based on three-year pooled data. However, the hip height at birth is not significantly correlated to the hip height at weaning ($P > 0.05$). These results demonstrated great performances of Angus Plus calves raised on 100% pasture in Hawaii subtropical climates. The combination of Angus with Brangus to produce Angus Plus cattle have the potential to contribute to the growing demand of forage-based production of high-quality natural and organic beef for the local and international markets

Key Words: Angus Plus cattle, Grazing, Growth

M20 Age at first calving and the longevity of beef cows of different breeds. F. Szabo* and I. Dakay, *University of Veszprem Georgikon Faculty of Agriculture*, *Keszthely, Hungary*.

The age at first calving, lifespan and longevity of cows have great importance in beef cattle husbandry because the cost of raising weaned calves depends largely on age at first calving and how long a cow remains in production. If cows are productive extendedly and raise more progeny, specific costs of raising each calf decrease proportionally. Consideration of lifespan and, specifically, longevity plays an important role in practical breeding. The objective of the present work was to evaluate the impact of breed type on age at first calving (AFC), age at culling (ACU), and longevity (LONG; the period between first calving and culling) in beef cows. A database of 2115 cows belonging to five breeds (Hungarian Grey, Hereford, Aberdeen Angus, Limousin and Charolais) and two crossbred genotypes (Simmental x Hereford F1, Simmental x Limousin F1) born between 1977-1992 was evaluated using multivariate analysis considering breed type, birth year, and birth month. The mean values of AFC, ACU and LONG obtained were 2.71, 9.47 and 6.77 years, respectively. Breed/genotypes and birth year had significant influence ($P < 0.01$) on each evaluated trait, whereas birth month statistically affected only the AFC. The period between first calving and culling (LONG) of the mentioned breed types were 8.95, 9.08, 8.28, 7.81, 7.91, 10.79, and 5.55 years, respectively.

Key Words: Age at first calving, Age at culling, Lifespan

M21 Determining the corn replacement value of wet brewers grains for feedlot cattle. J. W. Homm*, L. L. Berger, and T. G. Nash, *University of Illinois*, *Urbana*.

Due to increasing energy costs, breweries are marketing brewers grains as wet feeds. The purpose of this trial was to evaluate the corn replacement value of wet brewers grains (WBG) for finishing cattle. Two hundred heifers (287.8 ± 34.5 kg) were randomly assigned to four dietary treatments containing either 0%, 15%, 30%, or 45% WBG on a DMB. The control diet consisted of 15% corn silage, 75% whole high-moisture corn and 10% soybean meal-based supplement on a DMB. The control diet was balanced to contain 13.0% crude protein, 0.4% calcium, 0.3% phosphorus and 0.6% potassium. Two full weights were averaged at the initiation of the trial and carcass adjusted live weight was used to determine the final live weight. Heifers were pen-fed (5 pens per treatment, 10 heifers per pen) for 160 d. Live weight and feed efficiency were not significantly different between dietary treatments. Dry matter intake and average daily gain were quadratic ($P < 0.01$), where 15% and 30% WBG heifers consumed more feed and grew faster than 0% and 45% WBG heifers. Additionally, 15% and 30% heifers consumed more ($P = 0.01$) feed than 45% heifers. Heifers receiving the 15% and 30% WBG diets gained more ($P < 0.01$) than 45% heifers. Ultrasonic marbling was higher ($P < 0.05$) for heifers fed 0% WBG than heifers fed WBG at the start of the trial. Heifers fed 30% WBG had higher ($P = 0.03$) ultrasonic marbling scores than heifers fed 15% at the start of the trial. After 112 d on feed (DOF), heifers fed 30% WBG had higher ($\mathrm{P} = 0.03$) ultrasonic marbling scores than heifers fed 15% WBG. At harvest, carcass marbling tended ($\mathrm{P} = 0.06$) to be higher for heifers not fed WBG than those fed WBG. Carcass REA was larger ($\mathrm{P} = 0.05$) for the 15% and 30% WBG heifers than the 45% WBG heifers. Kidney, pelvic, and heart (KPH) fat increased linearly ($\mathrm{P} < 0.05$) as WBG increased in the diet. Additionally, 15% heifers had less ($\mathrm{P} = 0.04$) KPH fat than 30% heifers. These data indicate that feeding 15-45% WBG in feedlot diets supports performance and carcass characteristics similar to cattle fed a typical high-moisture corn finishing diet.

