somatic cell count (SCC) or California Mastitis Test (CMT). The tests were used to detect intramammary infection (IMI) for different DIM (2 to 8), parity statuses (heifer or cow), and a defined SCC threshold. Producer decisions for each cow included (1) test or no test, (2) if test is pursued, what type of test (CMT or SCC), and (3) a final decision: cull, segregate, administer antibiotics, or take no action. Each intermediate or final node of the model was associated with an economic outcome that the decision tree used to find the economically optimal pathway. The cost of subclinical mastitis was assessed as the aggregation of five factors: (1) milk loss, (2) milk premium loss, (3) premature culling, (4) clinical flare-ups, and (5) transmission to herd mates. These costs were a function of the lactation curve, milk price, defined SCC threshold, livestock prices, and a defined prevalence of contagious mastitis pathogens. Preliminary results indicate, in general, the selection of CMT and no action for negative cows. Seems that the administration of antibiotics could be a feasible option for positive cows, especially when a cow is in first parity (increased rate of cure), milk from a treated cow is used for heifer feeding, and the prevalence of contagious pathogens is high. The cost of mastitis under an optimal policy would vary between \$142 to \$225 per cow per 305-d lactation, and depend strongly on mastitis prevalence, SCC threshold, milk price, milk production level of cow, and parity.

Key Words: decision tree, mastitis cost, mastitis economic impact

T14 Effects of CpG ODN adjuvant on the immune responses elicited by a quadrovalent mastitis vaccine in dairy cows. S.-C. Lee[1] and J.-W. Lee*[2], [1]*Graduate Institute of Animal Vaccine Technology, National Pingtung University of Science and Technology*, *Neipu, Pingtung, Taiwan*, [2]*Department of Tropical Agriculture and International Cooperation, National Pingtung University of Science and Technology*, *Neipu, Pingtung, Taiwan*.

Staphylococcus aureus (*S. aureus*) and *Escherichia coli* (*E. coli*) remain to be common pathogens inducing bovine mastitis worldwide. Prevention of mastitis by using vaccines has not been very successful. Accumulated lines of evidence indicated that the efficacy of a vaccine can be enhanced by using bacterial DNA, or synthetic CpG oligodeoxynucleotides (ODNs), as the adjuvant. In the present study, a quadrovalent mastitis vaccine, containing formalin inactivated three strains of *S. aurues* (T5, T8, and smith compact) and *E. coli* J5, was formulated with or without a sequence of CpG ODNs that has been shown to be immunostimulatory to bovine cells. Eighteen healthy dairy cows were randomly assigned to three groups and received (1) the control (Freund's incomplete adjuvant, FIA, alone, n=6), (2) Vaccine + FIA (n=6), and (3) Vaccine + FIA + CpG (n=6). Serum antibodies specific to the four strains of bacteria and the expression of cytokines, including interferon-gamma (IFN-γ) and IL-4, in peripheral blood mononuclear cells (PBMC) in response to killed bacteria were analyzed by real-time PCR. In comparison with the control, titers of serum antibody specific to the three *S. aureus* strains were significantly (p < 0.05) increased.

Addition of CpG ODNs into the vaccine did not enhance the production of antibodies. However, PBMC from cows immunized with CpG ODNs as the adjuvant had a significantly increased expression of IFN-γ (11 v.s. 4 folds) and decreased expression of IL-4 (2 v.s 10 folds) at the transcriptional level. Results indicated that inclusion of CpG ODNs as the adjuvant in an inactivated mastitis vaccine can enhance Th1 type immune responses, which might be beneficial to the elimination of bacteria by phagocytes.

Key Words: vaccine, CpG, mastitis

T15 Intramammary glucocorticoid treatment during LPS-induced mastitis. O. Wellnitz, M. Saudenowa, and R. M. Bruckmaier*, *University of Bern, Vetsuisse Faculty, Veterinary Physiology, Bern, Switzerland*.

Therapeutically used glucocorticoids have dose-dependent effects on the immune system. Glucocorticoids such as prednisolone (Pred) are traditionally added to antibiotic intramammary injectors aiming to support the cure of the inflamed mammary gland. The goal of the study was to evaluate the effects of Pred at the dosage commonly used in intramammary injectors on the immune system of the mammary gland and to evaluate the influence of Pred on the mammary immune response to E. coli lipopolysaccharide (LPS) stimulation. Five healthy lactating dairy cows with quarter somatic cell counts (SCC) below 120 $\times 10^3$ cells/mL were intramammarily infused with either Pred (10 mg), LPS (100 μg), Pred+LPS, or saline solution (9 g/l) in one out of four quarters, respectively. Udders were completely emptied by machine milking every 12 h. SCC of each quarter, tumor necrosis factor alpha (TNF) in milk, and lactate dehydrogenase (LDH) in milk were measured at 0, 3, 6, 9, 12, 24, and 36 h. mRNA expression of TNF, interleukin (IL)-1beta, IL-8, IL-10, and lactoferrin (LF) were measured in milk cells at 0, 12, 24, and 36 h using qRT-PCR. Differences between treatments were considered significant if P<0.05. SCC increased in LPS stimulated quarters independent of Pred within 6 h until the end of the experiment. TNF milk concentrations increased immediately after LPS stimulation independent of Pred lasting until the 12 h milking. Milk LDH was elevated at the 9 h sample in the LPS quarters and at the 12 to 36 h samples in the LPS+Pred quarters. SCC, TNF, and LDH remained unchanged in the control quarters and in the Pred treated quarters. mRNA expression of TNF, IL-1beta, IL-8, IL-10, and LF increased in LPS treated quarters independent of the presence of Pred. No changes in mRNA expression of these factors in milk cells were observed in controls and Pred treated quarters. In conclusion, stimulation of udder quarters with LPS had a pronounced effect on the mammary immune response. The investigated parameters responded to LPS as typically expected. Based on the measured parameters no immune modulating effects of Pred were observed in healthy udder quarters despite a slightly delayed LDH response.

Key Words: prednisolone, mammary immunity, cow

Breeding and Genetics: Dairy Cattle Breeding II and Rabbit Breeding

T16 Ketosis – Managable by breeding strategies? F. Rehbock[1], G. Freyer[2], F. Klug[3], and N. Vukasinovic*[4], [1]*Landesforschungsanstalt für Landwirtschaft und Fischerei M-V, Institut für Tierproduktion*, *Dummerstorf, Germany*, [2]*FBN, Unit Genetics and Biometry*, *Dummerstorf,* *Germany*, [3]*Alexandrastr. 4*, *Graal-Müritz, Germany*, [4]*Newsham Choice Genetics, STL Research Center*, *Chesterfield, MO*.

Improving health and fertility is an economic prerequisite for increasing longevity and life performance in dairy cows. According to the literature, ketosis has been reported to be the cause for 9 to 26% reduction

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in milk yield, 26 to 37% shorter productive life, and 27 to 46% increase in fertility problems. Ketosis can be a trigger for other diseases as well as an accompanying disease. Generally, it has been assumed that this metabolic disorder occurs in cows in the second lactation and upwards. However, recent studies indicated an increased rate of ketosis in the first lactating cows, which can be explained by their most negative energy balance in the early lactation, caused by intensive selection on high milk yield in the first lactation. This relation will be studied further. Previous studies found high genetic variability and a significant differentiation among offspring groups regarding ketosis incidence. That suggests that ketosis could be managed by breeding. Simulation studies showed that considering milk protein percentage in the selection index aimed at an optimum combination of yield and content traits let to a significant reduction of ketosis rate in the offspring. Sires with high breeding values (BV) for protein percentages had also a better BV for general health and an increased length of productive life. Further, metabolic and endocrine parameters were not related to energy balance and should not be used for selection purposes. On the other hand, selection for increased feed intake leads to reduction in energy deficit and thus indirectly to reduced rate of ketosis.

Key Words: ketosis, health, functional traits

T17 Genetic parameters and breeding values estimated under heterogeneous variances of two groups for type records of Holstein cows in Japan. T. Baba*[1], Y. Masuda[1], Y. Goto[2], and M. Suzuki[1], [1]*Obihiro University of A and VM*, *Obihiro, Japan*, [2]*The Holstein Cattle Association of Japan, Hokkaido branch*, *Sapporo, Japan*.

