Tissue sample treatment and storage was assessed using hooves of six beef cattle (24 and 28 months) from an abattoir. Tissue samples from the sole and white line of each claw (5 and 2 of International Foot Map) and kept in sealed plastic bags at room temperature until conditioning from physiological moisture content (0) and relative humidity (RH) 11, 33, 58, 75 and 97%; sample thickness (0.05 and 0.3 mm); storage duration in plastic bags 2°C for 0, 48, 96, 144 and 192 hours and freezing (-20°C) for 7, 14 and 28 days. After treatment tissue samples were tested 12 times for punch resistance (PR) and elastic modulus (EM) using a Texture Analyser. Samples were tested for DM content. Increase in DM resulted in a significant (P<0.01) linear increase in the PR (N) of the sole (PR= 0.490; DM: 24.39, Rsq.= 0.54) and the white line horn (PR= 0.430; DM: 24.87, Rsq.= 0.64). The EM (N/mm2) of the sole horn was significantly (P<0.01) positively exponentially related to the DM (EM= 0.0602e0.1012x, Rsq.= 0.81). DM varied from 63.7 to 89.1%, PR of the sole horn from 6.24 to 24.66N, PR of the white line horn from 2.17 to 18.60N and EM from 85.5 to 751.9N/mm2. The days (1 to 8) taken to analyse the samples and freezing for up to 28 days had no significant effect on the DM and PR of the sole and white line horn. There was a significant (P<0.01) increase in the EM of the sole horn when samples were frozen for 28 days. PR increased in a positive significant (P<0.001) linear in relation to the thickness (mm) of the area tested (PR= 6.679 + 34.531 thickness, Rsq.= 0.66).

Key Words: Hoof, Beef Cattle, New Methods

Breeding and Genetics - Livestock and Poultry: Dairy Cattle II

555   Performance and physical conformation of first parity backcross Holstein x Jersey cattle and their Holstein contemporaries. K. A. Weigel*, T. J. Halbach, C. Maltecca, and P. C. Hoffman, *University of Wisconsin*, *Madison*.

The experimental population for the present study consisted of 194 backcross females, which were the offspring of 7 young Jersey x Holstein sires and 167 lactating Holstein dams, as well as 90 pure Holstein females, which were the offspring of 57 young Holstein sires and 83 lactating Holstein dams. These animals were born from November 2003 to January 2007 at the University of Wisconsin - Madison Integrated Dairy Facility. All first parity crossbred cows (N=40) and Holstein cows (N=23) were classified for linear type traits by a trained evaluator between 50 and 200 d postpartum. A linear model, which included fixed effects of classifier, days in milk, and pen, indicated that crossbred cows had shorter stature (P<0.0001), more strength (P<0.05), lower dairy form score (P<0.10), more slope from hooks to pins (P<0.01), narrower rump (P<0.0001), steeper foot angle (P<0.01), closer front teat placement (P<0.10), and straighter rear legs when viewed from the rear (P<0.05). Mean differences in body depth, rear legs when viewed from the side, fore udder, rear udder height, rear udder width, udder cleft, udder depth, teat length, and udder tilt were not significant. Crossbred cows were 35 kg lighter (P<0.10) at first calving, however, mean birth weight of their calves did not differ. Likewise, mean body condition score at first calving did not differ, nor did mean body condition score at breeding. Peak milk yield of crossbred cows was 4 kg lower (P<0.05), although fat and protein percentage did not differ. Based on these data, it appears that crossbreeding may improve mobility traits and reduce maintenance feed costs (through decreased body size), albeit at the expense of milk production.

Key Words: Dairy, Crossbreeding, Type

556   Crossbreds of Jersey/Holstein compared to pure Holsteins for production, fertility, and udder traits during first lactation. B. J. Heins, L. B. Hansen, A. J. Seykora, A. R. Hazel*, J. G. Linn, and D. G. Johnson, *University of Minnesota*, *St. Paul*.