Key Words: Wet brewers grains, Beef, Performance

Breeding and Genetics I

M22 Crossbreed dairy cattle production in the tropical area in Mexico. R. Lopez*, C. Vite, J. G. Garcia-Muñiz, and P. A. Martinez, *Universidad Autonoma Chapingo*, *Chapingo, Mexico*.

The objective was to determine the effect of grade of crossing (G), lactation number (LN), calving season (CS), parity (P) and its interactions on milk yield per lactation (TMY), daily MY (DMY), MY per day of calving interval (CIMY), peak milk yield (PMY), days to peak milk yield (DPMY), lactation length (LL), age at first calving (AFC), days open (DO), and calving interval (CI) of ¾ Zebu (Z) x ¼ Swiss (S), 3Z1S; ¾ Holstein (H) x ¼ Z, 3H1Z; ¾ S x ¼ Z, 3S1Z; ½ H x ½ Z, HZ; and ½ S x ½ Z, SZ cows. Records of 237 lactations of 230 cows collected from 1997 to 2004 in three commercial dual-purpose farms of Veracruz, México, were analyzed. Cows were grazing tropical pastures and were supplemented with 3.0 kg of TMR per cow per d at milking time. Moreover, cows were machine milked twice a day applying 0.25 mL of commercial Oxytocin (Oxytocin-S, Intervet, Tonisvorst, Germany) at each milking to help milk down. Milk yield per lactation, DMY, CIMY, PMY, DPMY, LL, DO and CI were analyzed with a linear model of fixed effect including G, LN, P, and CS; whereas AFC was analyzed with a linear model of fixed effects including G, LN, and year and season of birth of cows. Results indicated cows genotype had affected ($P < 0.05$) TMY and LL. In contrast, cow genotype did no affect ($P > 0.05$) DMY, PMY, CIMY and DPMY . The range of MY in 270 days of milking was 2719 ± 511, 4961 ± 416, 4349 ± 231, 4070 ± 238, and 3676 ± 175 kg for 3Z1S, 3H1Z, 3S1Z, HZ and SZ, respectively. Likewise, LN did influence TMY, DMY, PMY, and CIMY, however, did not show any impact on LL. In contrast, P and calving season did not have an influence on all the traits studied. Cows 3H1Z had better AFC than 3S1Z, HZ, and SZ (33.0 vs. 39.6, 33.2 and 34.9 mo, respectively). In addition, F1 animals showed sorthest DO and CI than the others genotypes. In conclusion, the crossover of locally adapted breeds with European breeds reduce the age to the sexual maturity especially in the F1 animals and increase MY.

Key Words: Dual-purpose cattle, Supplementation, Tropical forages

M23 Influence of the reproductive system on gestation length and birth weight of Nelore Cattle in the sub-tropical area of Bolivia.

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In Bolivia, the genealogic registration system is based solely on gestation length (GL) from the last reported AI or embryo transfer (ET) to the date of calving. Some ET calves have been rejected for registration because their GL was more or less than the established 305 d. The objective of this study was to determine the influence of reproductive system (RS), ET, or AI on GL and birth weight (BW) of Nelore cattle in Bolivia. A total of 2,062 observations from three herds over two years in the Bolivian Nelore Cattle Association were analyzed with mixed model procedures. Included in the model were the fixed effects of RS, sex of calf (SX), month of birth (BM), and their interactions. Age of dam was a covariate and sire of calf was considered a random effect. The interaction of BM × RS was significant ($P < 0.001$) for mean BW. The combination of ET and November BM of calf resulted in greater mean BW (36.4 ± 0.5 kg). Smaller mean BW resulted from the combination of ET and October BM of calf (31.8 ± 3.2 kg). Mean BW of male calves was 2.0 kg greater ($P < 0.01$) than BW of female calves. Significant effects ($P < 0.01$) for GL were BM, RS, SX, BM × RS, RS × SX. Cows mated by AI with December calf BM had greater ($P < 0.05$) GL and cows mated by ET with September calf BM had the shortest ($P < 0.05$) GL. Of the four RS × SX combinations, cows with male AI calves had the greatest ($P < 0.001$) GL (297.5 ± 0.8 d) and cows with male and female ET calves had the shortest GL (292.0 ± 0.8 d). Sire effects were important ($P < 0.001$) for both BW and GL. Correlation of AI and ET with both BW and GL were low (< 0.25 for both). These data show that variation exists for gestation length between AI and embryo transfer births and suggest that the previously determined gestation lengths should be revisited if both AI and embryo transfer calves are to qualify for inclusion in the genealogic registration of the Bolivian Nelore Cattle Association.