Type records in Japan are obtained from progeny test (PT) and herd enrollment for type (HE). However, farms participate in PT are selected randomly from those farms that provide milk records to the Hokkaido Dairy Milk Recording and Testing Association, but on the other hand, HE are voluntary. The objectives of this study were to estimate genetic parameters and breeding values for type traits when assuming that residual variances of its two groups are heterogeneous.Type traits and pedigree information of 705,453 animals were obtained. PT and HE of animals were 157,544 and 147,772, respectively. Genetic parameter and breeding value for two groups were estimated on assuming that only residual variances were difference (Model 1). And, as compared with results of Model 1, estimated values were obtained when their heterogeneity wasn't taken into account (Model 2). Breeding values for type traits were calculated from variance components obtained in Model 1 and 2. Breeding values estimated in Model 1 also assumed that residual variance are heterogeneous. Spearman's rank correlation cofficients of breeding values obtained from Model 1 and 2 were calculated.In examining the results in Model 1, we found that the residual variances estimated for type traits in PT were larger than in HE. Therefore, heritabilities in HE were higher values except in front teat placement. Heritabilities in Model 2 were likely to be mostly intermediate values between PT and HE. Correlations of breeding values between Model 1 and 2 were 0.999 in all traits for both sire and cow. For the top of breeding values in Model 2, there was little variability in correlations in cows and sires and when there was it was greater in cows. Therefore this result indicated that heterogeneity of residual variance in two groups didn't need to be assumed for sires.

Key Words: genetic parameter, breeding value, heterogeneous variance

T18 Estimation of genetic parameters for maturity of lactation using a test day model in Japanese Holsteins. Y. Masuda* and M. Suzuki, *Obihiro University of Agriculture and Veterinary Medicine*, *Obihiro, Japan*.

Test day milk yield for dairy cattle was affected by within-lactation and age (i.e., lactation curve and maturity of lactation). The straightforward approach to account for the contribution of maturity to additive genetic effects is to include the random regressions on age in the models. The objective of this study was to estimate genetic parameters for maturity of milk production by using a test day model with additive genetic curve over the life of Holsteins in Japan. Data included 1,011,634 test day records with first five lactations from 39,954 cows calving between 1985 and 2005. A single trait model was employed which contained random regressions both on days in milk (lactation curves) and on age at testing (curves for maturity). Permanent environmental effect was modeled as maturity curves and lactation curves common to all parities, while the additive genetic effect was only considered as a curve of maturity. Third order Legendre polynomials were fitted to animal genetic effects and two permanent environmental effects. Covariance components were estimated via Gibbs Sampling with GIBBS3F90 program. Heritability estimates of test day milk yield ranged from 0.20 to 0.25. Heritability of maturity rate was 0.09 when maturity rate was defined as the difference in total milk production from a cow 50-55 mo old and 30-35 mo-old cow. The model applied in this study provides a genetic curve for maturity for each cow. This approach needs lower computational demands for prediction of gentic maturity rate compared to multiple-parity random regression models.

Key Words: maturity, random regression, test day model

T19 Bayesian analysis of random regression using B-splines to model test-day milk yield of Holstein cattle. A. B. Bignardi*[1,3], L. El Faro[2], G. J. M. Rosa[3], F. F. Silva[3,4], V. L. Cardoso[2], P. F. Machado[5], and L. G. Albuquerque[1], [1]*Universidade Estadual Paulista*, *Jaboticabal, São Paulo, Brazil*, [2]*Agência Paulista de Tecnologia dos Agronegócios*, *Ribeirão Preto, São Paulo, Brazil*, [3]*University of Wisconsin*, *Madison*, [4]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brazil*, [5]*Universidade de São Paulo*, *Piracicaba, São Paulo, Brazil*.

A total of 152,145 weekly test-day milk yield records from 7,317 first lactations of Holstein cows distributed across 93 herds in southeastern Brazil were analyzed. Test-day milk yields were classified into 44 weekly classes of days in milk (DIM). The contemporary groups were defined as herd-year-week of test-day. The model included direct additive genetic, permanent environmental and residual effects as random, and fixed effects of contemporary group and age of cow at calving as covariable. Mean trends were modeled by a cubic regression on orthogonal polynomials of DIM, and additive genetic and permanent environmental effects were estimated using B-splines. Residual variances were modeled by step function with 6 variance classes. A total of 12 models, considering different combinations of linear, quadratic and cubic B-splines and up to six knots, were considered. Estimates of (co) variance components were obtained using Bayesian inference, assuming flat bounded priors, and employing a Gibbs sampling algorithm as implemented in the program RRGIBBS. A single chain with 400,000 samples was run for each model, discarding the first 10,000 samples as burn-in period. Models were compared by residual mean square error (MSE) as well as by a weighted (by number of days in interval) average of estimates of residual variances (RES). Results indicated a better fit for the model employing cubic B-splines to both random effects, with knots at 1, 10, 19, 26, 35 and 44 weeks (78 parameters). For this model,

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the heritability estimates were higher in the 1st week and between the 29th and 36th weeks, varying from 0.21 (3rd week) to 0.42 (1st week). Genetic correlation estimates between adjacent controls were high and close to one, and became smaller as the distance between controls increased. Negative genetic correlation estimates were observed between the 1st and the 6th weeks onwards and between the 2nd and 15th weeks onwards controls. Results indicated that a random regression model fitting basis functions of cubic B-splines is well suited to model the dynamic of milk yield over the lactation period.

Key Words: Bayesian, B-splines, test-day

T20 Study on genetic evaluation for linear type traits in Holstein cows. D.-H. Lee[1], S.-H. Oh*[2], and N. C. Whitley[2], [1]*Hankyong National University*, *Ansung, Gyeonggi, South Korea*, [2]*North Carolina A&T State University*, *Greensboro*.

The objective of this study was to determine better methods to evaluate genetic performance of individual animals with linear type traits of dairy cows, especially focusing on comparative traits, and to estimate actual data for genetic variances. Data used in this study was collected from 118,290 Holstein dairy cows between the years of 2000 and 2004 by Korea Animal Improvement Association (KAIA). Only data of more than five tested cows by Herd-Appraisal date and of individuals having more than ten daughters were included to increase the reliability of the data analyses. Outliers were removed and the records of individuals having one or both of parents were included in the analyses. The data used in the analysis is a total of 30,204 records of the selected traits, which was collected from 26,701 individuals having pedigree information. Herd-Appraisal date, year of age, lactation stage (grouped by month), and time lagged for milking were assumed as fixed effects on the model. Animal additive genetic effects considering pedigree relationship, and residual errors were assumed with random effects. Year of age at appraisal date was classified from one to nine years of age, assigning the value of nine years of age for animals that were greater than or equal to nine years of age. Five comparative traits were investigated in this study, general stature composite (GSC), dairy capacity composite (DCC), body size composite (BSC), foot and leg composite (FLC), and udder composite (UDC). In the present study, the greatest breeding values for GSC were estimated for Canada with the breeding values for USA lines increasing for 10 years starting in 1989 but tending to the decrease after that until 2004. For DCC, the breeding values for USA and Canadian lines showed similar patterns until 1999, after which the breeding values for the USA lines declined sharply. For BSC, Korea, Canada and USA data followed similar trends, but the breeding values of the USA decreased starting in 1999. In the US, selection indexes were based primarily on milk yield traits until methods for evaluating other traits began to emerge.

Key Words: Holstein, linear type traits, genetic evaluation

T21 Comparison of Swiss and New Zealand cows in a pasture-based milk production system. P. Kunz*, V. Piccand, and P. Thomet, *Swiss College of Agriculture*, *3052 Zollikofen, Bern, Switzerland*.