Jersey/Holstein crossbreds (n = 76) were compared to pure Holsteins (n = 73) for 305-d milk, fat, and protein production, days open, number calving a second time, and udder traits during first lactation. Cows were housed at two University of Minnesota research facilities and calved from September 2003 to May 2005. Jersey/Holstein crossbreds were bred to Montbeliarde sires, and Holstein cows were bred to Holstein sires. Best Prediction was used to calculate actual production (milk, fat, and protein) for 305-d lactations. Adjustment was made for age at calving and herd-year and records less than 305 d were projected to 305 d. Jersey/Holstein crossbreds (249 kg) and pure Holsteins (251 kg) were not significantly different for fat production, but pure Holsteins had significantly higher milk (7179 kg vs. 6600 kg) and protein (224 kg vs. 209 kg) production than Jersey/Holstein crossbreds. Least squares means for days open were 136 for Jersey/Holstein crossbreds and 159 for pure Holsteins. Jersey/Holstein crossbreds had a higher percentage of cows that calved a second time than pure Holsteins, (87% vs. 77%) respectively. Udder clearance, front teat placement, and teat length were measured during first lactation. Udder clearance was measured from the ground to the bottom of the udder and front teat placement was the distance between the front teats. Age at calving, herd-year, stage of lactation, breed, and random effect of sire within breed were included in the statistical model. Jersey/Holstein crossbreds had significantly less udder clearance than pure Holsteins, (47.2 cm vs. 54.6 cm) respectively. Jersey/Holstein crossbreds and pure Holsteins were not significantly different for front teat placement (15.3 cm vs. 13.7 cm) and teat length (4.5 cm vs. 4.4 cm), respectively.

Key Words: Crossbreeding, Heterosis, Production

557   SNPs in the 3'UTR of Stearoyl-CoA desaturase gene in Canadian Holsteins and Jerseys. P. M. Kgwatalala, E. M. Ibeagha-Awemu*, J. F. Hayes, and X. Xhao, *McGill University*, *Ste Anne De Bellevue, Quebec, Canada*.

Stearoyl-CoA desaturase (SCD) catalyzes the synthesis of conjugated linoleic acid (CLA) and monounsaturated fatty acids (MUFA) in the mammary gland. A two to three-fold variation in CLA and desaturase index have been reported among animals on the same diet. We hypothesized that SNPs in the 3´UTR of the SCD gene result in different 3'UTR regulatory variants which influence the production of SCD enzyme and consequently its activity in the mammary gland, which may explain some observed variations in CLA and MUFA

content of milk fat between Holsteins and Jerseys and within these breeds. The main objective of our study was therefore to determine the existence of SNPs in the 3'UTR of the SCD gene in Canadian Holsteins and Jerseys. Genomic DNA from 46 randomly selected Holsteins and 35 randomly selected Jerseys was used for selective amplification and direct sequencing of the 3'UTR of the SCD gene. A total of fifteen SNPs (G1571T, G1644C, C1763A, T2053C, A2584G, T2668C, A3007G, C3107T, G3208A, T3290C, G3497A, G3682A, A4399T, C4533T and G4881A) were uncovered in the 3'UTR of the SCD gene. The SNPs linked together resulting in 3 regulatory variants in Holsteins: H1 (G1571G1644C1763C2053 A2584 C2668 A3007 C3107 G3208T3290 G3497 G3682A4399C4533G4881), H2 (G1571G1644A1763 C2053 A2584 C2668 G3007 C3107 G3208T3290 G3497 G3682 A4399 C4533G4881) and H3 (T1571C1644A1763T2053 G2584 C2668 G3007 T3107 A3208 C3290 A3497A3682 T4399T4533A4881) and only H1 and H3 variants in Jerseys. The H1 regulatory variant was the most prevalent in both breeds suggesting it may be the wild regulatory variant at the SCD locus, followed by the H3 variant. The search for functional motifs in the 3´UTR region of the SCD gene revealed the presence of internal ribosome entry site (IRES) motif in the H1 regulatory variant and its total absence in the other two regulatory variants. SNPs in the 3'UTR of the SCD gene may thus contribute to existing variations in CLA and MUFA content of milk fat between and within Holsteins and Jerseys.