Key Words: Reproductive system, Gestation length, Birth weight

M24 Synchronization effects on parameters for days open.

M. T. Kuhn, J. L. Hutchison, and R. H. Miller*, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD*.

The purpose of this research was to determine if synchronization affects parameters related to days open. If synchronization alters genetic or error variances, for example, adjustments could be made to the daughter pregnancy rate evaluations to account for these effects. Synchronization information on individual cows or herds is not currently available. Thus, a chi-square criterion, based on first service only, was used to distinguish between herds that are likely synchronizing and those that are not. Variances were estimated by REML for each synchronization group using a linear model that included the effects of herd-year, year-state-month, parity, permanent environment, animal, and error. The genetic covariance between synchronized and non-synchronized records was also estimated. There were 19,198 synchronized cows and 15,429 non-synchronized cows from 2,903 herds (264 synchronized, 2,697 with non-synchronized records) used for estimation. Herds were randomly selected for inclusion. Calving years spanned 1995 to 2002 and over half the herds had 3 or fewer years of available data. To avoid selection bias, cows were required to have first lactation which further limited the number of eligible cows for each herd. The genetic correlation between synchronized and non-synchronized records was 1.0. However, there were differences in variances. Genetic and permanent environmental variances were higher for non-synchronized records while error variance was higher for synchronized records. The net effect was slightly higher heritability (0.04 vs 0.03) and higher repeatability (11.6% vs 5.7%) for non-synchronized records. Preliminary results indicated only a slight improvement in sire PTA when days open records were adjusted for these differences in variances. Further research will focus on possible improvements for identifying synchronization herds as well as use of second services to further differentiate herds and perhaps better identify differences in parameters.

Key Words: Estrus synchronization, Days open, Genetic evaluation

M25 THRGIBBS1F90 for estimation of variance components with threshold and linear models.

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THRGIBBS1F90 is a FORTRAN program for the analyses of multiple categorical and linear traits. The program is part of a family of programs based on BLUPF90. All programs in this family share common modules and utilize the same common parameter file. Models supported are those with sire, animal, and dominance and maternal effects, random regression, single and multitrait. THRGIBBS1F90 uses Gibbs sampling using by default flat priors. Options allow for restarting the analysis and setting up informative priors. The program creates output files "gibbs_samples" that contains the model information and Gibbs samples, and "solutions". A version of the program exists that stores the log of marginal densities in a file; this is to provide possibility to calculate Bayes Factors and Deviance Information Criteria. POSTGIBBSF90 is a program that analyzes Gibbs samples obtained from THRGIBBS1F90 and other Gibbs sampling programs. It calculates posterior means and standard deviations, highest probability density, effective sample size, and autocorrelations between samples. It also draws graphs of chains and distributions of Gibbs samples. Two kinds of graphs are available for help in determining burn-in period and convergence properties of each parameter. The first graph shows samples for selected parameters, and the second graph shows the distribution of the samples for one parameter. Graphing is by GNUPLOT. The source codes and binaries can be downloaded from http://nce.ads.uga.edu/~ignacy/newprograms.html. They can be compiled with a variety of FORTRAN compilers in Unix, Linux or Windows environments, including 64 bit.

Key Words: Threshold model, Gibbs sampler, Variance component

M26 Methodology for prediction of bull fertility from field data.

M. T. Kuhn* and J. L. Hutchison, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD*.

Simulated data were used to compare alternative models for prediction of bull conception rate (CR) using field data. Two modeling aspects were investigated: an expanded service sire (SSR) effect vs a single term for SSR and linear vs threshold model. In practice, factors such as stud, inbreeding, or age may affect a bull's fertility. Estimating these factors as separate terms in the model (expanded SSR effect), and then adding them back to the bull solution to form the bull's final prediction, may improve accuracy by using more data to estimate the individual components. Simulated data included the effects of herd, SSR, and cow, where the SSR effect had 3 components. Each of 20 replicates had 100,025 cows with a maximum of 7 breedings per cow and an overall mean CR of 0.35. There were 250 sires per replicate and 595 herds, ranging in size from 35 to 5,000 cows. The expected number of services per bull ranged from 270 to 5,900. Accuracy (correlation of predicted and true SSR effect) and bias were used to compare models. The underlying variable was also analyzed with the true linear model to assess the maximum accuracy for this simulated data. The expanded SSR effect was superior to the single SSR term in all models. However, the additional terms, contributing to the SSR prediction, must be fit as random effects to avoid bias. The linear and threshold models had the same accuracy (86.6%), which was only 4.6% lower than that for the true model for the underlying variable. However, the threshold model showed some bias while the linear model did not. Use of exact variances in the calculation of probabilities from threshold model solutions may improve the threshold model estimates. It is well known that the binomial distribution is approximated by the normal distribution and that this approximation improves as sample size increases. All herds in this simulation had a relatively large number of matings. Thus, further research will determine the effect of subclass sample size on differences between the linear and threshold models.

