

in duodenal EAA proportions ranged from as low as 11.1 to 11.2% of total EAA for phenylalanine to 12.3 to 14.3% of total EAA for lysine. Although profile of EAA (individual EAA as a % of total EAA) reaching the duodenum differed ($P = 0.02$) for all 10 of the EAA, duodenal flow did not differ ($P = 0.10$ to 0.65) for 8 out of the 10 EAA. Specifically, duodenal flow of arginine increased linearly ($P = 0.01$) whereas duode-

nal flow of tryptophan decreased linearly ($P = 0.002$) as forage intake decreased from 105 to 30% of maintenance. Our results demonstrated that balancing intestinal essential amino acid supply in beef cattle can be accomplished with proper RUP supplementation.

Key Words: Restricted intake, Amino acids, Supplementation

Breeding & Genetics: Dairy cattle breeding for production traits

147 Individual curve fitting of Italian Simmental cow milk test day data. N.P.P. Macciotta*¹, D. Vicario², G. Pulina¹, and A. Cappio-Borlino, ¹Università di Sassari, ²Italian Association of Simmental cow Breeders.

The evolution of milk production over time can be modelled by several mathematical linear and non-linear functions. Observed differences in fitting of average lactation curves of homogeneous groups of animal for the most commonly used lactation models are rather small. On the other hand, a very wide range of goodness of fit can be observed for individual lactation pattern, essentially due to the random biological variation between cows and not to the inadequacy of the mathematical model used. Therefore, in order to study the effects of some systematic environmental factors on the shape of lactation curves, it is more useful to fit a simple model whose parameters possess a clear, technical significance to curves that are not too far from the typical lactation pattern. In this study, the incomplete Wood's gamma function $y=a(bt)\exp(ct)$ was fitted to 13,739 lactations of Italian Simmental cows, with at least 7 records each and with the first recorded test day within the 15th days in milking, of six parity classes (1 to 6). The overall mean adjusted r-square was 0.71. A reduced data set of 6830 regular lactation curves was extracted with the constraints of having the b parameter positive and the adjusted r-square greater than 0.75. Values of parameter a, b and c were analysed with a linear model in order to evaluate the effect of herd, parity, year and season of calving on the lactation curve shape. Parity affected all the three parameters, with primiparous cows having the lowest values for the a (12.82) and c (-0.00417) parameter, thus indicating a lower level of production and a higher persistency of lactation in comparison with older cows. Also calving season affected all the parameters, with highest values of the scale parameter a for cows calving in March and April. Finally an increasing trend for the level of production and lactation persistency has been observed during the period considered (1989-1999).

Key Words: Lactation curve, Italian Simmental

148 Estimates of genetic parameters and lactation curves with a cubic spline model for Holstein cows treated with bovine somatotropin. B. J. DeGroot*¹, J. F. Keown¹, S. D. Kachman¹, and L. D. Van Vleck², ¹University of Nebraska, Lincoln, NE, ²USDA, ARS, USMARC, Lincoln, NE.

The objective was to estimate genetic parameters and response to bovine somatotropin (bST) from individual test-day milk yields with a cubic spline model for first three lactations. A total of 263,034 test-day milk records of Holstein cows treated with bST and 405,265 test-day records of untreated cows that calved between 1996 and early 2002 were obtained from Dairy Records Management System, Raleigh, North Carolina. Estimates of (co)variances for a cubic spline with five knots were obtained with REML. Estimates of heritabilities for test-days and estimates of genetic and phenotypic correlations between test-days were obtained from estimates of variances and covariances from the cubic spline analysis. Genetic parameters were estimated at the average day within each of the ten 30-d test day intervals. The cubic spline model included herd test-day, age at first calving, treatment, and treatment by linear as fixed effects and treatment by spline as random effects. Cubic splines were fitted for the overall lactation curve within treatments, additive genetic effects, and permanent environmental effects. The cubic splines used five intervals determined by days 0, 50, 135, 220, and 310. The treatment differences were measured for bST treated and untreated cows. Estimates of heritability for test-day one to test-day ten ranged from 0.09 to 0.16, 0.10 to 0.17, and 0.10 to 0.18 for lactations one, two, and three. Estimates of genetic correlations for milk yield at pairs of test-days ranged from 0.99 to 0.45 for lactation 1, 0.99 to 0.32 for lactation 2, and 0.99 to 0.35 for lactation 3. The differences of 3.17, 2.27, and 2.30 kg between treated and untreated cows at day 100 were maintained until about day 220 of lactations one, two, and three. Estimates of

heritability increased over the course of the lactation and estimates of genetic correlations decreased for pairs of test-days further apart.

