Breeding and Genetics: Applications and Methods in Animal Breeding—Dairy

W182   Epidemiology of synchronization programs for breeding management in US dairy herds. A. H. Souza*[1,2], P. A. Carvalho[1], R. D. Shaver[1], M. C. Wiltbank[1], and V. Cabrera[1], [1]*Department of Dairy Science, University of Wisconsin, Madison,* [2]*Ceva Sante Animale, Libourne, France.*

The aim of this study was to evaluate the use of synchronization programs in US dairy herds. Reproductive records from DHIA (AGSource, Agritech, and DRMS) were analyzed. The final data set included artificial insemination records from 2008 to 2012 and restricted to AI-breedings with confirmed pregnancy outcome. Only herds reporting at least 30 breedings in the last 12 mo were included. A total of 1,142,821 breeding records from 40 states were available for the 1st analysis. Breeding codes were classified within herd into either AI-to-estrus (EAI) or synchronized-AI (SAI) based on weekly insemination profile for each herd. Within-herd, synchronized breedings were assumed when more than 30% of the breedings happened on the same day of the week, remaining breedings for the same herd were considered non-synchronized. Overall, 29.9% of the breedings happened after the use of synchronization programs, with great variation throughout states. The leading states in terms of proportion of SAI that reported more than 5,000 breedings were SD = 56%, WI = 46%, IA = 43%, OH = 40%, MI = 32%, NY = 29%, PA = 27%, MN = 24%, VA = 23%, and SC = 23%. Out of all SAI breedings, 78% happened on Thursdays and Fridays. There were no significant differences in conception results between SAI (32.6%) and EAI (33.4%), with no interactions with breeding month. Herd size information was available for a further data set from WI herds with 207,506 breedings. Findings in regards to herd size and use of SAI at 1st AI in herds in WI are shown in Table 1, which indicates that SAI is used in most 1st postpartum AIs and larger herds seem to use more SAI at 1st AI and have lower days to 1st AI without compromising conception outcomes. In summary, these results indicate that most dairy herds in US use synchronization strategically as part of their breeding program. Supported by Accelerated Genetics.

Table 1.

Herd size	ME305 (kg)	SAI – 1st AI (%)	DIM at 1st AI (d)	P/AI at 1st AI (%)
<300 (n = 54,199 AI)	13,104[a]	47.4[a]	80.2[a]	36.5[a]
300-1000 (n = 89,336 AI)	14,082[b]	66.4[b]	76.0[ab]	35.5[a]
>1000 (n = 63,971 AI)	14,527[c]	75.3[c]	72.0[b]	35.1[a]

Key Words: dairy farm, timed AI, synchronization

W183   Effects of different stall type and bedding materials on lactation length, milk yield and some health problems in dairy herds. N. K. Kara*[1], A. Galiç[2], and M. Koyuncu[1], [1]*Uludag University, Bursa, Turkey,* [2]*Akdeniz University, Antalya, Turkey.*

This study was carried out to determine effects of 2 different stall types and 3 different bedding materials on lactation length, milk yield and some health problems in dairy herds. 477 lactation cows in 37 herds in Bursa were examined. Mean of lactation length (day) and milk yield of cows in the same herd was calculated to determine the effects. A *t*-test was used to compare the means of free-stall or tie-stall herds, and one-way ANOVA was used to compare the means of herds with concrete, sand or rubber bedding. To test the association between stall type or bedding material and some health problems, Chi-squared test was used. According to the results, a significant difference was determined between 2 stall types, in terms of milk yield ($P < 0.01$), while mean of milk yield and lactation length of herds with rubber bedding were found higher than the others ($P < 0.01$). The associations between stall type and repeat breeding, dystocia and retained placenta were found to be significant ($P < 0.01$, $P < 0.01$ and $P < 0.05$, respectively). Also, it was found that repeat breeding and clinical mastitis were associated with bedding material ($P < 0.05$ and $P < 0.01$, respectively). The results of the present study indicate that by providing suitable stall type with better bedding materials, animals can be kept healthy, expenditures on medical treatments can be minimized and consequently profitability can be increased.