Key Words: Bull fertility, Threshold model

M27 Comparison of Brown Swiss, Holstein and Brown Swiss x Holstein crosses for production, somatic cell score and days open.

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The objectives of this study were to compare milk, fat, and protein yield, somatic cell score, days open, and age at first calving between Holstein (HO) and Brown Swiss (BS), and among BS and HO crosses and backcrosses. A minimum of five first lactation cows entering a herd in the same year was required and only cows with a first lactation record and a registered HO or BS sire were retained. Data from 16 herds included 5,148 total records from 1,604 HO, 736 BS, 238 BS x Ho (SH), 19 HO x BS, and 60 BS x SH backcrosses (SSH). Data was retrieved through PCDART or Dairy Comp 305 for lactations one through five. Average daily milk, fat, and protein yield, SCS, days open, and age at first calving were analyzed using the MIXED procedure of SAS. The fixed effects were days in milk, age, parity, and breed. Random effects included cow and residual error. Breed effects were significant for all yield traits and age at first calving, approached significance for days open ($P = 0.12$), but were not significant for SCS ($P = 0.48$). Least square means (LSM) for daily milk yield were 32.5 kg for HO, 28.0 kg for BS, 31.4 kg for SH, and 28.8 kg for SSH. Least square means for daily fat yield were 1.17 kg for HO, 1.12 kg for BS, 1.22 kg for SH, and 1.14 kg for SSH. Daily protein yield LSM were 0.98 kg, 0.93 kg, 1.00 and 0.93 kg for HO, BS, SH, and SSH, respectively. Days open LSM were 159.1, 156.2, 148.3, and 149.2 for HO, BS, SH, and SSH respectively. Heterosis in SH crosses for yield traits ranged from 3.83% for daily milk yield to 6.56% for daily fat yield. Heterosis estimates were -5.93% for days open and -2.29% for age at first calving in SH crosses. Milk yield of SH were less than HO, but fat and protein yields were increased slightly. Days open and age at first calving were reduced with SH compared to the BS and HO. Brown Swiss may be effective in crossbreeding systems with HO.

Key Words: Crossbreeding, Holstein, Brown Swiss

M28 Heritability estimates of milk yield and electronically recorded daily body weight.

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The objectives of this study were to estimate the heritability of daily body weight and to estimate the genetic correlation between body weight and daily milk production. The Afiweigh cow body weighing system records the weight of every cow exiting the milking parlor. The Afiweigh system was installed at the Penn State dairy herd in August of 2001 and in July of 2004 at the Virginia Tech dairy herd. Daily body weight and milk yield were available for 542 Penn State Holstein cows and 120 Holstein cows from the Virginia Tech dairy herd. Body weight and milk yield recorded after 365 days in milk were eliminated. Outliers were detected by generating a body weight and milk yield curve for each cow and daily records more than four standard deviations from the predicted curves were removed. A total of 159,388 daily body weights and 235,144 daily milk records from the Penn State herd were analyzed with a two-trait animal model in ASReml. The model included lactation, age, date and days in milk as fixed effects and animal, permanent environment, and error as random effects. Average daily milk yield was 36.5 kg and average body weight was 654 kg. Heritability estimates for body weight and milk yield were 0.62 and 0.21, respectively, and repeatability estimates were 0.86 and 0.66, respectively. The genetic correlation estimate between body weight and milk yield was -0.61 with a standard error of 0.13. The phenotypic correlation estimate was -0.33 with a standard error of 0.04. Body weight can be measured accurately as cows exit the milking parlor and could be used to generate genetic evaluations for body weight. The genetic and phenotypic relationship between body weight and milk yield was negative, indicating that most body weight differences at the Penn State dairy herd may be due to differences in body condition.

Key Words: Daily body weight, Milk yield, Genetic correlation

M29 Genetic differences between Holstein maturity rates in the Netherlands and United States.

