Breeding and Genetics: Dairy Cattle

W23   Identification of small heat shock proteins in the bovine genome.   S. Schepis and M. Worku*, *North Carolina Agricultural & Technical State University, Greensboro*.

Protein-damaging stresses, including heat shock, cold, altered pH and oxygen deprivation induce the expression of a subgroup of molecular chaperones, called heat shock proteins (Hsp), which consist of several protein families designated by their molecular weight, such as the Hsp90, Hsp70, Hsp60, and the small Hsp (sHsp) families. Small heat shock proteins (sHsp) with a molecular mass of 15–30 kDa are ubiquitous and conserved. This large family of proteins is present within the prokaryotic and eukaryotic cell as large oligomeric complexes, ranging in size from 200 to 800 kDa. Unlike the high molecular weight Hsp, which are involved in protein folding in vivo, under normal conditions, sHsp play an important role in protecting organism from stress. The sHsp share an evolutionarily conserved sequence of 80–100 amino acids, located in the C-terminal region, and called "alpha-crystallin domain." Ten active genes for sHsp have been identified in the human genome. This project focused on 10 α-crystallin related Hsps belonging to the sHsp molecular chaperone family: HspB1- HspB10. It is anticipated that the recently completed annotated sequence of the cattle genome will lead to identification of genes for disease resistance and higher quality meat. The purpose of this project was to determine if genes coding for human sHsp are found in the bovine genome, and if so, how highly the sequences were conserved across the 2 species. The NCBI search engine, BLAST, and CLUSTALW on Biology Workbench were used. Homologs of 10 α-crystallin human small heat shock protein (sHsp) molecular chaperone family (HspB1- HspB10) were found within the bovine genome and single nucleotide differences identified in silico. The sequence for human sHspB9 expressed exclusively in the testis and cancerous tissue did not identify related sequences in the bovine.

Key Words: heat shock protein, bovine, human

W24   Use of partial least-square regression to predict SNP when some animals are genotyped with low density marker panels.   C. Dimauro*, G. Gaspa, R. Steri, S. Sorbolini, E. Pintus, and N. P. P. Macciotta, *University of Sassari, Sassari, Italy*.

Genome wide selection exploits information from dense marker platforms (usually 50K-60K) to predict genomic breeding values (GEBV) for livestock. However, costs of analysis are expensive for high density marker (HDM) platforms, allowing the genotyping of only a few thousand animals. A decrease in costs could be reached by using low density marker (LDM) chips, but, in this case, a unavoidable reduction in GEBV accuracy is expected. An alternative could be the use of both reference (REF) and prediction (PRED) populations of animals genotyped with HDM and LDM chips, respectively. Missing genotypes in the PRED population could be reconstructed using a suitable mathematical model which exploits information from REF population. In this work the partial least square regression (PLSR) is used at this purpose. A data set, generated for the XII QTLs-MAS workshop, which simulated a genome with 6 chromosomes and 6,000 equally spaced biallelic SNP for 5,865 animals, was used. It was split into 2 data sets, the REF with 4,665 animals and 6,000 SNP and the PRED with 1,200 individuals and 3,000 SNP. The PLSR, applied separately for each chromosome, was used to predict the 3,000 missing SNP in the PRED population. Different scenarios of missing SNP sampling in PRED and decreasing size of REF population were tested. Goodness of prediction was evaluated by calculating correlations between actual and predicted data. Best results were obtained when unknown SNP were chosen evenly spaced along the chromosome and all 5,865 individuals in the REF population were used. In this case, the mean correlation between actual and predicted data was 97%. As the size of REF population decreased to 2,000 individuals, the mean correlation reached a value of 94%. Therefore, if an adequately large REF population is used, the PLSR technique is able to predict with high accuracy the missing SNP in other animals genotyped with a LDM platform. This research was funded by FAR 2008.

Key Words: PLSR, SNP

W25   Multiple trait genetic evaluation of linear type traits using genomic and phenotypic information in US Holsteins.   S. Tsuruta*[1], I. Aguilar[1,2], I. Misztal[1], A. Legarra[3], and T. J. Lawlor[4], [1]*University of Georgia, Athens*, [2]*INIA, Las Brujas, Uruguay*, [3]*INRA, Castanet-Tolosan, France*, [4]*Holstein Association USA Inc., Brattleboro, VT*.