Key Words: Heritability, Genetic correlations, Milk yield

149 Environmental sensitivity of genetic merit for milk, fat and protein yield estimated by a random regression model. M. P. L. Calus* and R. F. Veerkamp, ID-Lelystad.

Environmental sensitivity of genetic merit for milk, fat and protein yield was estimated using a random regression model to evaluate the effect of combining these traits in an economic index for different herd environments. To describe herd environments fourteen environmental parameters were defined based on the data available. Variance components and breeding values of sires for milk, fat and protein yield were modeled as a function of an environmental parameter. Up to the third order polynomial random regressions were applied. Fixed linear and quadratic regressions were included for age at calving and fixed effects to account for herd-year-season groups. A fixed polynomial regression was applied to the environmental parameters, to account for the average level in each herd. The residual variance was modeled for ten different groups, to account for heterogeneous residual variances in the model. ASREML was used for all analyses. Herd-year peak date of calving, herd average protein, body condition score, calving interval and age at calving gave most environmental sensitivity, mainly resulting from a change in scale of the genetic and residual variances for extreme herds and little re-ranking. The sire variances of milk, fat and protein yield followed more or less the same pattern across the environmental scale. Most genetic correlations across environments were close to unity for each individual trait. The change in variances had a large scaling effect on the economic weights, but the effects were similar for milk, fat and protein yields. Therefore, also very little re-ranking occurred based on the economic index, but the use of high merit bulls seemed more beneficial in herds with peak date of calving in the fall or winter, high average protein, high body condition score, short calving intervals and young age at calving.

Key Words: Environmental sensitivity, Random regression model, Environmental parameter

150 Estimation of genetic parameters for test-day records of French Holstein cows with an AI-REML algorithm. T. Druet*, F. Jaffrézic, and V. Ducrocq, Station de Génétique Quantitative et Appliquée, INRA.

Genetic parameters for lactation test-day records of French Holstein cows were estimated as a first step towards the implementation of a national genetic evaluation with a test-day model. Test-day records were considered up to 335 days in milk. The fixed part of the lactation curve was modeled with regression splines with 6 knots. Genetic parameters were estimated with an Average Information REML algorithm where the average information matrix and the first derivatives of the likelihood functions were pooled over 10 samples. This approach made it possible to handle larger data sets. The logarithm of the residual variance was modeled with several parametric functions of days in milk such as polynomial function or regression splines. Quartic Legendre polynomials were used to estimate (co)variances of random effects. The estimates were within the range of most other studies and were very close to those obtained in a previous study where lactation length was limited to 305 days. The largest genetic variance was in the middle of the lactation while residual and permanent environmental variances mostly decreased during the lactation. The resulting heritability ranged from 0.17 to 0.37. For a large part of the lactation genetic correlations were higher than 0.90. For both the genetic and permanent environmental variances, the first two eigenvalues represented more than 90 % of the total variation. The corresponding eigenvectors seemed to make sense biologically. They were used as covariables to estimate the genetic

parameters in the three first lactations. Flexible functions were used to model the residual variance in order to take into account the extra residual variation not explained by the eigenvectors. Resulting genetic correlations among lactations were high.

Key Words: Genetic parameters, Test-day model

151 Estimation of genetic correlations among production, body size, udder, and productive life traits over time in Holsteins. S. Tsuruta¹, I. Misztal¹, T. J. Lawlor^{*2}, and L. Klei², ¹University of Georgia, Athens GA, ²Holstein Association USA Inc., Brattleboro VT.

Genetic parameters can change over time for several reasons. The use of a random regression model allows us to account for changes in a large number of variances and covariances over time and does not require any prior assumptions about how the parameters will change. Genetic correlation among milk, fat, productive life, body size, and udder traits in 40,838 Holsteins were estimated over a 15 year time period (cows born from 1979 to 1993). The model included registration status, herd-year, age group, and stage of lactation as fixed effects; additive genetic effects with random regressions on year of birth using the third order Legendre polynomials; and residual effects with heterogeneous variances using the interval method via Gibbs Sampler. Additive genetic variances for milk, fat, and body size increased over time while those for productive life and udder traits were constant. Residual variances for milk, fat, body size, and udder traits also increased over time, but those for productive life were relatively constant. As a result, heritability estimates for milk, fat, productive life, and body size were constant, and those for udder composite slightly decreased. Genetic correlations between milk production with fat yield and productive life have decreased, while the correlation of milk with body size and udder composite has increased over the years. Genetic correlations between productive life and the other traits decreased for the last decade. These changes can largely be explained by changes in selection emphasis that has taken place within the Holstein breed.