Key Words: Singl Nucleotide Polymorphisms, SCD Gene, Regulatory Variants

558   Estimation of yields for long lactations using best prediction. J. B. Cole*[1], P. M. VanRaden[1], and C. M. B. Dematawewa[2], [1]*Animal Improvement Programs Laboratory, USDA, Beltsville, MD*, [2]*Virginia Polytechnic Institution and State University, Blacksburg.*

Lactation records of any length now can be processed with the selection index methods known as best prediction. Previous programs were limited to the 305-day standard used since 1935. Best prediction (BP) was implemented in 1998 to calculate lactation records in USDA genetic evaluations, replacing the test interval method used since 1969 to calculate lactation records of any length at dairy record processing centers. Best prediction is more complex but also more accurate, particularly when testing is less frequent. Programs were reorganized to output better graphics, give users simpler access to options, and provide additional output, such as BP of daily yields. Simple diagnostic plots are now available for milk, fat and protein yields and somatic cell score, and BP of individual daily yields, test day yields, and herd lactation curves can be obtained by the user for production of publication-quality figures. Test-day data for Holstein cows were extracted from the national dairy database, including lactations longer than 305 d. Records from first through fifth parities were included if lactation lengths were at least 250 d, records were made in a single herd, at least five tests were reported, and only twice-daily milking was reported. After edits, 171,970 first- and 176,153 later-parity records were available. Lactation lengths averaged 362 d in first and 369 d in later parities. 23.9% of first and 27.5% of later parities were longer than 305 d, and 3.3% and 3.4%, respectively, were longer than 500 d. Average yields at any day in milk were estimated using a 4-parameter exponential function. Correlations among test day yields were estimated using an autoregressive matrix to account for biological changes and an identity matrix to model daily measurement error. Autoregressive

parameters (r) were estimated separately for first- (r=0.998) and later-parity (r=0.995) cows. These r were slightly larger than previous estimates due to the inclusion of the identity matrix, which accounts for test day variation. Many cows can produce profitably for >305 days in milk, and the revised program provides a flexible tool to model these records.

Key Words: Best Prediction, Milk Yield, Long Lactations

559   Genetic parameter estimates for days open by using a random regression model to analyze data from a long-term designed selection experiment. G. A. Gutierrez*, M. H. Healey, and P. J. Berger, *Iowa State University, Ames.*

The objective of this study was to estimate genetic parameters for days open (DO) by using a covariance function(CF)-random regression model. Data were collected at the Ankeny dairy research farm at Iowa State University from 1986 to 2004. A total of 3830 records from Holstein cows (n=766) were used in the analysis. Data were restricted to less than 6 parities. All cows were required to have a first parity record, but all cows did not have an opportunity to have completed all parities. Data were analyzed using two models: 1) a repeatability animal model, fixed effects for line of sire selection (high or average PTA fat plus protein), year-season, parity, and linear-Legendre polynomial (LLP) for age at calving(Average=39, min=20, max=90, and SD=16 mo), random effects for animal and permanent environment; and 2) random regression model, fixed effects as defined above for model 1, random LLP coefficients for additive genetic and permanent environment effects. Analyses were implemented by using ASREML v1.1. The covariance matrix of random regression coefficients was used to define the CF for the additive genetic and permanent environmental (co)variances across the trajectory of age at calving from 20 to 90 mo. In model 1, estimated values of heritability and repeatability for DO were 0.08 and 0.09, respectively. In model 2, the additive genetic variance tended to increase with age at calving. Heritability estimates were 0.07,0.08,0.09,0.10,and 0.10, respectively, at 24, 36, 48, 60 and 72 mo. The genetic correlation between records at different ages was fixed at 0.99. The percentage of phenotypic variance explained by permanent environmental variance varied from 3 to 19% across the 5 fixed ages. Repeatability ranged from 0.17 to 0.29. Permanent environmental correlations were highly variable; $r_{(24,36)}$=0.88, $r_{(24,48)}$=0.06, $r_{(24,60)}$= -0.48, and $r_{(24,72)}$= -0.65. Implication of this research is that CF-random regression approach gives a better description of the full (co)variance structure for repeated measurements of DO across a trajectory of age at calving than the repeatability model.