Genetic evaluation was conducted for linear type traits using combined genomic and phenotypic data in US Holsteins. Single nucleotide polymorphism (SNP) markers from the Illumina BovineSNP50 genotyping Beadchip, consisting of 38,416 SNP on 30 chromosomes, were used available for 6,931 bulls. A unified approach proposed by Aguilar et al. (2010) was used to estimate genomic evaluations with single trait (ST) and multiple trait (MT) models. Three analyses of 5 linear type traits (stature, strength, body depth, dairy form, and rump angle with heritabilities 0.45, 0.27, 0.34, 0.30, and 0.34) were conducted, utilizing 8,865,120 records in 2009 and 7,715,925 records in 2004. The EBV were calculated using 2009 and 2004 data sets with phenotypes (traditional genetic evaluation) and a 2004 data set with phenotypes and genotypes (unified approach). Coefficients of determination (R^2) and regressions on 2004 genomic EBV were calculated for 1,307 young bulls with at least 50 daughters in 2009 using daughter deviations from 2009 MT traditional evaluations. The EBV for 2004 traditional evaluation were parent average (PA). The R^2 from regressing daughter deviations on ST PA, MT PA, ST genomic, and MT genomic predictions were 0.34, 0.34, 0.54, and 0.54, respectively, for stature. Corresponding R^2 for strength were 0.25, 0.29, 0.40, and 0.44, respectively. In general, R^2 for ST and MT genomic models were 13-19% and 14-18% higher, respectively, than those of PA (28-42%). The regressions with MT were slightly (0.01-0.02) higher than those with ST, indicating less bias. The genomic evaluation by MT is more accurate for selected traits than by ST. The improvement in accuracy from ST to MT in genomic predictions follows a similar improvement in PA. Preliminary results show that, with a small modification in the unified approach, bias can be essentially eliminated at the cost of a small reduction in R^2.

Key Words: genomic selection, linear type traits, US Holsteins

W26   Genotype by environment interaction: Effects of nutritional management on production traits.   M. W. Dekleva*[1], C. D. Dechow[1], J. M. Daubert[1], S. Bauck[2], J. W. Blum[3], and G. A. Varga[1], [1]*The Pennsylvania State University, State College*, [2]*IGENITY Livestock Production Business Unit, Duluth, Georgia*, [3]*University of Bern, Switzerland*.

The objective of this study was to determine the effect of nutritional management factors on the level of genetic expression for milk, fat, and protein yield. Intakes of dry matter, crude protein and net energy of lactation (NE_L) in addition to 305 d yield were available for 970 cows from 11 tie-stall herds in Pennsylvania. All herds were visited monthly

to measure 24-h intake. Feed samples were collected on each visit and analyzed for dry matter percentage, crude protein percentage and NE_L (MCal/kg) content. Sire PTA for yield was available for all 970 cows, while 881 cows were genotyped and received an Igenity Profile Score (IS) for milk, fat, and protein where 1 corresponds to the lowest, and 10 corresponds to the highest genetic potential for yield. Multiple regression models were fit for 305 d milk, fat and protein yield. Fixed effects were herd averages for kg of dry matter refusals (DMR), ration crude protein percentage (CP), NE_L and the interactions of these herd averages with PTA or IS, herd-year-season, and lactation. Permanent environment was included as a random effect. For daughters of bulls that differed in PTA for milk by 500 kg, there was a 151.5 kg difference in milk yield at the tenth percentile for DMR compared with a 584.8 kg difference for cows at the ninetieth. A difference of 25 kg for sire PTA fat corresponded to a difference of 17.9 kg of fat yield for herds in the tenth percentile for CP and 51.5 kg for herds in the ninetieth. A change of one unit in Igenity Score corresponded to a difference of 1.87 kg of fat yield for cows at the tenth percentile for NE_L., compared with a 6.91 kg difference for cows at the ninetieth percentile. The results indicate that response to selection was reduced in herds that did not provide cows with adequate intakes of dry matter, crude protein and NE_L.

Key Words: genotype, environment, production

W27   Evaluation of the effect of inbreeding on age at first calving in Holstein cattle.   J. Bezdicek* and J. Riha, *Agrovyzkum Rapotin s.r.o.*, *Rapotin, Czech Republic*.

The objective of this study was to examine the effect of inbreeding depression on age at first calving (d) in Holstein cows. The databases included cows (173,000) that calved in the years 1995–2006 at farms in the Czech Republic. Inbred cows were matched with their outbred contemporaries (n = 811) based on sire, farm of first calving, year and period of calving (±2 mo), and dam's breeding value for milk production (±5%). Inbred cows and their matched outbred contemporaries were subsequently divided according to inbreeding coefficients of the inbred cows (F_x = 1.25%; F_x = 12.5%; F_x = 25%, and other). The data were analyzed with StatSoft Inc. Statistica 8 using descriptive statistics and paired *t*-tests. The GLM procedure of SAS Inc. was used to analyze the effects of inbreeding depression. Age at first calving increased when the level of inbreeding increased. Within the observed groups (F_x = 1.25%; F_x = 12.5%; F_x = 25.0% and all animals), the average age at first calving for inbred cows (for their outbred contemporaries) was 820 (818); 835 (822); 844 (822) and 832 (820) d. In the groups F_x = 25% and other, differencies between inbred and outbred cows were highly significant ($P < 0.001$). There was also greater variability for groups of inbred cows (s_x = 83.2 d) compared with groups of outbred contemporaries (s_x = 63.4 d). Inbred cows also had significantly ($P < 0.01$) lower breeding values for milk (20.8 kg) than in outbred contemporaries (63.6 kg). Overall, this study confirmed an increase in age at first calving in inbred cows compared with their outbred cohorts.

