting inferences to the assumed forms of component distributions. Hence, a nonparametric or semi-parametric modeling that avoids the prior specification of distribution forms is a logical choice to assess such uncertainty. Dirichlet process prior represents the

cornerstone of modern nonparametric Bayesian modeling by allowing in a relatively easy way, the relaxation of the parametric assumptions. A total of 3,214 test day milk yield records from 341 cows with complete lactations were analyzed using a parametric and a nonparametric hierarchical model. A three stage hierarchical model was assumed, where the first stage describes the conditional distribution of the data. Wood's incomplete gamma function was used. At the second stage, the joint distribution of the lactation curve parameters was assumed to be normal in the parametric case and unknown with a Dirichlet process prior for the nonparametric model. Posterior means of heritability for the three parameters of the lactation curve were 0.24, 0.27 and 0.14 using the parametric model and 0.16, 0.32 and 0.14 using the nonparametric model. Those changes were behind the Monte Carlo errors. Non-negligible changes were observed also for the genetic correlations between the lactation parameters. The posterior mean of the precision parameter of the Dirichlet process was 5.7. This small value does not support the normality assumption for the distribution of the lactation curve parameters used in the parametric case.

Key Words: Nonparametric, Dirichlet, Milk

197 Changes of genetic correlation between milk production and body size over time in Holsteins using random regression models. S. Tsuruta*¹, I. Misztal¹, T. J. Lawlor², and L. Klei², ¹University of Georgia, Athens, GA, ²Holstein Association USA Inc., Brattleboro, VT.

The objective of this study was to investigate changes of genetic correlations between milk production and body size traits with random regressions on year. Genetic parameters for production traits (milk, fat, and protein yields), linear type traits (stature, strength, body depth, and thurl width), and the body size composite (BSC = stature \times 0.50 + strength \times 0.25 + body depth \times 0.15 + thurl width \times 0.10) in Holsteins were estimated using bivariate (production and type) random regression models. About 40,000 first lactation cows with linear type scores obtained from Holstein Association USA Inc. and with 305-d production records obtained from USDA-AIPL were used in this analysis. Some of the protein records were missing. The first order Legendre polynomial for additive genetic effects was included in the models as linear random regression on year at calving. Heritability estimates for BSC increased over the years, ranging from 0.30 to 0.44. The genetic correlations between milk yield and BSC were positive and constant (0.09 to 0.10). The genetic correlations between fat yield and BSC increased in the 1980s but were stable (around 0.10) in the 1990s. The genetic correlations between protein yield and BSC were also positive, but decreased from 0.15 to 0.10 in the 1990s. The genetic correlations between milk yield and each linear type trait were all positive and relatively stable over time; especially, those for body depth were higher (0.14 to 0.16) than for other linear type traits. These results indicate that the trend of larger cows producing more milk has not changed for the last 20 yr.

Key Words: Genetic correlation, Body size, Random regression

Dairy Foods

Whey Proteins: Structure, Production, Function, and Future

198 β -Lactoglobulin: Properties, Structure and Function. L. Sawyer*, *The University of Edinburgh.*

β -Lactoglobulin (BLG) is the major whey protein of ruminant species. It is present also in the milks of many, but not all, other species. Its amino acid sequence and 3-dimensional structure show that it is a member of the lipocalin family that includes a widely diverse series of molecules most of which bind small hydrophobic ligands and may act as specific transporters, as does serum retinal binding protein. BLG appears to bind a wide range of ligand molecules but it is still unclear whether this is its physiological function. During heat treatment in milk processing plants, BLG is believed to be a major initiator of aggregation and hence fouling of heat-exchangers. It has also been linked to milk allergy. In reviewing the physicochemical properties of the protein, emphasis will be placed upon those studies that give insight into the behaviour during unfolding and denaturation under a variety of conditions. Further, by considering the lipocalin family in general, and in particular the species

distribution of BLG, some speculation as to the physiological function can be made.

Key Words: β -Lactoglobulin, Structure

199 Heat-induced reactions involving β -lactoglobulin and other milk proteins in milk, whey, and model systems. L. K. Creamer*¹, G. A. Manderson¹, Y-H. Hong², P. Havea¹, Y-H. Cho³, H. Singh⁴, A. Bienvenue⁵, and R. Jimenez-Flores⁵, ¹NZDRI, Palmerston North, New Zealand, ²Chonnam University, Kwanju, Korea, ³Mass. General Hospital, Boston, MA, USA, ⁴IFNHH, Massey University, Palmerston North, NZ, ⁵DPDC, Calpoly, San Luis Obispo, CA, USA.

Heat treatment of milks is an essential step in modern dairy processing and the effects can be far-reaching in terms of product functionality and the heat-induced gelation of whey protein concentrate (WPC) solutions is important in functional food applications. Heating WPC solutions or milk beyond pasteurisation causes some of the individual whey proteins