Key Words: bedding material, stall type, lactation length

W184   Genetic and phenotypic trends for milk yield in Holstein populations in Mexico. H. O. Toledo[1], F. J. Ruiz[2], C. G. Vazquez[1], J. M. Berruecos[1], and M. A. Elzo*[3], [1]*Universidad Nacional Autonoma de Mexico, Ciudad de Mexico, DF, Mexico,* [2]*INIFAP, Queretaro, Queretaro, Mexico,* [3]*University of Florida, Gainesville.*

The objectives were to evaluate genetic and phenotypic trends from 2007 to 2011 for milk yield in 3 Holstein populations representing 14% of the milk production in Mexico. Data consisted of first-lactation milk yields adjusted to 305 d, adult equivalent and 2 milkings/d. Records were from the Holstein Association of Mexico (HAM; n = 43,668), the National Bank of Dairy Information (NBDI; n = 120,217), and the National Breeding Program of Mexico (NBPM; n = 163,885) which included records from HAM and NBDI. Best Linear Unbiased Predictions of breeding values (BV) were computed with ASREML using a mixed animal model. Fixed effects were herd-year-season. Random effects were animal and residual. Weighted and unweighted yearly means of sire BV were computed for HAM, NBDI, and NBPM. Weights were numbers of daughters per sire per year. Weighted yearly means of sire BV in NBPM were also computed by country of origin (USA, Canada, México, Other). Lastly, yearly means of cow BV and phenotypic values (PV) were obtained for HAM, NBDI, and NBPM. The mean BV and PV of cows for milk yield in the HAM, NBDI, and NBPM populations increased between 2007 (BV = 108.4 ± 5.7 kg; PV = 217.3 ± 25.4 kg) and 2011 (BV = 242.9 ± 3.3 kg; PV = 486.3 ± 14.0 kg). Differences between yearly means indicated that cow BV from HAM tended to be higher than cow BV from NBDI (from 32.2 kg in 2009 to 47.2 kg in 2010). Holstein sires from the US tended to have substantially higher yearly mean BV for milk yield (from 722.4 kg in 2008 to 991.3 kg in 2010) than Holstein sires from Mexico. Breeders from HAM tended to choose sires with higher BV for milk yield (401.9 ± 15.1 kg) than those from NBDI (396.5 ± 11.0 kg). However, differences in weighted yearly means (from 221.9 kg in 2008 to 101.8 kg in 2010) suggested that NBDI breeders used sires with higher BV for milk yield more frequently than HAM breeders. Greater utilization of sires with increasingly higher BV for milk yield allowed dairy breeders in Mexico to consistently increase cow genetic and phenotypic means from 2007 to 2011.

Key Words: genetic trend, phenotypic trend, milk yield

W185   Genetic parameter estimates for rump traits and teat length in a multibreed dairy cattle population in Thailand. B. Wongprom[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1],

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Hip width (HW, cm), pin width (PW, cm), hip to pin length (HP, cm), hip height (HH, cm) and teat length (TL, cm) of cows are important for reproduction and production efficiency of a dairy business. Most dairy cattle in Thailand and other Asian tropical countries are multibreed where Holstein is a major component breed (mean = 87%; SD = 9%) and both purebred and crossbred animals are regularly selected as parents of the next generation. The objective of this study was to estimate genetic parameters for rump traits (HW, PW, HP and HH) and TL of dairy cattle in a multibreed dairy population in Thailand. The data set consisted of pedigree and phenotypic information for HW, PW, HP, HH, and TL from 868 cows located in 122 farms across Thailand. The data were analyzed using a multiple-trait animal model that accounted for the fixed effects of herd, Holstein fraction, and age of cow, and the random effects of animal and residual. An average information-restricted maximum likelihood procedure was used to estimate variance components. Estimates of variance components were subsequently used to compute heritabilities and genetic correlations. Means and SD were 55.13 cm and 4.91 cm for HW, 18.49 cm and 2.40 cm for PW, 51.74 cm and 3.27 cm for HP, 134.07 cm and 5.52 cm for HH, and 5.07 cm and 1.43 cm for TL. Heritability estimates were high for HW (0.42 ± 0.10), medium for PW (0.23 ± 0.09) and HP (0.25 ± 0.10), and low for HH (0.11 ± 0.08) and TL (0.12 ± 0.09). Most genetic correlations ranged from medium (0.35 ± 0.28 between HP and PW) to high (0.91 ± 0.45 between PW and HH). The only low correlations were between TL and PW (0.14 ± 0.39) and between TL and HH (0.19 ± 0.54). These estimates of heritability and genetic correlations indicated that it would be feasible to develop a genetic improvement program for rump traits and teat length in this multibreed population.