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Maturity rate of Dutch and US Holstein cows were compared by examining sire predicted transmitting abilities (PTA) for milk yield for each of the first 3 parities. For each bull with US daughters, PTA that included data from parity 1 (PTA_1), parities 1 and 2, and parities 1 through 3 were calculated from US records with first-parity calving dates from 1960 to 1998. Then PTA for contributions from only parity 2 (PTA_2) and parity 3 (PTA_3) were estimated based on numbers of daughters with first, second, and third parities. Parity-specific Dutch estimated breeding values (NLD_1, NLD_2, and NLD_3) were from August 2005 evaluations. To determine whether maturity-rate differences were genetic, comparisons were made across generations. Coefficients for regression of son PTA on sire PTA calculated within sire and son birth years for PTA_1, PTA_2, PTA_3, $PTA_2 - PTA_1$, $PTA_3 - PTA_1$, and $PTA_3 - PTA_2$ were 0.42 to 0.47; most had standard errors of 0.01. Similar regression coefficients for Dutch evaluations were 0.35 to 0.50. Maturity rates of US and Dutch daughters of the same bull were compared. Correlations among parity-specific bull evaluations were calculated within birth year of bulls. Correlations for 2,850 bulls with ≥500 US daughters were 0.88 between PTA_1 and PTA_2, 0.84 between PTA_1 and PTA_3, and 0.96 between PTA_2 and PTA_3; corresponding correlations for Dutch evaluations of 269 bulls were 0.92, 0.89, and 0.98, which are considerably higher than parity correlations assumed in the Dutch evaluation model. Correlations between $PTA_2 – PTA_1$ and $NLD_2 – NLD_1$ was 0.66 for 539 bulls with ≥50 daughters and 0.82 for 93 bulls with ≥500 daughters. Corresponding correlations were 0.61 and 0.83 between $PTA_3 – PTA_1$ and $NLD_3 – NLD_1$ but much lower (0.18 and 0.70) between $PTA_3 – PTA_2$ and $NLD_3 – NLD_2$. Differences in maturity rate of bull daughters were quite consistent across countries and transmitted to granddaughters in both countries through bull sons. Accounting for maturity differences should increase evaluation accuracy for bulls that deviate substantially from population mean.

Key Words: Maturity rate, Milk yield, Parity

M30 Estimation of genetic parameters for maturity of lactation in Japanese Holsteins.

Y. Masuda* and M. Suzuki, *Obihiro University of Agriculture and Veterinary Medicine*, *Obihiro, Japan*.

Models used in genetic evaluations of yield traits for dairy cattle usually include age at calving as a fixed effect. The models ignore the contribution of maturity with age to the additive genetic effect. The objective of this study was to estimate genetic parameters of maturity for milk production using a random regression model for Holsteins in Japan. Data consisted of 50,067 305-d milk records for 24,185 cows in the first five lactations calved between 1975 and 2000. Individual lactation yield was calculated with the test interval method using monthly test day records. An animal model with random regressions on age at calving from 20 to 84 mo, was employed. A third order Legendre polynomial was fitted for animal genetic and permanent environmental effects. (Co)variance components were estimated with the AIREMLRES program, and the residual variance was considered in the model as a function of age at calving. Heritability estimates of 305-milk yield at 24, 36, 48, 60, 72 and 84 mo of age were 0.38, 0.34, 0.32, 0.30, 0.27 and 0.21, respectively. Genetic correlations between milk yields at 24 and 36, 48, 60 72 and 84 mo were 0.92, 0.84, 0.78, 0.74 and 0.74, respectively. Additive genetic and permanent environmental variances decreased after 60 mo of age while the residual variance gradually increased until 80 mo of age. The first eigenvalue for the genetic covariance matrix explained 99.6% of the variation; therefore a second order Legendre polynomial may be sufficient to estimate genetic variances. The corresponding eigenfunction was positive and approximately constant over the ages. This approach provides the genetic curve for maturity and more precise genetic evaluations rather than a multiple-trait model based on parities if a cow has repeated records across lactations.

Key Words: Maturity, Milk yield, Random regression

M31 Genetic parameters for birth weight, dystocia, gestation length, and perinatal mortality in Holstein cattle.