Key Words: Genetic parameters, Random regressions, Selection

152 Identification of environments for AI progeny testing schemes that yield the highest heritability and correlation with second-crop evaluations for yield and type traits. N. R. Zwald* and K. A. Weigel, UW-Madison, Madison, WI.

The objective of this study was to determine if differences in heritability and correlation with second-crop evaluations existed between progeny-test environments, and to identify optimal herd characteristics for testing of AI young sires. Without a proper environment, animals may not be given the opportunity to express their true genetic potential and genetic evaluations of sires progeny tested in these environments could be inaccurate. Missing and inaccurate identification adds to this problem in some herds. To examine this problem, data from all first classifications of young sire daughters were examined from 1993 to 2001. Data from 480,927 animals in 20,650 herds from 16,844 AI sires were used for this analysis. Only 254,891 animals (47%) had a sire-identified dam, and only 132,953 (27.6%) had a classified dam. Herd average phenotypic score was divided into three equal groups, defined as high phenotypic average score (> 80 points), intermediate phenotypic average score (74-80), and low phenotypic average score (< 74 points). Correlations between sire PTAT and actual daughter score for the three environments were (0.15, 0.11, 0.09) respectively. Actual daughter classification scores were regressed on sire PTAT to determine the differences between environments. Regression coefficients were (1.05, 0.78, 0.48) respectively. This research shows that there are considerable differences between progeny testing environments and that every effort should be made to progeny test bulls in environments with acceptable herd average phenotypic score. This will allow animals to more fully express their genetic potential. The current situation favors bulls proven in environments with a higher herd average phenotypic score.

Key Words: Progeny test, Type evaluation, Genotype by environment interaction

153 Accuracy of foreign dairy bull evaluations in predicting US evaluations for yield. R. L. Powell*, A. H. Sanders, and H. D. Norman, Animal Improvement Programs Laboratory, Agricultural Research Service, USDA.

The addition of foreign daughter data to domestic dairy bull genetic evaluations has been shown to improve prediction of future domestic evaluations in a study of mainly US bulls. This study evaluates the accuracy of Interbull evaluations, based only on foreign daughters, in predicting the latest US yield evaluations, based only on US daughters, thus focusing on foreign bulls. February and August Interbull evaluations from 1995 through 2002 were used. For 652 Holstein bulls, the most recent Interbull evaluations solely from foreign daughter data were matched with February 2003 USDA evaluations based only on US daughters, thus providing a pair of evaluations based on different daughters. For the Interbull evaluations, mean reliability on the US scale was 84% and the mean US reliability for February 2003 evaluations was 78%. Correlations between these Interbull and US evaluations were .88, .82, and .88. for milk, fat, and protein, respectively. Interbull evaluations overestimated the US PTA by an average of 34, 0.4, and 0.7 kg, with standard deviations of the difference of 197, 7.5, and 5.5. Considering only those 153 bulls with US reliability of 90% or higher, correlations were similar to those seen overall for milk (.87) and protein (.88), but higher for fat (.87). Expected correlations were .81 for all 652 bulls and .91 for the 153 bulls. Thus, the actual correlations were higher than expected for all bulls but lower than expected for bulls with the highest US reliabilities. For the higher US reliability bulls, Interbull evaluations underestimated milk, fat, and protein by an average of 7, 0.3, and 0.4 kg, respectively, with standard deviations of differences, 167, 6.2, and 4.6. None of these mean differences between evaluations from foreign and US daughters are large and the correlations indicate that Interbull evaluations based solely on foreign daughters are good predictors of the US evaluations for yield.

Key Words: Genetic evaluation, Interbull, Evaluation accuracy

154 Standardization of lactation records for variance of Mendelian sampling to reduce bias in evaluations of bull dams. G. R. Wiggans*, P. M. VanRaden, and J. L. Edwards, Agricultural Research Service, USDA, Beltsville, MD.

Evaluations of bull dams may be biased upward because of preferential treatment or contemporaries with extremely low yields. Variance of Mendelian sampling (MS) was standardized to determine if such an adjustment of lactation records could improve accuracy of estimated breeding values (EBV) of bull dams. For Holstein data included in February 2003 USDA evaluations, MS variances were calculated within herd and 5 yr of first calving group. To regress estimates for small herds, the population estimate was included with a weight of 20. The ratio of the population MS standard deviation to the within herd-5 yr group value was used to adjust phenotypic yields. This ratio was limited to a maximum range of 0.5 to 2.0, with the range further limited based on mean herd yield to avoid over adjustment. To minimize effect of unreliable evaluations of females, MS was calculated using maternal grandsire EBV instead of dam EBV. At each round of iteration, this male index was subtracted from current EBV, and the result was adjusted for amount of information. To assess effect of the MS variance adjustment, EBV were calculated excluding records from calvings after 1997. Means of parent EBV were calculated for recent bulls using subset EBV with and without MS variance adjustment. Correlations (r) between February 2003 bull EBV and parent mean for the subset were higher with adjustment. Similarly, regression (b) of EBV on parent mean was closer to 1 with adjustment, and mean EBV minus parent mean (bias) was lower. Mean EBV of the top 100 cows was reduced with adjustment. Twenty percent in the top 50,000 cows for milk yield were different with adjustment. The largest drop was 1324 kg EBV. Standardization of MS variance improved accuracy of EBV.