Key Words: Days Open, Random Regression, Holstein

560   Construction and application of a bovine high-density SNP assay. C. P. Van Tassell*[1], L. K. Matukumalli[1,4], C. Taylor[5], T. P. L. Smith[3], T. S. Sonstegard[1], R. D. Schnabel[2], M. V. B. De Silva[1], G. R. Wiggans[1], G. Liu[1], S. Moore[6], and J. F. Taylor[2], [1]*USDA, ARS Beltsville Agricultural Research Center, Beltsville, MD*, [2]*University of Missouri, Columbia*, [3]*USDA, ARS, US Meat Animal Research Center, Clay Center, NE*, [4]*George Mason University, Fairfax, VA*, [5]*Illumina, Inc., San Diego, CA*, [6]*University of Alberta, Edmonton, AB, Canada.*

Bovine genomics has entered a new era and has been transformed by the availability of the whole genome sequence data. An additional resource currently under development is a 60,000 single nucleotide polymorphism (SNP) array that will soon be made commercially available. Targeted content for this SNP array includes all chromosomes with even-coverage throughout the bovine genome. The SNP array will be used in several large-scale genotyping projects, with over 10,000 animals genotyped. Resulting genotypes for Angus, Brown Swiss, Holstein, and Jersey animals will be used to construct breed specific haplotype maps and develop genomic selection procedures to enhance the prediction of genetic merit via integration with predictions from the national cattle evaluation. To date, nearly 2.5 million putative SNP have been predicted and/or obtained from publicly available databases. Validation of these SNP by resequencing has resulted in a wide range of success rates (from <40% to ~90%) correlating to the source of the in silico derived SNP. To supplement coverage for the design of the proposed SNP assay, we have generated over 24 million short DNA sequence reads and have identified approximately 50,000 new putative SNP among these sequences. Validation of these SNPs is currently in progress. The final assay is expected to be available by mid-summer, 2007.

Key Words: Genome Selection, Single Nucleotide Polymorphism, Marker Assisted Selection

561   Estimation of genetic parameters with random regression models using test-day records beyond 305 days in milk. J. Bohmanova[1], F. Miglior*[2,3], and J. Jamrozik[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [3]*Canadian Dairy Network, Guelph, ON, Canada*.

Effect of inclusion of test-day records recorded after 305 days in milk on variance components estimates was investigated. Currently, only test-day records measured ≤305d are utilized in the Canadian genetic evaluation. Since increasing number of cows has longer lactation than 305d, it is of interest to also include test-day records measured after this cut-off point. However, such a change requires re-estimation of variance components. Two data sets were sampled from the Canadian national database. Data were test-day yields of milk, fat and protein and somatic cell score from the first three lactations of Canadian Holsteins recorded from 1988 to 2006. The first data set consisted of 96,756 test-day records of 6235 cows, with days in milk from 5 to 365d. The second data set was a subset of the first one and comprised 89,429 records with days in milk ≤305d. The pedigree file contained 18,178 animals. A multi-trait multi-lactation random regression model (RRM) with fixed effects of herd x test-date and fixed regression on days in milk nested within age x season class was implemented. Legendre polynomials were used to model fixed and random regression for additive genetic and permanent environmental effect. Heterogeneous residual variance was modeled with a step function with four intervals. Variance components were estimated using Bayesian procedures via Gibbs sampling. Posterior means of the parameters were estimated using 90,000 samples after 10,000 burn-in iterations. The problem of overestimation of variances at the edges of lactation connected to use of RRM with Legendre polynomial was observed with both datasets. However, with the first dataset (containing later test-day records) the increase in estimates occurred at larger days in milk and estimates of additive genetic variance of milk yield at 305d were by 1, 4 and 7 kg^2 lower. Adoption of RRM with later test-days can provide better prediction of 305d breeding values due to utilization of more data and better genetic parameters. Confirmation of predictive ability of RRM with the new parameters is in progress.

Key Words: Random Regression, Test Day Model, Variance Component

562   Selection of dairy cow families for superior pregnancy rate. C. N. Vierhout*, S. P. Washburn, R. L. McCraw, E. J. Eisen, and J. P. Cassady, *North Carolina State University, Raleigh*.