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Data from a long-term dairy sire selection experiment at Iowa State University were analyzed to estimate heritability, direct and maternal genetic relationships among four traits expressed at the birth of a calf; dystocia (1=assisted, 0=unassisted), perinatal mortality (1=alive, 0=dead at birth), birth weight [kg], and gestation length [days]. This research implements a multiple trait animal model evaluation for genetic prediction of animal merit for direct genetic effect of sires and dams on their progeny and maternal genetic effects. This application is unique in its ability to model genetic and environmental factors associated with each measurement and simultaneously account for different distributional properties of discrete data, i.e., dystocia and perinatal mortality, and the symmetric normal distribution of traits with a continuous scale of measurement, i.e., birth weight and gestation length. Perinatal mortality and dystocia have high direct, 0.67, and maternal, 0.45, genetic correlations. These two traits, however, are not controlled by the same genes because the direct-maternal genetic correlation of -0.67 for dystocia and -0.48 for perinatal mortality. Birth weight and gestation length also add information about genetic merit for calving performance because they are moderately correlated with dystocia and perinatal mortality. The sign and magnitude of these genetic correlations suggest a multi-trait genetic evaluation of animals for calving performance. Adequate information exists to begin development of a calving performance index. A calving performance index is expected to enable breeders of dairy cattle to optimize the health and well-being of replacement animals and reduce the incidence of dystocia and perinatal mortality. The antagonism between direct and maternal genetic effects led to the development of a sire-maternal grandsire threshold model for national calving ease genetic evaluations in August, 2002. This research confirms the need to include maternal effects in the evaluation for dystocia and perinatal mortality.

Key Words: Binomial-Gaussian mixed model, Multiple trait, Dystocia

M32 Phenotypic relationships between multivariate measures of lactation curve shape and somatic cell count in Italian Simmental cows.

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Multivariate factor Analysis (MFA) and Principal Component Analysis (PCA) are dimension reduction techniques able to extract from the correlation matrix of milk test day records new latent variables related to lactation curve shape. In this paper, MFA and PCA were applied to a data set of 16,364 lactations of Italian Simmental cows, each with seven TD records for milk yield and Somatic Cell Count (SCC). The aim was to study relationships between lactation curve shape and two measures of SCC: lactational geometric mean of SCC (LGSCC) and lactational means of Somatic Cell Score (LSCS). MFA extracted two latent variables, related with level of production in early lactation (PEL) and lactation persistency (PERS) respectively, whereas PCA yields a leading component related to the average level of production (AVY) and a second component positively related with tests of early lactation and negatively with tests of the second part of lactation (SLOPE). Both for MFA and PCA, latent variables were able to explain more than 80% of the original variance. Correlations between indexes of lactation curve shape obtained with MFA and measures of somatic cells are favourable, i.e near zero or negative as in the case of PERS. Around zero are also correlations of the principal component related with level of production whereas positive and slightly higher (0.18) is the correlation between LSCS and SLOPE, indicating that curves with higher peaks and more pronounced slope in the second part of lactation tend to have higher values of SCC. Results of the present study highlight the ability of both MFA and PCA to extract latent variables related to lactation curve shape that, with the exception of the variable SHAPE, show very low or negative correlations with measures of SCC along the lactation.

Table 1. Correlations among different measures of lactation curve shape and lactational means of somatic cells

	PEL	PERS	AVY	SLOPE	LGSCC	LSCS
PEL	-	0.10	0.75	0.64	0.01	0.03
PERS		-	0.73	-0.66	-0.13	-0.20
AVY			-	0.00	-0.07	-0.11
SLOPE				-	0.11	0.18
LGSCC					-	0.78

Key Words: Lactation curve shape, Somatic cell count

M33 Genetic variation of lactation gross energy efficiency and its association with a number of traits in Holstein dairy cattle.

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Improving a cow's biological efficiency for converting feed to milk is an important goal for dairy industry. This study was conducted to estimation of genetic variation in gross energy efficiency of lactation (GEE) and its association with some of other traits in Holstein dairy cattle. 3503 monthly records of individual feed intake and composition and milk yield and composition were collected from 906 Holstein lactating cows in 3 herds. Energy content of milk (out put energy) was estimated according to National Research Council's model. GEE calculated as energy content of milk yield over net energy intake. Genetic parameters were estimated using Derivative Free approach of Restricted Maximum Likelihood procedure based on multi-trait animal models, with fixed effects of herd-year-season, parity number, lactation stage (months after parturition) and random effects of animal additive genetic and permanent environment. GEE was weakly heritable (0.09). Dry matter intake (DMI) and milk fat yield (FY) had low heritabilities (0.12 and 0.15, respectively) and milk yield (MY) fat corrected milk (FCM) and milk protein yield (PY) were moderately heritable (0.26, 0.29 and 0.34, respectively). GEE had high positive correlations with FY (0.80) and PY (0.57), high negative correlation with DMI (-0.32) and moderate positive correlations with MY and FCM (0.13 and 0.15, respectively). The results of this study showed that GEE is not a worthwhile criterion for direct selection in breeding programs, but can be improved by indirect selection through correlated response to protein yield, FCM or milk yield selection.