MS variance adjustment

Yield trait	Correlation		Regression coefficient		Bias		Mean EBV of top 100 cows	
	No	Yes	No	Yes	No	Yes	No	Yes
Milk	0.773	0.782	0.742	0.787	-75.8	-58.5	2716.2	2565.9
Fat	0.721	0.727	0.693	0.763	-3.3	-2.5	110.3	94.7
Protein	0.807	0.816	0.715	0.779	-2.5	01.9	88.8	77.9

Key Words: Heterogeneous variance adjustment, Evaluation bias, Mendelian sampling

155 Development of a selection index for the Reggiana dairy cattle breed. M. Fioretti¹, V. Palucci*¹, and F. Miglior², ¹Associazione Italiana Allevatori, Rome, Italy, ²Agriculture and Agri-Food Canada, CDN, Guelph, ON, Canada.

The Reggiana population is a dairy cattle breed reared in the province of Reggio Emilia, located in the Italian Po Valley. Milk from this breed has been mainly used for the production of Parmigiano Reggiano cheese. The Reggiana breed has shrunk from 84,000 cows in 1940 to 200 animals in 1984, having been replaced by much more productive Holstein-Friesian cows. Thanks to government support the breed was recovered in the last two decades, and currently close to 1000 cows are milk recorded. Selection has been based mainly on milk yield and produced moderate genetic progress for production (60 kg milk/yr, 2.5 kg fat/yr and 1.5 kg protein/yr) and phenotypic and genetic decrease for protein percent. In order to invert the negative genetic trend for protein percentage, unsuitable for Parmigiano Reggiano production, a selection index was developed that accounted for milk price for cheese production. The new index with economic weights of -26%, +7% and +67% emphasis for milk, fat and protein yield respectively, was found to increase protein percentage 10-yr genetic progress, and to greatly increase protein yield genetic progress (3.3 kg/yr), leaving milk and fat yields at normal levels (61 kg milk/yr and 2.5 kg fat/yr).

Key Words: Dairy cattle, Selection index

156 Analyses of heat tolerance for milk in Holsteins using different sources of heat-stress information. I. Misztal*, S. Oseni, and S. Tsuruta, *University of Georgia, Athens, GA, USA.*

The purpose of this study was to evaluate parameters of alternative models for analysis of test day milk under various levels of heat stress. Data included 81,674 first parity milk test days on 10,162 cows in FL. Also available were daily temperature-humidity indices (THI) from public weather stations in FL. Models included the effects of herd-test day, age class, days in milk class, frequency of calving, and additive and permanent environment implemented as linear random regressions. Models differed by the choice of covariables used in random regressions. The choices were: a) THI during the test day measured at the nearest public weather station, b) average THI across all weather stations for the month of test day, and c) solutions of month of test-day computed in a fixed model. The last model would correspond to a norm reaction model. Lowest production in models a) and b) corresponded to July, and lowest

production in model c) corresponded to August-September. Constant terms in the random regression could be interpreted as regular effects, and linear terms as heat-tolerance effects. Genetic correlations between the constant and linear additive effects were -0.42 for a), -0.46 for b), and -0.76 for c). Correlations between additive effects in a) and b) were 0.96 (regular) and 0.94 (heat-tolerance). The same correlations in a) and c) were 0.95 and 0.56. Genetic variance for the heat-tolerance effect corresponding to the peak of heat stress was 20% higher for c) than for b). For genetic analyses of heat tolerance, average monthly THI per state provided comparable information to daily THI from nearby weather stations. The heat tolerance effect in the norm reaction model accounts not only for the effect of heat stress due to current THI, but also for additional factors such as accumulated effects of heat stress or varying forage quality over time.

Key Words: Dairy cattle, Heat stress, Random regression

157 Comparison of Holstein, Holstein-Jersey crossbred, and Holstein-Normande crossbred first-parity cows for milk, fat, and protein production and SCS during the first 150 days of lactation. B. J. Heins¹, L. B. Hansen*¹, and A. J. Seykora, ¹University of Minnesota, St. Paul.