Key Words: age at first calving, inbreeding, Holstein

W28   Age at first calving in Holstein cattle in the United States.   J. Cole and D. Null*, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*.

Heifer rearing costs account for 15 to 20% of the total expense of milk production, and the decline in fertility of US Holsteins is well documented. Earlier age at first calving (AFC) may improve profitability and fertility. Records for 400,000 U.S Holstein cows born on or after January 1, 1997 were selected by random sampling of herd codes and used to estimate (co)variance components and breeding values. Phenotypic AFC averaged 788 ± 89 d, and ranged from 540 to 1095 d. The model included random animal and residual effects, and a fixed herd-year-season (HYS) of birth effect. Herd-year-season of birth was included to avoid confounding between sires and period-of-birth, and groups were required to include at least 10 observations. The 4 seasons were defined as: December to February, March to May, June to August, and September to November. Heritability averaged 0.027 ± 0.003 across the 6 data sets, which is lower than some literature estimates, and consistent with earlier, unpublished studies on US Holsteins. Predicted transmitting abilities for AFC of active bulls ranged from −13 to +14 d, and averaged −1.9 ± 3.6. Correlations were calculated among sire PTA for bulls with reliabilities of lifetime net merit (NM$) of at least 90%. Age at first calving had favorable (negative) correlations with milk (−0.22), fat (−0.18), and protein yield (−0.23), SCS (−0.05), productive life (−0.01), NM;(−0.18), heifer conception rate (HCR; −0.18), and persistency of milk (−0.12), fat (−0.13), and SCS (−0.02). Unfavorable (positive) correlations were found with cow conception rate (0.04) and protein persistency (0.04). Daughter pregnancy rate (DPR) was uncorrelated with AFC (0.001; $P > 0.05$). Excessive AFC has a negative effect on yield and lifetime profitability, which is reflected in these correlations. Genetic trend was estimated by regression of sire PTA for AFC on birth year, and was slightly negative, decreasing by −0.09 d per year ($P < 0.01$). Routine genetic evaluation of AFC is desirable because it provides dairy producers with an additional tool for managing reproduction in their herds.

Key Words: age at first calving, fertility, genetic evaluation

W29   Relationship of reason for lactation termination with genetic merit of Holsteins in the United States.   H. D. Norman, J. R. Wright, and S. M. Hubbard*, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*.

Reasons that producers report to 4 dairy records processing centers for why individual cows exit the herd (lactation termination codes) were examined for 6.2 million US Holsteins with lactation records that ended in 2007 and 2008 to determine their relationship to genetic merit. The most frequent termination reasons were lactation ended normally and cow stayed in the herd (68%), cow died (5%), and cow was sold for low production (4%), reproductive problems (4%), or mastitis (4%) or for dairy purposes (3%); 9% of lactations had no reason specified. For cows with normally ended lactations, mean predicted transmitting ability (PTA) and standard deviations (SD) were 135 ± 271 kg for milk, 5 ± 10 kg for fat, 4 ± 8 kg for protein, 2.95 ± 0.38 for somatic cell score (SCS), 0.8 ± 1.4 mo for productive life (PL), 0.1 ± 0.9% for daughter pregnancy rate (DPR), and net merit (NM) was $115 ± 132; corresponding means and SD for parent averages (PA) were 117 ± 219 kg milk, 4 ± 8 kg fat, 4 ± 6 kg protein, 2.95 ± 0.37 SCS, 0.6 ± 1.3 mo PL, 0.1 ± 0.9% DPR, and $98 ± 111 NM. Mean PTA and PA for all yield traits and PL as well as NM generally were lower for cows that did not end their lactations normally; lowest means were 18 kg for PTA milk, 1 kg for PTA fat, 1 kg for PTA protein, 0.2 mo for PTA PL, $37 for NM, 74 kg PA milk, 3 kg PA fat, 2 kg PA protein, 0.3 mo for PA PL, and $62 for NM for cows sold for low production and –0.2% for PTA DPR and –0.1% for PA DPR for cows sold for reproductive problems. Cows that aborted had the highest mean PTA for all yield traits (159 kg for milk, 5 kg for fat, and 5 kg for protein) and PA milk (125 kg). For SCS, PTA and PA were highest for cows with normally ended lactations and lowest (2.80 for PTA SCS and 2.81 for PA SCS) for cows that died; cows sold because of mastitis had mean PTA SCS of 2.91 and mean PA SCS of 2.90. Across termination categories, SD were similar for each

trait except SCS. In general, cows with lactations that ended normally were genetically superior for all traits except SCS.