Key Words: dairy, genetic parameter, type trait

W186   Genotype by environment interaction effect on lactation pattern and milk production traits in an Ethiopian dairy cattle population. G. Gebreyohannes[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], [1]*Kasetsart University, Bangkok, Thailand,* [2]*University of Florida, Gainesville.*

The objective of this study was to evaluate the effect of genotype by environment interaction (GEI) on lactation pattern and milk production traits in an Ethiopian multibreed dairy cattle population. The analyses used 4,488 lactation milk records of 1,320 cows born from 254 sires and 896 dams collected in 2 research centers (Bako and Holetta) from 1979 to 2010. Breeds present in the population were Horro, Boran, Friesian, Simmental and Jersey. Traits were lactation milk yield (LY), initial milk yield (IY), peak milk yield (PY), average milk yield per day (YD), lactation length (LL) and days to peak (DP). The effect of GEI was tested using a fixed linear model that considered herd-year-season, parity, environment (Bako and Holetta), breed and the interaction between breed and environment as fixed effects, and residual as a random effect. Lactation length was considered as a covariate for the analysis of LY. Least squares means (LSM) were compared among subclasses of each factor. All factors in the model affected LY, IY, PY, YD and LL ($P < 0001$). The effects of breed and breed by environment interaction on DP were not significant. All traits had significantly ($P < 0001$) higher LSM values in Holetta than Bako. Friesian crossbred cows in Holetta had significantly higher LSM for LY (2111.9 ± 16.87 kg), IY (9.2 ± 0.08 kg), PY (11.6 ± 0.08 kg) and YD (6.6 ± 0.05 kg) than Simmental and Jersey crosses. The LSM for LY, PY and YD were significantly ($P < 0.0001$) higher for Friesian and Simmental than for Jersey crossbreds in Bako. However, the LSM IY and LL were not significantly ($P > 0.05$) different among Friesian, Simmental and Jersey crossbred cows. The LSM of LY, IY, PY, YD and LL for Boran

and Horro were not different in both environments. In Holetta, the Jersey and Simmental were not significantly different for the LY, IY, PY and YD. Thus, Friesian sires can be recommended for crossbreeding with Boran or Horro in Holetta, and Friesian, Simmental and Jersey sires in Bako.

Key Words: dairy cattle, genotype by environment interaction, multibreed

W187   Impact of sire by region interaction on first-lactation traits of dairy cows raised under tropical conditions in Thailand. P. Yod-klaew[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], [1]*Kasetsart University, Bangkok, Thailand,* [2]*University of Florida, Gainesville.*

Initial yield (IY), peak yield (PY), days to peak yield (DP) and persistency (PS) are traits associated with milk yield (MY) in dairy cattle. Daughters of the same sire could have different lactation curve traits (IY, PY, DP, and PS) and MY in different regions. Thus, the objective of this study was to investigate the effect of sire-by-region interaction on first-lactation traits in 3 regions of Thailand. The data set contained 27,276 monthly test-day records from 2,431 first-lactation cows raised in 294 farms located in Central, Northeastern and Southern Thailand. Wood's gamma function was used to estimate IY, PY, DP, PS, and MY for individual cows using their monthly test-day records. A fixed linear model was used to avoid sire-by-region interactions due to unequal numbers of daughters per region. The fixed linear model included herd-year-season, calving age, Holstein fraction, and interaction between sire and region as fixed effects, and residual as a random effect. Sires were ranked in each region using their least squares means and correlations between sire rankings across regions were computed. Herd-year-season affected ($P < 0.001$) all lactation traits and calving age only influenced PY ($P = 0.02$). Holstein fraction had no effect on any trait and sire-by-region interaction had an effect only on PY and MY ($P < 0.001$). Correlations between sire rankings in the Central and Northeastern regions, Central and Southern regions, and Northeastern and Southern regions were low or close to zero for PY (-0.01 to 0.05) and MY (0.03 to 0.29). These results suggested that sires would affect their daughter's first-lactation PY and MY differently if they were located in different regions of Thailand. Thus, sires would need to be selected based on their genetic superiority in each region to optimize genetic improvement for milk production in this Thai population.

Key Words: dairy cattle, interaction, tropical

W188   Optimal age at first calving for US dairy cattle. J. B. Cole, J. L. Hutchison*, D. M. Bickhart, and D. J. Null, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Heifer rearing is a major expense for the US dairy industry that accounts for 15 to 20% of the total cost of producing milk. Selecting for an optimal age at first calving (AFC) in US dairy cattle could reduce these costs while still providing animals with high lifetime yields. Records from 9,502,802 Holstein (HO), 611,939 Jersey (JE), and 46,580 Brown Swiss (BS) cows with first calvings from January 1, 1997 to present were selected for analysis. A linear model included the fixed effects of herd-year of calving, year-state-month of calving, and AFC, grouped into 50-d intervals. The traits analyzed included, milk yield, composition, and persistency; fertility; and longevity. Contrary to current age adjustment factors, the highest first-lactation milk yield occurred at an AFC between 651 to 700 d (21 to 23 mo) for HO, resulting in an increase in milk production of 58 kg compared with animals with an AFC between 701 to 750 d (23 to 25 mo). Similarly, fat, protein, and persistency of milk in HO showed an increase of 1.86 kg, 2.08 kg, and 0.05, respectively, for the same AFC