The objective of this study was to determine if dairy cow families could be used to select for superior pregnancy rate. Holstein cow records in 13 southern states were obtained from Dairy Records Management Systems. Cows were included from historical records dating back to birth year of 1981 or 1982 as the foundation cows. Historical records included cows calving and completing lactations through August, 2005. Cows from various generations were then put in maternal family groups using dam identification within herd. Milk production and calculated pregnancy rate (based on days open) deviations were obtained within herd-year-season. A family value was calculated by averaging the first and second lactations across parity by degree of relationship to the individual (free of progeny information) for generation one though four. Each family entered into one of four quartiles based on average deviations milk production and one of four quartiles for average deviations in pregnancy rate. Analysis was performed on fifth generation members to determine if milk production and pregnancy rates in the fifth generation were significantly associated with historical performance of the respective cow families. Average of the standardized values for milk production has improved (-0.09 to -0.01) from generation one to five while pregnancy rate decreased from (0.17 to 0.05) in the same period for cow families having daughters represented in the fifth generation. After adjustments for sire predicted transmitting ability (PTA), maternal-grandsire PTA, and family quartile for milk or pregnancy rate in the model the effect of maternal cow family remained highly significant for pregnancy rate (P<0.0001, R^2=0.0147) and milk production (P<0.0001, R^2=0.010). Thus, there may be potential economic value in considering maternal family history for pregnancy rate when selecting future bull dams.

Key Words: Pregnancy Rate, Days Open, Female Fertility

563   Mapping of quantitative trait loci economic important traits in Canadian holstein bulls. D. Kolbehdari*, S. Moore, and Z. Wang, *University of Alberta, Edmonton, Alberta, Canada*.

A whole genome scan for mapping quantitative trait loci (QTL) for economic important traits was performed in this study. Fifteen hundred and thirty-six bovine single nucleotide polymorphisms (SNPs) were selected to design the genotyping assay. The SNPs were distributed throughout the genome based on bovine genome assembly (Btau_2.1) and design at the Bovine Genomic lab of the University of Alberta. A total of 462 Canadian Holstein bulls with general pedigree, 319 originating from 10 core sire families, were genotyped using the designed assay. Among these SNPs, 139 were not amplified well during the genotyping, and therefore were removed from the linkage analysis. The SNPs physical position and the orders were recomputed based on the updated 7.1 X Bovine Genome Assembly (Btau_3.1). The

average polymorphism information content of the SNPs was 0.287 (0 to 0.375). The average SNP heterozygosity was 0.329 (0 to 0.50). Initial linkage analysis using variance component approach for milk, fat and protein yield has detected QTL at regions of the chromosomes known to harbor QTL based on previous studies. It is anticipated that this study will validate some of the QTL already mapped and new QTL will be discovered.

Key Words: Mapping QTL, Linkage Analysis, Dairy Cattle

564 Economic value of a marginal increase in pregnancy rate in dairy cattle. A. De Vries*, *University of Florida*, *Gainesville*.

Objective of this study was to estimate the economic value of a marginal (1-percentage point) increase in 21-d pregnancy rate in dairy cattle. The computer simulation program DairyVIP (http://dairy.ifas.ufl.edu/tools) was used. Based on user-defined inputs such as lactation curves, 21-d service rates, probabilities of conception, feed intake, involuntary culling, body weights, and costs and prices, DairyVIP first optimizes breeding and replacement decisions for individual dairy cows and then calculates many herd statistics such as pregnancy rate and profit per slot per year. An average herd in the US was modeled. Key default values were: service rate 43%, probability of conception 40% and slightly decreasing by DIM, heifer price $1600, and milk price $31/cwt. Default pregnancy rate was 16% and profit per slot per year was $389. Service rates and probabilities of conception were changed simultaneously and similarly. The economic values of a 1-percentage point increase in pregnancy rate around 7%, 14%, 18%, 23% and 34% were $32.04, $14.49, $9.92, $6.76, and $3.31 per slot per year, respectively. The greatest contributing factors were reductions in herd turnover costs resulting from lower cull rates. Sensitivity analysis by changing the default heifer price, milk price, milk yield, and risk of involuntary culling independently by 20% revealed that heifer price had the most effect on the economic value of a marginal increase in pregnancy rates. When heifer price was $1920, economic values were respectively $41.93, $17.89, $11.84, $7.98, and $3.73. When heifer price was $1280, economic values were respectively $21.71, $10.59, $7.44, $5.27, and $2.72. Twenty percent lower risk of involuntary culling and less time to become pregnant before culling also increased the economic value of marginal increases in pregnancy rates, but typically not more than $2. Greater milk price and greater milk yield increased the marginal value only when pregnancy rate was greater than 14%. In conclusion, the economic value of a marginal increase in 21-d pregnancy rate is considerably greater at lower levels of pregnancy rates.