Key Words: lactation termination, genetic merit, Holstein

W30   Comparison of Holstein service-sire fertility for heifer and cow breedings with conventional and sexed semen.   H. D. Norman*, J. L. Hutchison, and P. M. VanRaden, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*.

Sire conception rate (SCR), a service-sire fertility evaluation implemented in August 2008, is based on up to 7 conventional-semen breedings for parities 1 through 5 (C_{cow}). The same procedure was used to derive SCR for other types of breedings: sexed semen for cows (S_{cow}) and conventional semen and sexed semen for primiparous heifers (C_{hfr} and S_{hfr}, respectively). For all 4 breeding types, SCR were based on breedings from 2006 through 2009. Service-sire age groups were consolidated for sexed-semen breedings because of a limited number of bulls. Only artificial-insemination Holstein bulls with $\geq$ 300 breedings overall and $\geq$ 100 matings during the last 12 mo in $\geq$ 10 herds were included. Number of bulls evaluated was 2,309 for C_{cow} breedings, 270 for C_{hfr} breedings, 25 for S_{cow} breedings, and 114 for S_{hfr} breedings; respective mean SCR reliabilities were 79, 82, 73, and 75%. Mean SCR for all breeding types was near 0, and standard deviations were 2.21% for C_{cow}, 2.57% for C_{hfr}, 2.39% for S_{cow}, and 4.34% for S_{hfr} breedings. Correlation between C_{cow} and S_{cow} SCR was 0.18, which resulted in a genetic correlation (r_g) for true SCR of 0.24; corresponding correlations for heifer breedings also were low: 0.08 and 0.11, respectively. Correlation between C_{cow} and C_{hfr} SCR was 0.67 (r_g of 0.82); correlation between S_{cow} and S_{hfr} SCR was 0.75 (r_g of 1.02). Among artificial-insemination organizations, absolute differences between mean SCR for conventional and sexed-semen breedings ranged from 1.44 to 4.52% for cows and 0.87 to 6.78% for heifers. Bull age effects were quite large for conventional semen but small for sexed semen. Results suggest that fertility rankings for sexed semen differ markedly from those for conventional semen and separate SCR are needed. Combining cow and heifer inseminations together in some manner would seem to be advantageous.

Key Words: sire conception rate, bull fertility, sexed semen

W31   Derivation of factors to estimate daily, fat, protein, and somatic cell score from one milking of cows milked three times daily.   M. M. Schutz*[1] and H. D. Norman[2], [1]*Purdue University, West Lafayette, IN*, [2]*USDA-ARS Animal Improvement Programs Laboratory, Beltsville, MD*.

The objective of this research 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 3 times (3x) per d. Daily milk weights were recorded automatically and samples were collected from 8 herds for each milking on test-day by Dairy Herd Improvement personnel. Following edits, 1721 records of 1236 first lactation (L1) cows and 2704 records of 1940 later lactation (L2) cows 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, 2 methods were compared with estimate factors or equations to predict daily F, P, and SCS. First, factors were estimated as the ratio of the sum of daily yield to the sum of partial yield within a parity-MINT class (13 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 ($2 \times 7 \times 8$) [Method 3] to jointly account for MINT and DIM. Separate factors were derived for milking 1, 2, and 3 for each trait in L1 and L2. Method 3 resulted in consistently strongest correlations between estimated and actual yields, and smallest variances of estimates, and root mean squared errors (rMSE) for all components in milkings 1, 2, and 3 in L1 and L2. Method 3 resulted in rMSE of 0.14 (F, L1), 0.22 (F, L2), 0.09 (P, L1), and 0.14 (P, L2) kg for milking 1; compared with rMSE of 0.18, 0.27, 0.12, and 0.16 kg from current factors for the same traits in L1 and L2. Differences in rMSE were similar for F and P for milking 2 and 3 and for SCS for all 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

W32   Derivation of factors to estimate daily milk yield from one milking of cows milked three times 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 Animal Improvement Programs Laboratory, Beltsville, MD*.