The high yielding dairy cow which is widespread in Switzerland is not suited to a production system based on roughage and very little concentrates. Investigations in Ireland and New Zealand have shown that the New Zealand Holstein Friesian population is well adapted to a pasture-based milk production system with seasonal calving. For this reason 72 pregnant Holstein Friesian heifers with at least two generations of New Zealand ancestry were imported from Ireland in 2006 and placed on twelve dairy farms in Switzerland. The objective was to investigate over 3 years (2007 - 2010) the attributes of cows adapted to a roughage-based seasonal production system under Swiss conditions. The amount of feed over one year was composed of 65 - 70% grazed pasture, 20 - 25% conserved roughage and at most 300 kg of concentrates. For comparison, pairs of Swiss and New Zealand (HF-NZ) cows were established with similar age (±6 months) and calving date (± 35 days) on the twelve farms. The Swiss cows consisted of 14 Brown Swiss (BS), 13 Fleckvieh (FV) and 18 Holstein Friesian (HF-CH) breeds. Body weight (BW) in the first lactation was higher in Swiss than in NZ cows (BS: 494 kg, HF-NZ: 472 kg; FV: 560 kg, HF-NZ: 473 kg, HF-CH: 572 kg, HF-NZ: 483 kg). Milk yield was higher in HF-CH (5441 kg energy corrected milk (ECM)) than in HF-NZ (4818 kg ECM) cows, but lower in FV (5027 kg ECM) than in HF-NZ (5508 kg ECM) and in BS (4366 kgECM) than in HF-NZ (5047 kg ECM) cows. Efficiency (kg ECM/ kg metabolic BW) was higher in HF-NZ (49.9) compared to BS (41.7) and higher in HF-NZ (54.3) compared to FV (43.8) but similar between HF-NZ (46.9) and HF-CH (46.7). The results show advantages for NZ compared to BS and FV cows but there are also individual Swiss cows with similar attributes. Additional variables are currently being analysed, which will hopefully help to achieve the aim of finding the key attributes of cows adapted to a pasture-based seasonal production system.

Key Words: lactating cows, breed, pasture

T22 Udder health traits as related to economic losses in Friesian cattle. H. G. El Awady[1] and E. Z. M. Oudah*[2], [1]*Kafr El Sheikh University*, *Kafr ElSheikh, Egypt*, [2]*Mansoura University*, *Mansoura, Egypt*.

A total number of 4752 lactation records of Friesian cows from 2000 to 2005 were used to determine the relationship between somatic cell count (SCC), udder health traits (UHS) and economic losses in milk production. Studied traits were milk yield traits {i.e., 305-milk yield, (MY), fat yield (FY) and protein yield (PY)} and udder health traits {i.e. SCC, mastitis (MAST) and udder quarter infection (UDQI)}. Least square analysis was used to estimate the fixed effects of month and year of calving, parity and stage of lactation on different studied traits. Data were analyzed using Multi-trait Derivative Free Restricted Maximum Likelihood to estimate the genetic parameters. The effects of SCC, MAST and UDQI on milk traits were also studied. Unadjusted means of MY, FY, PY and SCC were 3936, 121, 90 kg and 453,000 cells/ ml, respectively. All fixed effects were significantly (P<0.01) affect all traits except the effects of month of calving on both FY and PY was not significant. The SCC, MAST, UHS and UQI increased during winter and summer than spring and autumn. Additionally, SCC and MAST noticeably increased with advancing in parities. Increasing SCC from 300,000 to 3000,000 cells/ml increased UDQI from 5.5 to 23.2%. Losses in monthly and lactationally milk yields per cow ranged from 14 to 89 and from 105 to 921 kg, respectively. Losses in monthly and lactationally milk yields per cow ranged from 14 to 89 and from 105 to 921 kg, respectively. Losses in monthly and lactationally milk yields return per cow at the same level of SCC ranged from 24.5 to 155.75 LE and from 50.8 to 1612 LE, respectively. Heritability estimates of MY, FY, PY, SCC, MAST, UHS, UDQI were 0.31, 0.33, 0.35, 0.14, 0.23, 0.13, and 0.09, respectively. All milk production traits phenotypically and genetically correlated negatively with SCC, MAST and UDQI. It could be concluded that the SCC can be used as a perfect tool for UHS and milk quality. The use of SCC thresholds for parities and stages of lactation to detect intra-mammary infection improve quality parameters over a fixed threshold of 200,000 cell/ml.

Key Words: udder health, genetic parameters, dairy cattle

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T23 Comparing random regression models to analyse first lactation daily milk yield data in Murrah buffaloes by Bayesian inference. F. C. Breda Mello[*1], L. G. de Albuquerque[3], R. F. Euclydes[2], H. Tonhati[3], and A. B. Bignardi[3], [1]*Universidade Federal de Roraima*, *Boa Vista, Roraima, Brazil*, [2]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brazil*, [3]*Faculdade de Ciências Agrárias e Veterinária / Universidade Estadual Paulista*, *Jaboticabal, São Paulo, Brazil*.

Random regression models were used to estimate genetic parameters for test day milk yield in buffaloes using Bayesian inference. Data comprised 17,935 test-day milk records from 1,433 buffaloes. Different orders of fit of the Legendre orthogonal polynomials (LP) for the regression of random effects were considered. The term LP(ij) was adopted, where i and j indicate the order of fit for additive genetic and permanent environmental effects, respectively. All twelve models included fixed effects of contemporary group, milking number and age of buffaloes as covariate. In addition, residual variances were considered to be heterogeneous with six classes of variances. Models were compared based on residual mean square (MSR) errors and estimates of genetic parameters. The models LP46, LP56 and LP67 presented the smaller MSR estimates. The three models differed little in the partition of phenotypic variance into genetic, permanent environmental and residual variance. The differences in the heritability estimates between models were detected at the beginning (0.34 and 0.45) and at the end of lactation (0.40 and 0.50). Ignoring heritabilities for milk yield in the first and final weeks of lactation, the estimates ranged from 0.19 to 0.30, which was highest between week 9 and week 19. In general, models LP46, LP56 and LP67 yielded similar estimates of the genetic parameters, though, models LP67 and LP56 resulted in a higher degree of interdependence between additive genetic and permanent environmental random regression coefficients. This finding might explain the difficulty in convergence to distribution stationary observed when processing the analyses with these models. In addition, LP56 and LP67 yielded negative genetic correlations between the initial and mid-lactation (after week 9). The results indicated that a model using fourth- and sixth-order polynomials for additive genetic and permanent environmental effects, respectively, was appropriate to describe the changes in variances that occur along the buffalo lactation curve.

Key Words: Bayesian inference, buffaloes, milk yield

T24 Genetic parameters estimation for milk yield of buffaloes Murrah breed using parametric functions. F. C. Breda[*1], R. F. Euclydes[2], L. G. de Albuquerque[3], H. Tonhati[3], and A. B. Bignardi[3], [1]*Universidade Federal de Roraima*, *Boa Vista, Roraima, Brazil*, [2]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brazil*, [3]*Faculdade de Ciências Agrárias e Veterinária/ Universidade Estadual Paulista*, *Jaboticabal, São Paulo, Brazil*.

The objective of this study was to evaluate random regression models, which used different parametric functions and residuals variances classes for describing the milk production genetic variation of buffaloes, through genetic parameters estimates and broad range of model comparison criteria. Twenty seven random regression models were used to adjust 17,935 test day milk records of 1,433 buffaloes. The models include fixed effects of contemporary group, milking number and age of buffaloes as covariable. The additive genetic and permanent environmental effects were modeled through random regression models, using Wilmink and Ali and Schaeffer functions and Legendre orthogonal polynomial. Models were compared by Akaike's information criterion (AIC), Bayesian information criterion (BIC), Log likelihood function, information theoretic measure of model complexity (ICOMP), weighted residual variance (VRP) and an index that considered all model comparison criteria mentioned. The Ali and Schaeffer function (AS) presented better values of LMV, VRP and ICOMP to the model with 42 residuals variances classes (ASHE42); AIC and index for model with 17 residuals variances classes (ASHE17); and BIC for model that considered homogeneous residual variance (ASHO). However, ASHE42 didn't differ of ASHE17 for the likelihood test. Additionally, the additive genetic and permanent environmental variances and correlation produced by ASHE17 and ASHO were similar, not justifying the use of models more parameters to describe the changes in variances that occur along the lactation curve. Heritability estimates ranged from 0.18 to 0.31 and were higher at the week 8 to 17, indicating larger genetic variability in this period. The genetic correlation among test days were positive and decreased with the increase in lag between tests, except at the initial weeks. Random regression models were efficient in describing the milk production genetic variation, except at the beginning and at the end of the lactation. The ASHO is recommended to model the test day milk yield of Murrah buffaloes, in genetic evaluation programs.

Key Words: buffaloes, milk yield, random regression

T25 Estimation of heritability of monthly test day milk yield at different calving seasons in Holsteins of Khorasan province of Iran. R. Lotfi[*1], H. Farhangfar[2], and A. Shoorideh[3], [1]*Tarbiat Modares University*, *Tehran, Iran*, [2]*Birjand University*, *Birjand, Iran*, [3]*Jihade Agriculture of Razavi Khorasan*, *Mashhad, Iran*.