Key Words: Gross energy efficiency, Genetic parameters

M34 Bayesian heritability estimates of monthly test day milk yields for Iranian Holsteins.

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A total of 18360 monthly test day milk yields collected from 2104 Iranian first lactation Holsteins (progeny of 279 sires) calving between 1993 and 2004 was used to estimate heritability of milk yield at each month of lactation using Bayesian statistical method in a random regression test day animal model. The records analysed were obtained from a large-size dairy farm (Astan-e-Quds) consisting of two herds in Khorasan province of Iran. In the random regression model, fixed environmental effects of herd test date (HTD with 273 levels) and covariables (linear and quadratic) of cow age at recording time as well as random effects of direct additive genetic and permanent environment were included. Orthogonal legendre polynomials of order 4 (cubic) were also included in the model to take account of milk yield variation over the course of the lactation at two genetic and environmental levels. Random regression analysis was undertaken using RRGIBBS software in which Bayesian heritability estimates of test day milk yields were obtained through 100000 rounds Gibbs sampling. The results showed that months 1 and 9 of the lactation had the lowest (0.164) and greatest (0.339) heritabilities respectively. The average heritability of monthly test day milk yields at the second part of the lactation curve was generally higher than the first part of the lactation curve (0.202 vs. 0.310) suggesting that accuracy of predicting breeding value for candidate animals could increase as milk yield at the second part of the lactation curve is used in genetic evaluation programme.

Key Words: Bayesian estimate, Test day milk, Iranian Holstein

M35 Estimation of phenotypic and genetic trends for milk and fat yield traits in Khorasan province Holsteins of Iran by using a univariate model.

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A total of 17971 first lactation milk records from Holstein heifers, calving from 1990 to 2003 in 133 herds, was used to estimate phenotypic and genetic trends by implementing an animal model. In the model, fixed effects of herd-year-season of calving, age at first calving as well as random effect of additive genetic effect were included. Heritability of first lactation milk yield was found to be 0.28 and statistically significant. Genetic and phenotypic trends were 9.824 and 139.162 Kg/year respectively for milk yield and -0.0616 and 4.349 kg/yr indicating that environmental improvement contributed a major part of annual milk and fat yield traits increase in Holstein cows of Khorasan province.

Key Words: Genetic and phenotypic trends, Holstein, Khorasan

M36 Comparison of lactation and test day models for genetic evaluation of 305-day milk trait in Iranian Holstein heifers.

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A total of 179,460 monthly test day milk records obtained from 17,946 Iranian Holstein heifers (trice a day milking) distributed in 287 herd and calved from 1986 to 2001 was used to predict breeding value of animals. Monthly test day milk production was analyzed by applying a covariance function in which the effects of herd, year of calving, season of production, age at test day, genetic merit and permanent environmental effects were included. Orthogonal legendre polynomials up to order 5 was also implemented in the covariance model to take account of genetic and environmental aspects of milk production variation over the course of lactation. In the present research, predicting of breeding value of animals based upon using 305-day and monthly test day milk yields was compared. The results indicated that ranking of ten top sires, dams as well as progenies changed as the genetic evaluation of animals switched from the traditional (based on 305-day milk yield) to the new method that was based on the covariance function. Regression analysis of average breeding value of progenies on first year of their calving showed that the amount of genetic trend obtained from the covariance function for 305-day milk yield was greater than that of the lactation model (11.607 vs 3.860 Kg/year) over the period of 16 years of calving. The phenotypic trend for lactation milk yield was 92.97 Kg per year that it was significant statistically. This indicates that a large proportion of annual increase of milk production of Holstein heifers in Iran has been due to environmental rather than genetic improvement.

Key Words: Genetic evaluation, Covariance function, Iranian Holsteins

M37 Phenotypic study of lactation curve in Iranian Holsteins.

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A total of 136250 monthly test day milk records collected from 13625 Iranian Holstein heifers (3x milking) calved between 1991 and 2001 and distributed in 264 herds, was used to study the effects of some environmental factors influencing lactation curve parameters as well as production characteristics. Wilmink function (Yt = W0 + W1t + W2e-0.05t) was fitted to individual lactations. The results of least squares analysis of variance indicated that herd, year and month of calving had a very high significant effect on all traits under consideration. Correlation analysis showed that parameter W0 had a negative and significant relationship with parameters W1 and W2 while it was positively significantly correlated with milk at peak time and 305-day milk yield. Simple linear regression analysis of adjusted means of 305-day milk yield, days to reach peak yield as well as peak milk yield on year of first calving also revealed that there was a phenotypic increase of 137.152 Kg, 0.535 day and 0.434 Kg per year respectively.