The objective of this research was to derive factors to predict daily milk yield when milk is sampled once per d for cows milked 3 times (3x) per d. Milk weights for all 3 milkings were recorded automatically by 8 herds and collected by Dairy Herd Improvement supervisors on test-day. Following edits, 196,725 daily milk weight records of 2235 first lactation (L1) cows and 346,508 records of 3385 later lactation (L2) cows remained. Factors currently in use to adjust single milking yields for milking interval (MINT) were applied. Also, 3 methods were compared with estimate factors or equations to predict daily milk yield. First, factors were estimated as the ratio of the sum of daily yield to the sum of partial yield within a parity-MINT class (13 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 ($2 \times 7 \times 8$) [Method 3] to jointly account for MINT and DIM. Separate factors were derived for milking 1, 2, and 3 for each trait in L1 and L2. Method 3 resulted in consistently strongest correlations between estimated and actual yields, and smallest variances of estimates, and root mean squared errors (rMSE) for milkings 1, 2, and 3 in L1 and L2. Method 3 resulted in rMSE of 3.12 (Milking 1, L1), 3.26 (Milking 2, L1), 3.25 (Milking 3, L1), 4.52(Milking 1, L2), 4.72 (Milking 2, L2)and 4.57 (Milking 3, L2) kg; compared with rMSE of 3.58, 3.66, 3.59, 5.13, 5.41, and 5.09 kg, respectively, from current factors for the same milkings for L1 and L2. The multiple regression methodology (Method 3) appears to provide the most accurate prediction of daily milk weight from a single milking for herds milking 3x daily.

Key Words: milking interval, adjustment factor, milking frequency

W33   Genetic relationship between milk urea nitrogen and milk constituents in Holstein dairy cows.   N. Ghavi Hossein-Zadeh*[1] and M. Ardalan[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Guilan, Rasht, Iran*, [2]*Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran*.

The objectives of this study were to estimate the heritability of milk urea nitrogen (MUN) concentration and describe the genetic and phenotypic relationship between MUN and other milk constituents in Iranian

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Holstein dairy cows. Lactation records including MUN data obtained from 57301 dairy cows on 20 large dairy herds in Iran between January 2005 and June 2009. Genetic parameters were estimated using an animal model with covariates for days in milk and age at first calving, fixed effects for season of calving and effect of lactation number, and random effects for herd-test day, animal, permanent environment, and residual error. Coefficient of variation for MUN was 38.76%. Estimated heritability for MUN was 0.14. Phenotypic trend of MUN increased significantly over the years. Also, phenotypic correlations of MUN with milk production traits were close to zero. The genetic correlation was close to zero for MUN and lactose percentage (- 0.07); was moderately positive for MUN and net energy concentration of milk (0.24), fat percentage (0.23), protein percentage (0.34), total solids (0.29), solids-not-fat (0.31), and milk yield (0.25), and was negative for MUN and somatic cell score (- 0.14). Herd-test day explained 52% of the variation in MUN, which suggests that management adjustments at herd-level can reduce MUN. This study shows that it is possible to influence MUN by herd management and by genetic selection.

Key Words: milk urea nitrogen, dairy cattle, milk traits

W34   Genetic relationship between milk urea nitrogen and reproductive performance in Iranian Holsteins.   N. Ghavi Hossein-Zadeh*[1] and M. Ardalan[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Guilan, Rasht, Iran*, [2]*Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran*.

The objective of this study was to describe the genetic and phenotypic relationship between milk urea nitrogen (MUN) and reproductive traits in Iranian Holstein dairy cows. Lactation records including MUN data obtained from 57301 dairy cows on 20 large dairy herds in Iran between January 2005 and June 2009. Genetic parameters for MUN and reproductive traits were estimated with an animal model using ASREML. Herd-test-day or herd-year-season along with age at calving and days in milk were included as fixed effects in all models. Heritabilities for MUN and reproductive traits were estimated separately for first lactation, second lactation, and third lactation. Estimated heritabilities for MUN varied from 0.18 to 0.21. Heritability estimates were low for reproductive traits and ranged from 0.02 to 0.06 for different traits across parities. Except for days open, phenotypic and genetic correlations of MUN with reproductive performance traits were close to zero. Genetic correlations between MUN and open days were 0.22 in first lactation, 0.33 in second lactation, and were 0.46 in third lactation. On the other hand, phenotypic correlations between MUN at different parities were moderate (0.29 to 0.34), but genetic correlations between MUN at different parities were high and ranged from 0.84 to 0.97. This study shows that it is possible to influence MUN by genetic selection.

Key Words: milk urea nitrogen, dairy cow, reproductive traits

W35   Adjusted phenotypic trend estimation for peak milk yield of Iranian Holsteins milked three times daily.   H. Farhangfar*[1], M. Bashtani[1], and J. Modarresi[2], [1]*University of Birjand, Birjand, Iran*, [2]*Agricultural Jihad Organisation, Birjand, Iran*.