In this study, a total of 58513 monthly test day milk yields belonging to 13045 Iranian first lactation Holsteins during 2003-2008 and distributed in 113 herds were used to estimate heritability of monthly test day milk yield at different calving seasons. A test day repeatability animal model including fixed effects of herd-year of calving-stage of lactation (HYS), Holstein gene (linear covariable), age at calving (linear covariable) and also direct additive genetic and permanent environment random effects were used. Restricted maximum likelihood (REML) estimates of genetic and environmental variances were estimated for different calving seasons by DFREML software. The heritability estimates of monthly test day milk yield for different calving seasons of spring, summer, autumn and winter were found to be 0.16, 0.20, 0.23 and 0.09 respectively. Heritability estimates were highest for fall calvers followed by summer, spring and winter calvers. Different heritability estimates for calving seasons found in the present study indicate that additive genetic as well as environmental variations vary over the calving seasons suggesting that a greater genetic gain could be achieved over the generations as the genetic selection of candidates animals is practiced based upon the performance records of fall calvers.

Key Words: calving seasons, heritability, environment variation

T26 Genetic characteristics of energy balance for Iranian primiparous Holsteins using a fixed regression test day model. H. Farhangfar[*1], R. Lotfi[2], and M. H. Fathi Nasri[1], [1]*Birjand University*, *Birjand, Iran*, [2]*Tarbiat Modares University*, *Tehran, Iran*.

A fixed regression test day animal model was used to estimate genetic and environmental variance components of energy balance for Iranian primiparous Holsteins. The data set comprised a total of 51,402 monthly test day (thrice a day milking) milk yields, fat and protein percentages collected from 7111 first lactation cows calved between 2003 and 2008 in 113 herds distributed over the Khorasan province of Iran. Energy

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balance for individual months of lactation was estimated based upon a multiple regression model proposed by Friggens et al. (J. Dairy Sci., 2007, 90:5453-5467). In the data set, total number of sires and dams were 642 and 6117 respectively. Furthermore, average monthly test day milk yield, fat and protein percentage were 30.7 kg, 3.29% and 3.12% respectively. The overall mean monthly test day energy balance was found to be 21.3 MJ/d over the course of the lactation. In the model, herd-year-season of calving- stage of lactation was included as a contemporary fixed environmental effect. Moreover, linear covariates of Holstein genes, age at calving, milk yield, fat and protein percentages were taken into account. The cow number was also included in the model to account for direct additive genetic as well as permanent environmental random effects. DMU package was applied for genetic analysis of energy balance. The results showed that direct additive genetic, permanent and temporary (residual) variance components for energy balance were 3067, 687 and 74607 (MJ/d)2 respectively. Heritability and repeatability of the trait were found to be approximately 0.039 and 0.047 respectively indicating that a very low potential genetic variation is available for energy balance to be genetically improved by candidate's selection in the population.

Key Words: energy balance, genetic parameters, Iranian Holstein

T27 Estimation of genetic correlations among peak milk yield, energy balance and age at first calving for Iranian Holstein heifers. H. Farhangfar*[1], R. Lotfi[2], and M. H. Fathi Nasri[1], [1]*Birjand University*, *Birjand, Iran*, [2]*Tarbiat Modares University*, *Tehran, Iran*.

This study aimed to estimate genetic relationships among milk yield at peak time, energy balance and first calving age for Iranian first lactation Holstein cows. A total of 6994 records obtained from 6994 heifers calved between 2003 and 2008 was used. All milk records were thrice a day milking samples collected from 112 herds distributed over the Khorasan province of Iran. Energy balance for individual cows was estimated based upon a multiple regression model proposed by Friggens et al. (J. Dairy Sci., 2007, 90:5453-5467). In the data set, total number of sires and dams were 640 and 6028 respectively. In the data set, average milk yield, energy balance and first calving age were 32.28 kg, -316.45 MJ/d and 26.08 month respectively. A multivariate animal model was used to estimate variance and covariance components for genetic and environmental random effects through restricted maximum likelihood statistical method implemented in DMU package. In the model, herd-year-season of calving (as a contemporary fixed environmental effect) and linear covariate of Holstein genes were included. The cow number was also included in the model to account for direct additive genetic random effect. Heritability estimates of milk yield at peak time, energy balance and first calving age were 0.107, 0.008 and 0.047 respectively. At genetic level, peak milk yield was negatively correlated with energy balance (-0.68) and first calving age (-0.21). Genetic correlation between energy balance and first calving age was 0.83. Although peak milk yield had a negative environmental correlation with energy balance (-0.45) it was positively correlated with age at first calving (0.09). A negative environmental correlation (-0.05) was found between energy balance and first calving age.

Key Words: genetic correlation, energy balance, Iranian Holstein

T28 Mixed model analyzing of some environmental factors affecting average lactation somatic cell score in Iranian Holstein heifers. H. Farhangfar*[1], A. Abedini[1], K. Shojaeian[2], and M. H. Fathi Nasri[1], [1]*Birjand University*, *Birjand, Iran*, [2]*Zabol University*, *Zabol, Iran*.

To study the effects of some environmental factors affecting somatic cell score, a total of 13977 records from Iranian Holstein heifers (three times a day milking) was used. The number of cows, sires and dams were 13977, 871 and 12882 respectively. The records were collected from 183 herds between 2002 and 2006. The trait was defined as the average lactation somatic cell score (ALSCS) for individual cows. The somatic cell score was expressed as loge-transformed somatic cell count (logeSCC) from monthly test days measured in 1000 cells/ml. Mean ALSCS in the data file was 4.48. The data were subsequently analyzed by a mixed linear model. In the model, herd, year and season of calving, age at first calving and Holstein gene percentage (as linear covariates) and interaction between age and calving season were included as fixed environmental effects. Sire and the interaction between herd and sire random effects were also fitted in the model. Mixed procedure of SAS software was applied to fit the model. The results showed that herd and year of calving significantly (P<0.01) affected the ALSCS. The trait was not significantly affected by the Holstein gene percentage and two-way interaction terms included in the model. Although season of calving was found to be statistically a non-significant factor on the trait, Tukey-Kramer adjustment paired comparisons applied in the model revealed that spring and summer calvers had a significant (P<0.01) higher level of ALSCS than that of cows calving in fall and winter seasons. No significant differences were found between spring and summer and between fall and winter calvers. Restricted maximum likelihood estimates of sire, herd*sire and residual variance components for ALSCS were 0.011, 0.045 and 0.587 respectively indicating that a small genetic variation was available for the ALSCS.

Key Words: somatic cell score, Iranian Holstein, mixed model

T29 Genetic association between male fertility and prolificacy after artificial insemination with semen subjected to limited screening. L. L. Tusell*[1], R. Rekaya[2], M. López-Bejar[3], M. García-Tomás[1], O. Rafel[1], J. Ramon[1], and M. Piles[1], [1]*Unitat de Cunicultura, IRTA, Barcelona, Spain*, [2]*University of Georgia, Athens*, [3]*UAB, Barcelona, Spain*.

The aim of the study was to estimate the (co)variance components for male fertility (F), defined as success or failure of artificial insemination (AI) and male prolificacy (TB), defined as number of total born per litter, in a rabbit population selected for growth rate. Semen from 248 males was used to generate a total of 6,613 doses to inseminate 2,293 crossbred females applied 24 h after collection. Ejaculates were rejected only if individual motility was lower than 2 (from 0 to 5 scale), or if they had urine. A bivariate longitudinal mixed model for F and TB was assumed. Systematic effects included: concentration, building, batch-technician, physiological status of the female, and buck-age. Unrelated female, non-additive genetic plus permanent environmental effects of male, permanent environmental effect of male and day of AI, male additive genetic effect, and the residual term were included as random effects. Missing TB was predicted by data augmentation and Gibbs sampling was used for inference. The mean (s.d.) of the marginal posterior distribution for heritability was 0.12 (0.05) and 0.11 (0.04) for male F and TB, respectively, and the genetic correlation was very high 0.97 (0.05). Therefore, TB in prolific species could be considered as another measure of fertility. Under these conditions of AI, the additive genetic variation was higher than when natural mating or AI without any storage period was performed in rabbit, or after AI in other spe-

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cies. The random effect of male and day of AI was the most important for both traits, being 25.3% and 10.3% of the phenotypic variance for F and TB, respectively. This effect encompasses the strong source of variation that every ejaculate is subjected to during the handling of the male doses when AI is performed.