Key Words: Pregnancy Rate, Economics, Value

565 Relationships between locomotion and lesion score, punch resistance and Holstein (HUKI) conformation scores. B. Winkler[1] and J. K. Margerison*[2], [1]*University of Plymouth*, *Plymouth, UK*, [2]*Massey University*, *Palmerston North, New Zealand*.

Dairy heifers (n 20) were used to assess locomotion, lesions score (LS) in the sole horn and hoof samples were collected from all claws and analyzed for elastic modulus (ELM) and puncture resistance (PR), each measurement was replicated five times on the same area of each claw. All heifers were assessed (HUKI) for conformation. Elastic modulus of the tension test of the sole at day 100 postpartum was significantly ($P<0.01$) negatively correlated to locomotion score at 154 dpp ($R2 = - 0.61$). HUKI score for rear legs was significantly ($P<0.05$) and positively correlated to punch resistance of sole and white line horn at 40 days prepartum ($R2 = 0.55$ and 0.50) and elastic modulus of sole at 50 dpp ($R2 = 0..53$). HUKI score for feet was significantly ($P<0.01$) and positively correlated to punch resistance and negatively correlated to lesion score of white line area at 40 days prepartum ($R2 = - 0.50$) and to the number of days the animals were severely lame throughout the lactation ($LS > 4$ ($R2 = - 0.50$)). HUKI locomotion score was significantly ($P<0.05$) and positively correlated to punch resistance of the white line horn at 100 dpp ($R2 = 0.50$). HUKI total score for legs and feet was significantly ($P<0.05$ to 0.01) negatively correlated to punch resistance of white line horn at 150 dpp ($R2 = - 0.50$) and the number of days the animals were severely lame throughout the lactation ($LS > 4$ ($R2 = - 0.48$)). HUKI total final score was significantly ($P<0.05$ to 0.01) negatively correlated to punch resistance of white line horn at 50 and 150 dpp ($r = - 0.50$) and to the punch resistance of the sole horn at 150 dpp ($R2 = - 0.60$).

Key Words: Conformation, Lameness, Dairy heifers

Companion Animals: Pet Food Ingredients - Mining, Dredging, and Extrapolating Effective Nutrient Delivery

566 Advances in evaluating pet food ingredients: Methodologies. G. C. Fahey, Jr.*, *University of Illinois*, *Urbana*.

Many ingredients exist that may be included in complete and balanced diets for pets. Dogs and cats are unique in that they can spend considerable numbers of years in the senior and (or) geriatric states, making the list of potential dietary ingredients even longer than would be the case for other species. It is important that ingredients be described in detail in order to allow for maximal utilization of their nutrients. Several levels of evaluation exist, beginning with a thorough analytical description of the ingredient. Modern analytical methods allow for near complete descriptions of macronutrients and micronutrients. In vitro testing constitutes the next level of evaluation and is very useful in predicting digestive physiological behaviors. The third level of evaluation is conducted in vivo with an animal model (e.g., use of the cecectomized rooster to determine true metabolizable energy and true amino acid digestibility values). The fourth and final level of evaluation is conducted with the target species and can take a number of forms: palatability, growth performance, and tolerance assays; digestibility evaluations, both ileal and total tract; balance studies; and gestation/lactation performance tests.

Key Words: Pet, Nutrient Bioavailability, Ingredients

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