The main aim of this study was to estimate adjusted phenotypic trend for sample milk yield at peak time of thrice a day milking Iranian Holstein cows. A total of 212,889 sample milk yields (at third month of lactation) collected from 70,963 Iranian first lactation Holstein cows calving from 1997 to 2008 were used. All cows were milked 3 times a day: morning, noon and night. The number of herds was 739. The average milk samples were 10.792, 10.366 and 10.310 kg for morning, noon and night milking

respectively. To analyze the data, a fixed statistical linear model was used. In the model, fixed effects of herd, year and season of calving, time of milking as well as covariables of Holstein gene percentage, first calving age and days in milk were included. In the model, 2-way interactions between season of calving and time of milking and between year of calving and time of milking were also taken into account. For fitting the model General Linear Model (GLM) procedure of SAS program was applied. Results indicated that all effects except days in milk had statistically significant ($P < 0.01$) influences on milk samples at peak time. Morning sample milk yield was revealed to be significantly different from night sample ($P < 0.05$) while no significant difference were found between morning and noon and between noon and night milk samples. Linear regression analysis of adjusted milk sample yields on year of calving ($R^2 = 0.974$) showed a positive significant ($P < 0.001$) phenotypic trend of 0.168 kg for sample milk yield over the period of time. As the phenotypic trend consisted of genetic (resulted from genetic selection for high producing cows) and environmental trends (good dairy herd management practices such as appropriate ration formulation, and good animal health), further research is needed in future to be carried out to estimate genetic part of phenotypic improvement of sample milk yield in Iranian Holsteins.

Key Words: Iranian Holsteins, phenotypic trend, milk sample

W36   REML estimates of heritability and repeatability for monthly test day milk yield of primiparous Iranian Holsteins.   A. Seyed Dokht*[1], H. Farhangfar[2], A. A. Aslami Nezhad[1], and M. Tahmorespour[1], [1]*Ferdowsi University of Mashhad, Mashhad, Iran*, [2]*Birjand University, Birjand, Iran*.

In this research, a total of 634,949 monthly test day milk records collected from 72,523 Iranian Holstein first lactation cows calving between 1999 and 2008 were utilized to estimate heritability and repeatability using restricted maximum likelihood (REML) statistical approach. The records were obtained from 724 herds over 19 provinces in the country. All monthly test day records were obtained from 3-times a day milking cows. The average monthly test day milk yield in the whole data set was 29.11 kg (SD = 7.07 kg). A repeatability test day animal model was used. In the model, fixed contemporary group (combining province-herd-year of recording-season of recording), stage of lactation (10 stages), and covariables of Holstein gene percentage, days in milk nested in the stage of the lactation, and age of cow at recording (in month) were included. The random part of the model consisted of additive genetic, permanent environment and residual effects. The total number of animals (including daughters, sires and dams) in the pedigree was 101,601. DMU software was run in a Pentium 4 computer with 4 gigabyte memory to fit the animal model. Additive genetic, permanent environment and residual variance estimates were 4.352, 13.494 and 15.335 kg2 respectively. The results revealed that heritability and repeatability of monthly test day milk yield were 0.131 and 0.537 respectively. Low heritability of monthly test day milk yield obtained in this study indicates major part of the phenotypic variation for the trait under consideration is resulted from the temporary environment and model unexplained variation revealing that genetic selection based upon test day milk records may not be as cost effective as the traditional lactation model for which there is usually a higher heritability.

Key Words: Iranian Holsteins, genetic parameters, test day milk yield

W37   Correlation between milk components with regard to the season in Iranian dairy herds.   A. Laki*, S. Babaei, N. Hedayat-

Evrigh, M. Dehghan-Banadaky, and K. Rezayazdi, *Department of Animal Science, Campus of Agriculture, University of Tehran, Karaj, Tehran, Iran.*

Previous studies showed a positive correlation between somatic cell count (SCC), fat and protein, and a highly significant negative correlation between SCC and lactose content. The aim of this study was to determine the correlation between milk components in different seasons in Iranian dairy herds. All test-day data (n = 126,357), including milk composition measured by infrared test method at the Tehran milk quality laboratory, were collected from 124 commercial Holstein dairy herds in the State of Tehran during a 4-year period (2004–2008). Overall means for fat, protein, SCC, lactose, total solids, solids-not-fat, and milk urea nitrogen were 3.54%, 3.15%, 424,370 cells/ml, 4.54%, 11.52%, 9.12% and 17.43 mg/ml respectively. The data showed a statistically significant ($P < 0.01$) positive correlation between SCC and fat (0.04) and protein content (0.11), and between fat and protein (0.17); and a highly significant negative correlation between SCC and lactose content (−0.26). With regard to season, the correlation between fat and protein was lowest in spring (0.11) and highest in fall (0.188). Also the correlation between lactose and SCC was lowest in summer (−0.23) and highest in fall (−0.28). The correlation between protein and SCC was the lowest in spring and the highest in fall (Table 1).