Key Words: fertility, prolificacy, (co)variance

T30 Breeding values of fat and protein content in inbred and outbred cows. J. Bezdicek*[1], J. Subrt[1], R. Filipcik[2], and J. Riha[1], [1]*Agrovyzkum Rapotin Ltd.*, *Rapotin, Czech Republic*, [2]*MZLU v Brne*, *Brno, Czech Republic*.

The aim of this study was to explore the effect of inbreeding depression on production in holstein cows. Production (in kg of fat and protein) was presented in the form of breeding values. The data included holstein cows (253,286) calved in the years 1990-2006 at farms in the Czech Republic. For proper comparison each inbred cow was assigned to at least one outbred equal (2.063 equals in sum). Inbred cows with their outbred equals were matched on characteristics such as identical sire, first calving interval occurrence on the same farm, first calving occurring in the same year and period (±2 months) and dam reaching the same breeding value of milk production. The goal was to make doublets of inbred and outbred cows which were very similar in terms of origin (the same sire, dam with similar breeding value) and which would also produce under the same conditions and time. Inbred cows and their matched outbred equals were subsequently divided according to the inbreeding coefficient of inbred cows into three groups (F_X=1.25%, F_X=2.0-3.125%, F_X=4.0-12.5%). The data were analysed using PROC GLM of SAS. Both the observed milk components showed significant decrease in breeding value when the level of inbreeding was higher. Compared to their coevals, inbred cows showed lower breeding values. Within the observed groups (F_X=1.25%, F_X=2.0-3.125% and F_X =4.0-12.5%) the average breeding value of inbred cows (and their coevals) was, in kg of protein 4.76 (5.32); 4.36 (5.24); 3.20 (7.19) kg. A similar tendency was also apparent in the breeding value of inbred cows (coevals) in kg of fat 4.17 (4.89); 4.42 (4.72) a 3.42 (7.11). These summaries show clearly not only a decrease in kg of fat and protein connected to increased level of inbreeding but also lower values reached by inbred cows compared to their coevals. In this study we have shown a decrease in breeding values of kg of fat and kg of protein in inbred cows compared to their noninbred coevals. When the coefficient F_X was high (4.0-12.5), the decrease was significant or highly significant.

Key Words: inbreeding, Holstein, protein

T31 Genetic correlations of dry matter intake with fat corrected milk yield, body weight, and body condition score in eleven commercial tie-stall dairy farms. S. M. Hall*[1], C. D. Dechow[1], J. M. Daubert[1], M. D. Dekleva[1], J. W. Blum[2], G. A. Varga[1], C. R. Baumrucker[1], and W. Liu[1], [1]*Pennsylvania State University*, *University Park*, [2]*University of Bern*, *Bern, Switzerland*.

The objective of this study was to estimate genetic correlations of dry matter intake (DMI), with fat corrected milk yield (FCM), body weight (BW), and body condition score (BCS) in commercial tie-stall dairy farms. Dry matter intake, BW and BCS were recorded within 7 days of monthly DHI milk testing on 11 Pennsylvania dairy farms. In order to minimize disruption to the farm feeding routine, herd managers were instructed to distribute feed evenly for all cows. Any feed subsequently

moved to or taken from a cow was recorded by the research technician, and all feed refusals were weighed the following morning. Records from cows more than 280 days in milk or in greater than fifth parity were removed. A total of 1,158 daily DMI, 1,790 BCS and 984 BW observations from 587 cows were available for analysis. Fat corrected milk was retrieved from all prior lactation for cows in second lactation or greater, resulting in 42,931 daily FCM observations. Total DMI, total FCM, average BW, and average BCS for the first 280 days of lactation were derived with solutions estimated with a 4-trait random regression model. Total lactation traits were then analyzed with a 4-trait animal model in ASREML. The mean total DMI for the first 280 days was 6,031 kg, whereas mean FCM was 9,718 kg. Mean BW and BCS were 674 kg and 2.94, respectively. Heritability estimates ranged from 0.12 for BCS and DMI to 0.33 for BW. Dry matter intake was genetically correlated with more FCM (0.74), higher BW (0.66) and higher BCS (0.38). Standard errors for the genetic correlations were high, ranging from 0.37 (FCM and BW) to 0.58 (BCS). Phenotypic correlations of DMI with FCM (0.32), BW (0.30) and BCS (0.07) were all positive. Feed intake can be measured in commercial tie-stalls with sufficient accuracy to estimate genetic parameters for DMI. Dry matter intake was genetically correlated with higher FCM and BW.

Key Words: feed intake, heritability, genetic correlation

T32 Phenotypic and genotypic variation of bovine immune responses in Cohort dairy herds across Canada. K. A. Thompson*[1], N. Karrow[1], K. Leslie[1], M. Quinton[1], F. Miglior[2], and B. A. Mallard[1], [1]*University of Guelph*, *Guelph, ON, Canada*, [2]*Canadian Dairy Network*, *Guelph, ON, Canada*.

Infectious diseases contribute to substantial economic loss in the dairy industry with human and animal health implications. The immune system is a tightly genetically regulated system that largely controls response to infectious disease. Including estimated breeding values (EBV) of immune response (IR) traits in a selection index has the potential to improve inherent animal health. Cows and pigs classified as high IR (HIR) in University of Guelph research herds had increased responses to commercial vaccines, and other health and production benefits. Cows ranked as HIR in a large US commercial dairy herd had lower disease scores (Hernandez, 2008 PhD thesis, University of Guelph, DeLapaz, 2008 MSc thesis, University of Florida). The objective this study is to evaluate antibody-mediated (AMIR) and cell-mediated IR (CMIR) in 58 commercial herds across Canada to determine effects on health and performance. This will provide novel insight into IR phenotypes on a national scale to confirm results of a single herd. In collaboration with the Canadian Bovine Mastitis Network and National Cohort of Dairy Herds 690 Holsteins were systematically immunized with both a type 1 and a type 2 antigen to stimulate AMIR and CMIR, respectively. To classify cows as high (H) or low (L) responders, serum antibody was measured by ELISA. Skin-fold thickness measurements were taken to evaluate delayed-type hypersensitivity (DTH), a measure of CMIR. Genomic analysis will be performed to determine genetic profiles associated with these diverse IR phenotypes. National health and production records are available for correlation with IR. Preliminary results show measurable differences in AMIR and CMIR between cows, herds, and provinces, making it possible to identify H and L responders. Identifying H and L responders (phenotypically and by EBV) and genetic profiles of these phenotypes may make it feasible to include IR in breeding indices to improve health.

Key Words: immune response, breeding, genetics

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T33 Study on genetic parameters of conception rate and heat detection rate of NY Holsteins. C. Huang[1], S. Tsuruta*[1], I. Misztal[1], and T. J. Lawlor[2], [1]*University of Georgia*, *Athens*, [2]*Holstein Association USA Inc.*, *Brattleboro, VT*.

The purpose of this study was to estimate genetic parameters of heat detection (HD), conception rate (CR) and days open (DO). Because HD is not observed directly, two indirect measures of HD were created: HD1=minimum [21/service interval (SI), 1] and HD2=[0 if SI>21; 1 if SI≤21]. Field data were obtained from DRMS, Raleigh, NC and included milk and service records of NY Holsteins. Edits included only farms with herd-year size >50 and with approximately even daily insemination pattern; the last step was to eliminate herds using timed AI. The final data set included 115,405 cows with 244,967 service records from 1999 to 2003. Traits considered were CR as the binary outcome of each insemination, DO as the interval of calving date to last service date with limits of 21-250d, and the 2 indirect HD measures. Traits analyzed in the bivariate model were one of CR and DO and one of HD1 or HD2. Effects included in the model were DIM, season, milk yield, age at calving, AI status as fixed effects, herd-year, service sire, additive sire, and cow's permanent environment as random effects. The heritability estimates of CR, DO, HD1 and HD2 were 3.6-4.1%, 3.2%, 1-1.6% and 3.5-3.8%, respectively. The estimated genetic correlations were -0.73 (CR, HD1), -0.40 (DO, HD1), -0.26 (CR, HD2), and -0.14 (DO, HD2). The different sign of correlation was expected with CR and DO because the correlation between these traits is strongly negative. Previous studies on DO, CR, HD1 and HD2 using simulated data indicated large variability of estimated correlations between fertility and heat detection measures as a function of missing data and treatment of censoring and that the most accurate estimates were between CR and HD1. Further model refinements are necessary for unambiguous determination of the sign of the genetic correlation between the CR and HD.