First-parity Holsteins (n = 247), Holstein-Jersey crossbreds (n = 97), and Holstein-Normande crossbreds (n = 68) were compared for milk, fat, and protein production and SCS during the first 150 days of lactation. Cows were housed in six commercial dairies in California and calved from June 2001 to December 2002. Dependent variables for analysis were test-day observations from DHI. Independent variables were breed composition (H, HxJ, HxN), random effect of cow within breed composition, stage of lactation (4-30 d, 31-60 d, 61-90 d, 91-120 d, or 121-150 d), herd (1 to 6), milking frequency (2X or 3X), and interaction of breed composition and milking frequency. Breed composition was significantly different for milk and fat production and approached significance for protein production; however, there was not a significant difference of breed composition for SCS. Least-squares means for test-day milk production were 32.7 kg (H), 30.3 kg (HxJ), and 29.1 kg (HxN). For test-day fat production, least-squares means were 1.13 kg (H), 1.20 kg (HxJ), and 1.09 kg (HxN). Least squares means for protein production were 0.96 kg (H), 0.95 kg (HxJ), and 0.93 kg (HxN). Although not significantly different, least squares means for SCS were 2.3 (H), 2.8 (HxJ), and 2.5 (HxN).

Key Words: Crossbreeding, Production, SCS

Dairy Foods: Processed cheese, milk powder, and microbiology

158 Comparison of pilot-scale and RVA process cheese manufacture. L. E. Metzger*, P. Lehtola, and R. Kapoor, *MN-SD Dairy Foods Research Center, University of Minnesota, St. Paul, MN.*

Numerous formulation and processing parameters influence the functionality of process cheese. Consequently it is sometimes difficult to predict the functionality of process cheese based on the formulation used. However, a small-scale manufacturing and analysis method could be used to evaluate the influence of formulation parameters on the functionality of process cheese. The objective of this study was to compare process cheese produced on a small scale (20 g) in a Rapid Visco Analyzer (RVA) to process cheese produced on a pilot-scale (4.5 kg) Blentech twin screw (BTS) cooker. Three different formulation of process cheese (PC) and process cheese food (PCF) were produced in a RVA and in a BTS cooker. Each formulation was produced in triplicate in the RVA and in duplicate in the BTS cooker. In the RVA the temperature of the heating block was maintained at 80°C and the stirring speed was sequentially increased from 0 rpm to 500 rpm in two minutes. The RVA was stopped 1 min or 2 min after an increase in viscosity was observed for the short and long manufacturing profiles respectively. In the BTS cooker each formulation was heated to 80°C in 3 min and held an additional 4 min. A screw speed of 120 rpm or 140 rpm was used for the PC and PCF respectively. Texture profile analysis (TPA) and the RVA melt test were performed on all PC and PCF produced. The formulation used had a significant (P<.05) effect on the TPA hardness, hot viscosity, and melt time of the PC and PCF produced in the RVA and in the BTS cooker. However, the PC and PCF produced in the RVA had a significantly (P<.05) higher TPA hardness and melt time as compared to PC and

PCF produced in the BTS cooker. The RVA manufacturing time (short vs long) did not have a significant (P>.05) effect on any parameter for the PCF. However with the PC, the long manufacturing time significantly (P<.05) increased hot viscosity and melt time. Future research will focus on identifying RVA manufacturing profiles that produced PC and PCF that matches the functionality of process cheese produced on a pilot scale.

Key Words: Process Cheese

159 Salt whey ingredient. V. V. Mistry* and M. R. Acharya, *South Dakota State University.*

A method for manufacturing a salt whey ingredient (SWI) was developed (patent pending). Approximately 110 of kg salt whey was obtained for each of three replicates from salted curd that had been placed in barrels for draining and separated by centrifugal separation at 35°C. The skimmed salt whey was pasteurized at 63°C for 30 min, cooled to 20°C and condensed in a rising-film single-stage evaporator. The concentrate was spray dried in a single-stage spray drier to 3.3% moisture, 1.97% fat, 10.1% protein, 40.1% salt and 39.8% lactose and used in the manufacture of pasteurized process cheese and cheese spreads. The pasteurized process cheese formulations consisted of a blend of young (1- to 2-mo old) and aged (4- to 6-mo old) Cheddar cheese in equal proportions as follows: control pasteurized process cheese; control with no emulsifier; cheese with 2% SWI; cheese with 1.7% SWI but no emulsifier. For the cheese spread there were two formulations: control Provolone cheese