Table 1. Correlation coefficients between milk components in different season

Season	Fat & Protein	Fat & Lactose	Fat & SCC	Protein & Lactose	Protein & SCC	Lactose & SCC
Spring	0.11[b]	−0.02[a]	0.05[b]	0.04[b]	0.09[b]	−0.26[b]
Summer	0.187[b]	−0.08[b]	0.06[b]	−0.08[b]	0.11[b]	−0.23[b]
Fall	0.188[b]	−0.10[b]	0.04[b]	−0.14[b]	0.13[b]	−0.28[b]
Winter	0.16[b]	−0.03[b]	0.03[b]	−0.05[b]	0.11[b]	−0.27[b]

[a]significant at ($P < 0.05$); [b]significant at ($P < 0.01$).

Key Words: correlation coefficient, milk composition, season

W38   Comparison of fixed and random regression test day models in genetic evaluation of Iranian Holsteins for protein yield.   M. Bashtani*, H. Farhangfar, H. Naeemipour, M. R. Asghari, A. Arab, and M. Jafari Tarbaghan, *Birjand University, Birjand, Iran.*

The main objective was to compare 2 test day models (with fixed or random regressions) applied for genetic evaluation of protein yield trait in Iranian Holsteins. The data were 57,551 protein test day records from 7036 first parity Holstein cows calved between 2003 and 2006. Total number of herds (located in Razavi Khorasan province), sires, dams and animals in pedigree file were 138, 590, 6091 and 13117 respectively. Contemporary groups were defined based on combining herd - year - season of production - milking times (HYSM). The response variable was test day protein yield for which there was an average 918 gr (SD = 225.8 gr) in the whole data set. In fixed and random regression test day models, HYSM (fixed effect), calving age (linear and quadratic covariables), Holstein gene percentage (linear and quadratic covariables), and random effects of additive genetic and permanent environment were included. To take account of the shape of the lactation curve at phenotypic, genetic and environmental levels, orthogonal Legendre polynomials were also included in the models so that the order of the Legendre fit was level and cubic for fixed and random regression test day models, respectively. Fixed and random regression test day models were run using WOMBAT and DXMRR software, respectively. The results indicated there was a very high rank correlation coefficient (0.936) between predicted breeding values (PBV) which was statistically significant ($P < 0.001$). Averages PBV of progeny were found to be −0.209 and −0.037 gr for fixed and random regression test day models, respectively which were not significantly different from each other. It can therefore be concluded that fixed regression test day model could be used instead of random regression test day model in genetic evaluation of Iranian Holsteins for protein test day records in particular where computational capacity is limited for running a random regression test day model at the national scale.

Key Words: Iranian Holsteins, test day protein yield, random regression

W39   Estimation of udder composite in the Holstein population of Iran. M. R. Bakhtiarizadeh*, M. Moradi Shahr Babak, and A. Pakdel, *University of Tehran, Karaj, Tehran.*

The objective of the present study was to estimate the weights of udder type traits in udder composite (UC) of Holstein cattle in Iran. Records generated for first lactation Holstein dairy cows from 1991 to 2007 over 220 herds. The genetic parameters and relationships between udder traits and functional traits (milk yield, longevity, and somatic cell score (SCS)) were estimated and data (included udder type traits (udder depth (UD), fore udder attachment (FU), rear udder width (RUW), rear udder height (RUH), fore teat placement (FTP), rear teat placement (RTP), suspensory ligament (SL)), milk production, SCS and pedigree) were used by Animal Breeding Center in Iran. The genetic parameters were estimated by ASREML software and also SelAction software was used for estimating coefficient importance of functional traits. The equation $Y = Rg*v$ was used for estimating UC. In this equation, Y is weight of udder type traits in UC trait, Rg is the genetic correlation between the udder type traits and functional traits and v is importance coefficient of functional traits that were estimated from SelAction software. Heritability estimates for the udder type traits ranged from 0.1 (FU) to 0.19 (RTP). Heritabilities were 0.05, 0.07, and 0.28 for longevity, SCS and milk production, respectively. The genetic correlation among udder type traits and longevity ranged from 0.41 (UD) to −0.33 (RTP), among udder type traits and SCS ranged from 0.85 (RUW) to −0.6 (FU), among udder type traits and production ranged from 0.34 (RUW) to −0.31(UD). The importance coefficient of functional traits were 0.55, 0.38 and −0.07 for milk production, longevity and SCS, respectively. Finally the UC trait has been shown as follows (PTA is predicted transmitting ability): UC= (−0.091*PTAfu)+(0.015*PTAruh)+(−0.035*PTAruw)+(−0.015*PTAsl)+(0.134*PTAud) +(0.69*PTAftp) +(−0.015*PTArtp). In this study breeding goal was to decrease SCS and increase milk production and longevity by applying the UC trait. Consequently, each trait that has a desirable relationship with functional traits in the breeding goal has a higher coefficient in UC trait.