Key Words: conception rate, days open, heat detection

T34 Beta-casein enhancer (BCE) and evolutionarily conserved region 3 (ECR3) polymorphisms are associated with milk composition and management traits in dairy cattle. G. Rincon[1], M. Rijnkels[2], A. Islas[1], and J. F. Medrano*[1], [1]*University of California*, *Davis*, [2]*USDA/ARS Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine*, *Houston, TX*.

The bovine casein gene locus is located on BTA6 and comprises four genes: CSN1S1,CSN2, CSN1S2 and CSN3. In addition to the casein genes, there are five physically linked genes and a number of non-coding conserved regions that may play a role in regulation of gene expression. Beta-casein enhancer (BCE) and evolutionarily conserved region 3 (ECR3) are potential regulatory regions located in the casein gene cluster that are present in most species. In the present study we resequenced BCE and ECR3 genomic regions in a sample of 8 Brown Swiss, 8 Holstein and 8 Jersey cows that were unrelated in a three generation pedigree. Three SNPs were found in the BCE region (SNP_20586, SNP_20752, SNP_20827) and two SNPs were found in the ECR3 region (SNP_9109, SNP_9518). The SNPs were genotyped and tested for associations with milk production and management traits in 800 Holstein bulls from the UC Davis archival collection and 300 Holstein cows from farms in the California Central Valley. Bull PTA values were obtained from the USDA Animal Improvement Programs Laboratory (Beltsville, MD). Milk composition analysis was performed to obtain phenotypes in the cow population. The association analysis was developed using the SNP Variation Suite from Helixtree to test allelic associations with phenotypic variables. Significant results (p<0.01;

FDR<0.05) were observed for SNP_20752 in the bull population for milk yield, protein yield, productive life and somatic cell score PTA traits. The same SNP was also significantly associated with protein and casein percentages in the cow population. SNP_20586 and SNP_9109 were associated with PTA protein percentage in bulls. These results emphasize the importance of SNP variation in the BCE and ECR3 regions in relation to milk production and management traits in dairy cattle. To provide support to this finding, we are examining if different genotypes for BCE and ECR3 have an association with gene expression differences in the casein locus.

Key Words: casein cluster, milk production, management traits

T35 Comparison of superovulation, embryo recovery, and embryo transfers in lactating dairy cows and heifers. M. B. Gordon*, T. Pretheeban, and R. Rajamahendran, *University of British Columbia*, *Vancouver, BC, Canada*.

While reproductive performance in lactating dairy cows have dramatically decreased, fertility in dairy heifers still remains high. Some factors which may contribute to poor fertility include: poor oviductal and uterine environments, altered follicular dynamics and oocyte quality, reduced corpus luteum function and increased embryo mortality. The objectives of this study were to compare heifers to 2nd and 3rd parity cows with respects to response to superovulation and embryo recovery, and compare the uterine environment by comparing pregnancy data following the transfer of embryos collected from heifers to recipient heifers and 2nd and 3rd parity cows. Beginning 10 to 11 days after synchronization of estrus, standard superovulation treatment was carried out on 2nd and 3rd parity lactating dairy cows (n=23) and virgin heifers (n=32), with subsequent non-surgical embryo recovery 6 to 7 d after a timed double insemination (a.m. and p.m.). Heifers had a significantly higher response to superovulation treatment as indicated by the number of corpus lutea present on the day of embryo recovery (11.6 ± 1.0 vs. 5.8 ± 1.2; P=0.0007). The average number of viable embryos recovered from animals was 7.1 ± 0.9 and 2.7 ± 1.1 (P=0.002) for heifers and cows, respectively. Heifers also had significantly higher progesterone concentrations on an individual CL basis than cows on day 4 (3.82 ± 1.08 vs. 0.43 ± 1.23 ng/mL; P=0.05) and day 6 (3.11 ± 0.57 vs. 0.90 ± 0.65 ng/mL; P=0.02) post-insemination. Recipient animals were estrus synchronized for subsequent embryo implantation 6 to 7 days after estrus. Of the animals that were prepared for implantation, 63% of parity cows (n=27) and 60% of the heifers (n=35) were at the proper stage of the estrous cycle to receive embryos. Pregnancy rates of cows and heifers were 53.3% and 52.4%, respectively. This study suggests that heifers may ovulate superior viable embryos, and may produce better functional corpus lutea in the first 6 days after estrus, as indicated by high progesterone concentrations.

Key Words: superovulation, embryo transfer, fertility

T36 Effect of sexed semen on conception rate for Holsteins in the United States. H. D. Norman and J. L. Hutchison*, *Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

Effect of sexed-semen breedings on conception rate was investigated using US Holstein field data from January 2006 through October 2008. Sexed-semen breeding status was determined by a National Association of Animal Breeders' 500-series marketing code or by individual breeding information in a cow or heifer reproduction record from a dairy records processing center. Marketing-code 514 was not identified as sexed semen

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because that technology is a gender-bias semen that results in only 10% more female births than semen that has not been sex sorted. Sexed-semen breedings resulted in 91% female offspring. Only breedings with confirmed outcomes were included: 1,190,587 heifer breedings (of which 119,920 were sexed-semen breedings) and 9,835,105 cow breedings (of which 106,393 were sexed-semen breeding). Overall mean conception rates for sexed-semen breedings was 44% for heifers (compared with 57% for conventional semen) and 26% for cows (compared with 30% for conventional semen). For heifers, 80% of sexed-semen breedings were first breedings; 16%, second breedings; and 3%, third breedings, with conception rates of 45, 39, and 35%, respectively. For cows, 43% of sexed-semen breedings were during first lactation and 28% during second. For first-lactation cows, 51% of sexed-semen breedings were first breedings; 23%, second breedings; and 12%, third breedings, with conception rates of 29, 27, and 25%, respectively. For second-lactation cows, 47% of sexed-semen breedings were first breedings; 25%, second breedings; and 13%, third breedings, with a mean conception rate of 26% for the first 3 breedings. For bulls with >300 breedings, correlations between sire conception rates from sexed and conventional semen were 0.19 for heifer breedings (67 bulls) and 0.49 for cow matings (51 bulls). Corresponding correlations for bulls with >800 breedings were 0.32 (31 bulls) and 0.78 (15 bulls).

Key Words: sexed semen, conception rate, Holstein

T37 Derivation of factors to estimate daily fat, protein, and somatic cell score from one milking of cows milked twice daily. M. M. Schutz*[1], J. M. Bewley[2], and H. D. Norman[3], [1]*Purdue University, West Lafayette, IN*, [2]*University of Kentucky, Lexington*, [3]*USDA-ARS, Beltsville, MD*.

The objective was to derive factors to predict daily fat (F) and protein (P) yield and somatic cell score (SCS) when milk is sampled once per d for cows milked twice per d. Milk samples were collected for each milking on test-day by Dairy Herd Improvement personnel from herds recording milking times and milk weights automatically. Following edits, 2190 records of 1869 first lactation (L1) cows and 3363 records of 2931 later lactation (L2) cows in 25 2x herds remained. Factors currently in use to adjust single milking F and P for milking interval (MINT) were applied. No adjustments are currently in use for SCS. Also, 3 methods were compared to estimate factors or equations to predict daily F, P, and SCS. Factors were estimated as the ratio of the sum of daily yield to the sum of partial yield within a parity-MINT class (24 intervals in 2 parities) [Method 1] or as the sum of the ratios of daily yield to partial daily yield for each cow-day divided by the number of cow-days within parity-MINT class [Method 2]. Resulting factors from both methods were smoothed, applied to data, and residuals were regressed on days in milk (DIM). Regression equations (n=112) were also developed within parity-MINT-DIM classes (2x7x8) [Method 3] to jointly account for MINT and DIM. Separate factors were derived for am and pm milking for each trait in L1 and L2. Method 3 resulted in consistently stronger correlations between estimated and actual yields, and smallest variances of estimates, and root mean squared errors (rMSE) for all components in both milkings in L1 and L2. Method 3 resulted in rMSE of 0.12 (F, L1), 0.17 (F, L2), 0.07 (P, L1), and 0.10 (P, L2) kg for am milkings; compared to rMSE of 0.15, 0.20, 0.08, and 0.11 kg from current factors for the same traits in L1 and L2. Differences in rMSE were similar for F and P for the pm milkings and for SCS for both milkings. Work is ongoing to determine whether equations from Method 3 will allow accurate estimation of daily milk, F, P, and SCS when applied to other herds.