Key Words: Lactation curve, Wilmink function, Iranian Holsteins

M38 Estimation of genetic trends for milk production traits in Iranian Holsteins.

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In order to estimate genetic trends for milk production traits in Iranian Holsteins a total of 18989 adjusted 305d-2X-ME first lactation records collected from 18989 heifers calved between 1995 and 2001 and distributed in 202 herds over the country were used. The traits were milk, fat and protein yields as well as fat and protein percentages. A multiple trait animal model was utilized. The effects included in the animal model were fixed contemporary group of province-herd-year-season of calving, linear covariate of Holstein genes and random additive genetic effect. Restricted maximum likelihood estimates of variance and covariance components and best linear unbiased prediction of breeding value of individual cows for each trait were obtained by using MTC and MTJAAM softwares respectively. Genetic trends for the traits under consideration were estimated based upon simple linear regression analysis of BLUP solutions on year of first calving. The results obtained in this study revealed that the average breeding value of cows had a significant increase of +33.178 Kg per year ($P < 0.01$) for milk yield. At the same time, fat and protein yields had positive genetic trends of +245 g ($P > 0.05$) and +789 g per year ($P < 0.05$) respectively. In contrast to yield traits, the genetic trends calculated for fat and protein percentage showed an annual decrease of -0.011 % ($P < 0.001$) and -0.003 % ($P < 0.05$) respectively which were significant statistically.

Key Words: Genetic trend, Milk production traits, Iranian Holsteins

Forages and Pastures: Forage Quality

M39 Direct or sequential determination of ADF in legume forages.

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Objectives of this study were to compare ADF values of legume forages obtained from samples treated directly with acid detergent solution (direct, DP) or after extraction with NDF solution (sequential, SP) and the effect of the ADF extraction method on lignin quantification. Pastures (n=26) corresponding to nine harvest dates (HD) of alfalfa (AA), ten HD of birdsfoot trefoil (BT), and seven HD of red clover (RC) were evaluated. For each specie and HD, ADF and Lignin concentrations were determined in triplicate. The ADF was determined by filter bag technique (ANKOM Technology), corrected for ash. In SP, Na2SO3 was not included in NDF solution. Lignin was determined by extraction with 72% H2SO4 (Ligsa). Data were analyzed in a completely randomized design and the model included specie, extraction procedure, and their interaction. There was an interaction (P<0.02) of specie with extraction procedure for ADF concentration as ADF concentration determined by DP tended (P=0.10) to be greater than SP for AA (27.9 vs 26.4 ± 1.5) and lower (P<0.01) for BT (29.7 vs 32.1 ± 1.5) whereas ADF for RC (28.7 vs 29.4 ± 1.5) did not differ (P=0.55) between extraction procedures. There was an effect of ADF extraction method on Ligsa quantification as Ligsa was greater (P<0.01) for SP than DP for all legume species (8.57 vs 6.75 ± 0.44). It would be advisable to always specify the procedure followed in ADF quantification. Additional studies are required to establish equivalency between ADF determined by DP and SP, and the affects on nutritional fractions such as Ligsa and ADIN.

Table 1. Number of determinations resulting on equal or different concentrations for ADF or Lignin

Specie	Number	ADF Equal	ADF Different	Lignin Equal	Lignin Different
Alfalfa	9	4	5	7	2
Birdsfoot trefoil	10	3	7	5	5
Red clover	7	6	1	3	4

Key Words: ADF, Lignin, Extraction procedure

M40 Direct verses sequential analysis of acid-detergent insoluble nitrogen in forage legume hays.

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Acid-detergent insoluble nitrogen (ADIN) is thought to represent nitrogen that is not degraded during ruminal and post-ruminal digestion of forages by cattle. Forage ADIN can be determined following direct acid detergent extraction or following sequential extraction with neutral and acid detergents. In this study, we evaluated how direct verses sequential detergent extraction influenced the ADIN content of legume hays differing in polyphenol composition and degree of conditioning at harvest. In 2002 and 2003, first and second cuttings of polyphenol-free alfalfa, low to high tannin birdsfoot trefoil, and red clover with