interval. For JE, the highest yields occurred at 601 to 650 d (20 to 21 mo), with increases of 129 kg, 5.18 kg, 4.45 kg, and 0.12 for milk, fat, protein, and persistency of milk, respectively. The greatest yields for BS occurred between 701 to 750 d, although they did not differ from the yields of the 651 to 700 d or 751 to 800 d groups. Heifers from all breeds calving between 601 to 750 d showed an increase in heifer and cow conception rates compared with those calving later. Lifetime traits (up to 5 parities) showed the same optimal HO AFC, with differences between 651 to 700 d and 701 to 750 d of +589 kg, +21.14 kg, +18.23 kg, +11 d, and +0.90 d for milk, fat, protein, days in milk, and days open. For JE, differences between 601 to 650 d and 701 to 750 d were +1397 kg, +64.21 kg, +50.03 kg, +33 d, and +0.72 d, respectively. These results show that the optimal AFC is actually 75 to 130 d less than the breed averages published in 2010, suggesting that a reduction in AFC may improve profitability and fertility in HO and JE cattle.

Key Words: age at first calving, milk production, fertility

W189   Evaluation of genetic advance of production traits in Shenxing dairy farm from 2002 to 2012. G. Yao[1], H. Liming[2], L. Guanglei*[1,2], Z. Changbin[1], and F. Fengshou[1], [1]*Shanghai Dairy Breeding Center Co., Ltd., Shanghai, China,* [2]*State Key Laboratory of Dairy Biotechnology, Shanghai Bright Holstan Co., Ltd., Shanghai, China.*

Genetic trends of milk, fat and protein yield (305 d, 1st lactation) from the Shenxing dairy farm in Shanghai were evaluated for genetic trend by best linear unbiased prediction. Original data consisted of 13,548 production records between 2002 and 2012 were obtained from Dairy Herd Improvement (DHI) project of Shanghai Dairy Breeding Center. Generation interval from sire to daughter was 6.48 years and from dam to daughter was 5.84 years, with an average of 6.16 years. Heritability of milk, fat and protein yield was calculated by half-sister correlation analysis. Heritability estimates were 0.27, 0.16 and 0.14 for milk, fat, and protein yield. Average genetic trend for milk yield was about 71 kg per year over 11 years, an increase about 0.84% per year (60 to 67 kg per year in the first 6 years, about 0.71 to 0.79% of average genetic progress; about 70 to 86 kg in the later 5 years, approximately 0.82% to 1.01% of average genetic change). Average genetic advance of fat and protein yield were about 2.1 kg and 1.1 kg per year, the average genetic progress were about 0.45% to 0.82% in fat yield and 0.37% to 0.56% in protein yield. Our results showed that the genetic level of yield traits in Shanghai Holstein herd have increased in the past 11 years, and that meant the improvement project of Shanghai Holstein herd is effective.

Key Words: genetic advance, generation interval, heritability

W190   Genetic parameters for test-day milk, fat, protein and mozzarella yield using random regression models in buffaloes. N. Hurtado-Lugo*[1,2], R. Aspilcuelta[1], G. M.F. de Camargo[1], M. Cerón[2], and H. Tonhati[1], [1]*State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil,* [2]*University of Antioquia, Medellín, Antioquia, Colombia.*

Buffalo milk is used mainly for the production of milk derivatives due to the compositional and physicochemical quality of its components. Random regression models (RRM) can be applied to test-day milk yield as an alternative to standard procedures used for the genetic evaluation of longitudinal traits in dairy cattle. We aim was to estimate covariance functions for additive genetic and permanent environmental effects and, subsequently, genetic parameters for milk (MY), fat (FY) protein (PY) yields and mozzarella cheese production(MP) in buffaloes from Colombia using RRM with orthogonal Legendre polynomials (LP). Data of test-day MY, FY, PY and MP of 1884 first lactation buffaloes were analyzed. They were daughters of 228 sires from 14 herds in Colombia with calving between 1995 and 2011. For test-day, 10 mo classes of lactation days were considered. Herd-year test day was used as a contemporary group. The random effects in the model included: additive genetic effect, permanent environment and residual and the fixed effects of contemporary group, buffalo age at calving (linear and quadratic effect) and mean lactation curve of the population modeled by LP of 3rd order. The residual variances were modeled with homogeneous structures and many heterogeneous classes. The variance components were estimated using the statistical package WOMBAT. According to the REML test, the best model for MY was with 4 classes of residual variances, considering LP of 3rd and 5th order for additive genetic and permanent environment effects respectively. For FY, PY and MP, the best model was with 4 classes of residual variances, considering LP of 3rd and 4th order for additive genetic and permanent environment effect respectively. The heritability estimates for MY, FY, PY and MP varied from 0.38 to 0.05, from 0.67 to 0.11, from 0.50 to 0.07 and from 0.50 to 0.11, respectively. In general, the RRM were adequate do describe the genetic variation in test-day of MY, FY, PY and MP in Colombian buffaloes.