Key Words: milking interval, adjustment factor, milking frequency

T38 Best prediction of lactation yields accounting for regional and seasonal differences. J. B. Cole and D. J. Null*, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*.

In the United States, lactation yields are calculated using best prediction (BP), a method in which test day (TD) data are compared to breed- and parity-specific herd lactation curves that do not account for differences among regions of the country or seasons of calving. This may result in biased estimates of lactation yields. Data from 5,345,621 lactations of 348,123 Holstein cows with lactation lengths between 250 d and 500 d, records made in a single herd, at least _ve reported TD, and twice-daily milking were extracted from the national dairy database (NDDB). Herds were assigned to one of six regions of the country, individual lactations were assigned to three-month seasons of calving, and lactation curves for milk and fat yield were estimated by parity group (first versus later) for regions, seasons, and seasons within regions. The resulting curves were added to the BP software and tested against a validation dataset of 891,809 lactation records from 400,000 Holstein cows sampled at random from the NDDB. Mature equivalent (ME) milk and fat yields were calculated using the standard curves and the new curves. Differences between 305-d ME yields were calculated and tested for significance. Yields calculated using 50-d intervals from 50 to 250 DIM and using all TD to 500 DIM allowed comparisons of predictions for records in progress (RIP). Differences in ME milk ranged from 0 to 51 kg and were slightly larger for first- than later-parity cows, but were not significant (P > 0.05) in any case. Fat yields also did not differ significantly. Correlations of projected yields for 50-d intervals with yields using all TD data were similar across analyses. Differences among predictions averaged 57 kg lower for the new curves than for the standard curves using TD in the first 50 DIM, decreasing to 20 kg as TD from subsequent 50-d intervals were added. Complete lactation yields were similar for all curves, but projected yields for RIP were slightly more accurate when adjusted for regional and seasonal differences.

Key Words: best prediction, milk yield, regional effects

T39 Trends in international flow of Holstein genes. R. L. Powell*, J. R. Wright, and H. D. Norman, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*.

Holstein genes spread from Europe to much of the world through live cattle more than 100 yr ago. By the advent of artificial insemination, selection emphasis in North America had led to a specialized dairy strain that was in demand internationally. From 1995, genetic evaluations through Interbull more accurately identified the best bulls across countries. Many of the same bulls were used in many countries, particularly to sire sons for progeny testing, so a number of countries had bulls worthy of international consideration. Data from over 100,000 Holstein bulls and 27 countries in the January 2009 Interbull evaluation were used to examine changes over birth years in the direction of gene flow by examining the country of AI bulls' sires. Birth years ranged from 1986 to 2003. Percentage of bulls having a foreign sire was surprisingly steady, being 56% in 1986 and 55% in 2003, after a high of 65% for 1995 to 1997. Through 1991, nearly all AI bulls progeny tested in France, Germany, Italy, and The Netherlands were sired by bulls from other countries. For bulls from those countries born in 2003, 49 to 87% were by foreign sires. Although the United States used fewer foreign sires of sons, that portion has been about 25% for bulls born this decade. The United States provided the most foreign sires of sons every year, as high as 86%, with Canada second in most years; the two together contributed 56 to 97%. The "hot bulls" syndrome is evident from the dramatic changes in country of foreign sires from one

year to year. The Netherlands had not accounted for more than 4% of foreign sires until 12% in 1999 followed by 24, 18, and dropping to 5%. Frequency of German sires went from 1% in 2000 to 12% in 2001 while Italian sires went from 1% in 2001 to 14% in 2002. Sourcing of sires is a dynamic situation with the proportion of sires from a given country rapidly changing. The constant is that foreign sires produce the majority of Holstein bulls progeny tested. The portion of foreign sires has not shown much trend, but certainly the accuracy with which sires are chosen has improved.

Key Words: sires of sons, Interbull, genetics

T40 Holstein, Jersey and its cross affects fatty acid composition under grazing conditions. R. A. Palladino[1], F. Buckley[2], J. J. Murphy[2], R. Prendiville[1,2], and D. A. Kenny*[1], [1]*University College Dublin, Belfield, Dublin 4, Ireland*, [2]*Teagasc, Moorepark Dairy Research Centre, Fermoy, Co. Cork, Ireland.*

Dietary n-3 polyunsaturated fatty acids (PUFA) and conjugated linoleic acid (CLA) have beneficial properties for human health. Dairy cow breed affects PUFA concentration in milk but most work to-date has been conducted under TMR based systems. Additionally, there is little information about the cow breed and heterosis on concentrations of milk PUFA. The objective of this study was to compare milk FA concentration of two dairy cow breeds (Holstein and Jersey) and their F1 hybrid managed under a grazing system. Eighty-one spring-calving dairy cows (27 cows per treatment) were managed under a predominantly perennial ryegrass pasture during two experimental periods (June and July). Milk yield, fat, protein, lactose and fatty acids (FA) were recorded once a week during each period. Milk FA were analyzed by gas chromatography. Data were analyzed by ANOVA. Cow was used as random effect. Statistical model was $Y_{ij} = \mu + breed_i + period_j + breed_i \times period_j + error_{ij}$. No interaction was found for any of the variables studied over the two periods. Holstein cows had the highest milk yield, Jersey the lowest with the crossbred animals intermediate (P<0.01). Milk fat and protein were highest for Jersey, lowest for Holstein and the crossbred animals intermediate (P<0.01). Holstein had higher n3:n6 ratio (P<0.05), C18:2 n6, and the Ã¢Ë†â€9 desaturase index (P<0.01). Milk CLA also tended to be higher in Holstein (Table 1). Under the grazing conditions employed here, Holstein dairy cows produced more milk with a higher content of CLA, probably due to the higher mammary gland Ã¢Ë†â€9 desaturase enzyme activity observed. No evidence for any heterotic effects on milk related variables measured was found from this study.

Table 1. Effect of breed on milk FA composition

FA (g/kg of Total FA)	Holstein	Jersey	H x J	SED[1]	Significance[2]
t-11 C18:1 (VA)	44.4	45.2	38.4	3.95	NS
C18:2	5.9[a]	4.7[b]	4.6[b]	0.38	**
CLA	17.8	15.3	14.7	1.36	†
C18:3	6.6	6.0	6.6	0.35	NS
n3:n6	0.77[b]	0.99[a]	1.01[a]	0.100	*
Δ9 desaturase index[3]	0.09[a]	0.08[b]	0.08[b]	0.004	**

[a,b]Means within a row with different superscripts differ (P<0.05); [1]Standard error of the difference; [2]NS = not significant; † = P<0.10; * = P<0.05; ** = P<0.01; [3]C14:1/(C14:0 + C14:1).

Key Words: fatty acids, dairy breeds, conjugated linoleic acid

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T41 Logistic analysis of some environmental factors affecting multiple birth performance of Iranian indigenous goats. H. Farhangfar*[1], Y. Shamshirgaran[2], M. Esfandiari[3], and M. H. Fathi Nasri[1], [1]*Birjand University, Birjand, Iran*, [2]*Ferdowsi University of Mashhad, Mashhad, Iran*, [3]*Agricultural Jihad Organisation, Birjand, Iran.*

To study the effects of some environmental factors influencing multiple birth performance of Iranian indigenous goats a total of 815 records collected from 2000 to 2007 was used. All data were obtained from a breeding flock of Cashmere indigenous goat in southern Khorasan province of Iran. The number of kids and dams in the whole data set was 815 and 405 respectively. In the data, single birth was coded as 1 and the litter size greater than one was set to 2. A logistic regression model was subsequently used to analyze the multiple birth performance of the population. In the model, fixed environmental factors of year of kidding (2000-2007), number of kidding (kidding 1, 2, 3 and 4), and kid sex (male and female) along with linear covariate of kid weight at birth (2.11 kg, SD=0.44 kg) were included. The model was fit using logistic procedure of SAS software. The results showed that the number of kids born was significantly (P<0.01) influenced by all the factors considered in the model. Point estimation of odds ratio for the birth weight was found to be 0.077 indicating that the ewes with heavier kids tend to have more probability for the multiple birth. Taking account of female sex as the reference level, the odds ratio for male kid was 1.853 showing that ewes with multiple birth performance are expected to have a greater number of male progeny. The results found in this study also revealed that multiple birth probability was greater for the ewes kidding at the third time, followed by the fourth and second times than that of the first-kidding ewes.