Key Words: udder composite, type traits, genetic parameters

W40   Bayesian estimates of genetic parameters for cystic ovarian disease, displaced abomasum and foot and leg diseases in Iranian Holsteins via Gibbs sampling.   N. Ghavi Hossein-Zadeh*[1] and M. Ardalan[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Guilan,* [2]*Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran.*

The objective of this study was to estimate heritability and genetic correlations between cystic ovarian disease (COD), foot and leg diseases (FLD), and displaced abomasum (DA) within the first 3 lactations of

Holstein dairy cows. The records of 57,301 dairy cows on 20 large dairy herds in Iran between January 2005 and June 2009 were analyzed with univariate and bivariate threshold animal models, using Gibbs sampling methodology. The final model included the fixed class effects of herd-year, season of calving, parity of dam, the linear covariate effect of age at calving, and additive direct genetic effect of animal. Posterior means of heritability in first, second, and third lactations were 0.14, 0.18, and 0.20, respectively, for FLD; 0.08, 0.10, and 0.11 for COD; 0.05, 0.06, and 0.08 for DA. Posterior means of genetic correlations between diseases were low (from 0.02 to 0.12), within lactations; the largest estimates were for FLD and DA, and the lowest involved FLD and COD. Positive genetic correlations between diseases suggest that some general disease resistance factor with a genetic component exists. The results of this study indicated the importance of health traits for considering in the selection index of Iranian Holstein dairy cows.

Key Words: Bayesian methods, cystic ovarian disease, displaced abomasum

W41   Bayesian estimates of genetic parameters for metritis, retained placenta, milk fever, and clinical mastitis in Holstein dairy cows via Gibbs sampling. N. Ghavi Hossein-Zadeh*[1] and M. Ardalan[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Guilan*, [2]*Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran*.

The objective of this study was to estimate heritability and genetic correlations between the liabilities of clinical mastitis (CM), milk fever (MF), metritis (MET), and retained placenta (RP) within the first 3 lactations of Holstein dairy cows. The records of 57,301 dairy cows from 20 large dairy herds in Iran between January 2005 and June 2009 were analyzed with univariate and bivariate threshold animal models, using Gibbs sampling methodology. The final model included the fixed class effects of herd-year, season of calving, parity of dam, the linear covariate effect of age at calving, and the random direct genetic effect of animal. Posterior means of heritability for liabilities in first, second, and third lactations were 0.06, 0.08, and 0.09, respectively, for CM; 0.10, 0.12, and 0.11 for MF; 0.09, 0.07, and 0.10 for MET, and 0.07, 0.08, and 0.08 for RP. Posterior means of genetic correlations between disease liabilities were low or moderate (from −0.01 to 0.26). The results of this study indicated the possibility of considering health traits in the selection index of Iranian Holstein dairy cows.

Key Words: Bayesian methods, clinical mastitis, metritis

W42   Genetic relationships between somatic cell count, milk production and udder conformation traits in Iranian Holsteins. M. R. Sanjabi*[1], A. Gholibaigi Fard[2], R. Vaez Torshizi[2], A. Lavaf[2], and A. H. Ahadi[1], [1]*Iranian Research Organization for Science and Technology, Tehran, Iran*, [2]*Azad University, Karaj, Iran*.

Heritabilities and genetic correlations between milk yield (MY), fat percentage (FP), protein percentage (PP), somatic cell count (SCC) and udder type traits in 10 dairy Holstein herds near Tehran on 3500 lactations were evaluated. The DFREML software was used for calculation of variance components and heritabilities of individual traits, and genetic correlations were estimated using Harvey's software. Heritabilities were low for SCC (0.04), moderate for MY (0.19) and FP (0.24), and high for PP (0.48). For type traits, heritability estimates ranged from 0.04 to 0.55. The estimated genetic correlation between SCC and udder type traits varied from −0.78 to 0.51 and estimated genetic correlations between SCC and MY, FP and PP were 0.15, 0.03, and 0.04, respectively. In general, the cows with shallow and tightly attached udders and closer teat placement had lower somatic cell count and lower risk of mastitis. In summary, it appears that selection for improved udder conformation will reduce SCC and clinical mastitis among cattle selected for high milk production.

Key Words: dairy cattle, genetic parameters, somatic cell count