Key Words: Iranian indigenous goat, multiple births, logistic analysis

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T42 A neural networks approach for prediction fertility in rabbit using semen quality parameters. L. L. Tusell*[1], R. Rekaya[2], M. López-Bejar[3], M. García-Tomás[1], C. Andreu[3], O. Rafel[1], J. Ramon[1], and M. Piles[1], [1]*Unitat de Cunicultura, IRTA, Barcelona, Spain*, [2]*University of Georgia, Athens*, [3]*UAB, Barcelona, Spain.*

Several statistical techniques based on linear and nonlinear regression have been used to relate seminal quality with fertility showing limited predictability power. In this study, a Neural Networks approach is proposed to predict fertility based on seminal quality parameters. A total of 107 ejaculates from 27 bucks were used for insemination at two different dose concentration (10 and 40 millions of spermatozoa per mL) 24 h after collection. Ejaculates were rejected only if individual motility was lower than 2 (from 0 to 5 scale), or if they had urine. A feed-forward network with one hidden layer was used in the context of a multi layers feed-forward networks. Randomly, 79 records were used for the training process and the remaining 28 records were used for the validation step. Concentration of the ejaculate, individual motility, percentage of viable spermatozoa, acrosome-reacted spermatozoa, spermatozoa with morphological abnormalities of head, neck-midpiece and tail and spermatozoa with cytoplasmic droplet, age of the male and dose concentration were used as input nodes. An extra input node with fixed value equal to one was added. The hidden layer had 4 nodes. Fertility, defined as % kindling rate, was the only output of the network. Weights were updated after all the observations in the training set were presented to the network. A 100,000 iterations were performed with a learning rate of 0.45. The back propagation algorithm was used to optimize the network weights during the training process. The network approach performed reasonable well in predicting the kindling rate. In fact, the correlation

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between the observed and the predicted values using the training and the validation sets were 0.71 and 0.53, respectively.

Key Words: neural network, fertility, semen quality

Dairy Foods: Dairy Foods Processing/Cheese/Dairy Micro

T43 Understanding and controlling flavor and color development resulting from non-thermal browning (NTB) in cheese. A. Lopez-Hernandez*, N. Van Epps, and S. A. Rankin, *University of Wisconsin, Madison.*

Under certain conditions, some cheeses brown (i.e. parmesan, gouda) during the course of aging yielding concomitant changes in flavor and color. Very little definitive science exists to describe, define or control the reaction chemistry of non-thermal browning (NTB) in cheese from either the flavor or pigmentation perspective. There is a number of suggested pathways that attempt to explain these changes. Such pathways involve factors such as redox potential, available oxygen, the presence of α–dicarbonyl compounds, amino acid type and concentration, Mn^{2+} ions, and microbial tyrosinase activity. However, NTB still exists in the industry with no clear means of understanding or controlling its development. The aim of the present study was to define the chemical structures of flavorants and pigments generated through non-thermal browning mechanisms in cheese as an aid to understand and control its development. Our results showed that the pigments are stable to air exposure and soluble in some non-polar solvents, such as pentane and pentane-methylene chloride (2:1 v/v). The UV-Visible spectra of the extracts showed maximum absorption peaks at 400 and 450 nm. Volatile characterization revealed compounds specific to brown cheeses including lactones, ketones and pyran derivatives. The relative abundance of the compounds was found to be higher in those cheeses where browning and more intense aroma was more evident. Parallel studies in a cheese model systems demonstrated that α–dicarbonyls specific to fermentation showed little effect on the development of brown color. Extensive heat treatment of the cheese milk source also showed little effect on the development of brown pigmentation.

Key Words: non thermal browning, parmesan, maillard reaction

T44 Transcriptomic analysis of Camembert cheese fungal activity. C. Viel*, F. Boileau, A. Thériault, and S. Labrie, *Département des sciences des aliments et de nutrition, Centre de recherche en sciences et technologie du lait (STELA), Institut des neutraceutiques et des aliments fonctionnels (INAF), Université Laval, Québec, QC, Canada.*

Camembert cheeses are dynamic microbial ecosystems that evolve during ripening. The overall metabolic activity of the microbiota largely determines the quality of the cheeses. However, little is known about the genes expressed by the surface microbiota. We studied the transcriptome of a ready-to-eat Camembert cheese to gain a better understanding of the major activities of the fungi responsible for rind formation. Samples were collected from the rind of a Camembert cheese, inoculated on selective media, and three isolates were microbiologically characterized and further identified as *Penicillium camemberti*, *Geotrichum candidum*, and *Debaryomyces hansenii* by rDNA sequencing. High quality total RNA was obtained from the same rind and was analyzed by RT-PCR using a Bioanalyzer 2100. Specific primers revealed that the three species could be amplified from total RNA. mRNA was purified from the total RNA and retro-transcribed. A cDNA library was constructed. The sequence of the clones were compared to those in public databases.

Putative gene functions were attributed as follows: 26% were involved in metabolism, 20% in translation, 10% in cell signaling, 4% in survival (defense, stress, and repair), 4% in ion transport, 4% in transcription, 2% in apotosis, 2% in cell transport, and 3% in other functions, while 25% had unknown functions. The results of the present study will help guide the selection of biomarker genes that can be used to monitor fungal activities during cheese ripening.

Key Words: transcriptome, fungi, camembert

T45 Comparison of Hispanic cheeses from US and country of origin manufacturers. L. A. Jimenez-Maroto[1], A. Lopez-Hernandez*[1], B. Maldonado[2], and S. A. Rankin[1], [1]*University of Wisconsin, Madison,* [2]*Tecnológico de Monterrey, Campus Querétaro, Querétaro, México.*

There is anecdotal information that US-made Hispanic cheeses are criticized by Hispanic consumers for not being authentic compared to cheeses made in their countries of origin. In order to determine what characteristics define the authenticity of Hispanic cheeses several assessments were conducted including microbial testing, sensory profiles, chemical composition, and functional character. Commercial samples of three different types of Hispanic cheeses (fresh, pasta filata, aged) were acquired from domestic (n=44) and country of origin (n=40) manufacturers from three regions (Mexico, Central America, Caribbean). Proximate analysis was conducted using standard methods. A modified melt-flow apparatus was used to ascertain the melt character. Quantitative descriptive analyses (QDA) of cheese flavor, texture, and appearance were conducted by trained panelists (n=13) and the results analyzed using principal component analysis (PCA) and canonical analysis. Consumer panels comparing US and Mexican samples were conducted for each of the cheese types studied. None of the samples tested positive for the presence of food pathogens. Country of origin cheeses had higher moisture and pH, lower salt, similar lipid and protein content. Some of the non-US cheese products contained non-dairy ingredients, such as vegetable oils. Melt character of fresh and aged cheeses showed significant differences between domestic and country of origin samples, while pasta filata cheeses showed no significant differences. There were significant differences in salt, bitter, buttery, cowy, milkfat, oxidized, unclean and rancid flavor attributes. Consumer panels showed that Mexican consumers similarly rated US-made cheeses as highly authentic when compared to the Mexican-made samples. These results provide insight into the characteristics that define the authenticity of the Hispanic cheeses analyzed. Knowledge of these characteristics will aid U.S. manufacturers to produce a Hispanic cheese with more authentic qualities that will satisfy the demands of their Hispanic consumers.

Key Words: Hispanic cheese, sensory profile, melt character

T46 Partitioning of omega-3 fatty acids in Cheddar cheese curd and whey. C. Brothersen*, D. J. McMahon, and B. Pettee, *Western Dairy Center, Utah State University, Logan.*

Full-fat Cheddar cheese was made with milk fortified with omega-3 fatty acids and the partitioning of omega-3 fatty acids into the curd

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