Key Words: animal model, heritability, mozzarella

W191   Rate of genetic progress and breeding values in commercial dairy herds using young versus daughter proven sires. C. D. Dechow*[1] and G. W. Rogers[2], [1]*Penn State University, University Park,* [2]*Geno Global Ltd., Hamar, Norway.*

The objective of this study was to evaluate the rate of genetic progress and breeding values (BV) of cows in commercial dairy herds using young sires (YS) with genomic BV versus daughter proven sires (PS). Genotypes were simulated at 1000 loci for a nucleus herd of 1000 animals (500 bulls and 500 cows) born each year and a commercial herd with 500 cows born annually. Allele effects were −1 or 1 for all loci and accuracy was 100% for initial scenarios as BV was obtained by summing allele effects across loci. Young bulls and cows were selected beginning at 2 years of age and ending at 3, versus a range of 6 to 7 years for PS. Young sires and dams from the top 10% of BV were selected for the nucleus herd. Sires for commercial cows were selected from the top 10%, 25%, or 100% of the nucleus population. Thirty years of selection were simulated and results among scenarios were compared for years 11 to 30. The average generation interval for the nucleus herd was 2.22 years and the actual genetic progress of 0.75 additive genetic standard deviations per year was close to expectations from the genetic progress formula (0.79). The rate of genetic progress in commercial herds (0.73 to 0.77) was nearly identical to progress in the nucleus herd regardless of whether YS or PS were selected. The BV of cows in PS scenarios lagged behind cows in YS scenarios by 4 years when selection intensity was identical between YS and PS, which was equivalent to the difference in generation interval. The lag was reduced to 1.5 years when the top 10% of PS were selected versus the top 100% of YS. Scenarios were considered where accuracy was reduced by adding a random noise term to the BV before making selection decisions. Higher accuracy for PS further reduced the lag between YS and PS scenarios. It was concluded that the rate of genetic progress in commercial herds may not differ for YS versus PS selection strategies, but that average BV at a specific point in time will vary depending on differences in generation interval, selection intensity, and accuracy. Genetic progress predictions may need to consider interdependencies among selection pathways.

Key Words: genomic, genetic progress

W192   Evaluation of sources of variation and estimation of productive parameters using multi-trait animal models in dairy buffaloes in Pakistan. S. M. Suhail*[1,2], M. S. Qureshi[2], I. Ahmed[2], H. Akbar[1], M. J. Khan[1], and J. J. Loor[1], [1]*University of Illinois, Urbana, [2]KPK Agricultural University, Peshawar, Pakistan.*

Buffalo is the major source of milk production in Asia. Production performance of buffaloes raised at 3 state farms of Pakistan was studied using complete milk records from 5,026 lactations. Economic traits including lactation yield (LY), standard 305-d yield (SY), peak daily milk yield (PY), average daily milk yield (DY) and lactation length (LL) were studied. A general linear model (GLM) procedure was used to study the effect of herd, year, season of calving and sire nested into herd, parity and age at puberty × season of calving on production traits. Birth weight, square of birth weight, lactation length, calving interval, age at puberty and age at first calving were used as covariates. Average LY was 2,076 ± 4.94 (1,524 to 3,723 kg) while SY was 2,200 ± 5.93 kg (1,540 to 3,852 kg). PY and DY averaged 9.9 ± 0.05 and 7.1 ± 0.02, respectively. Mean LL was 294 ± 0.49 (181 to 435 d). Herd, sire nested into herd and parity had a significant effect on lactation yield, while the effects of year, season of calving, year × season and age at puberty × season were nonsignificant. Among covariates, birth weight and lactation length had a significant effect on lactation yield. Similarly, standard 305-d milk yield was significantly affected by sire within herd and parity. Among covariates birth weight, square of birth weight, lactation length and calving interval affected the SY. Year and season of calving and their interaction affected PY. Among covariates the length of lactation affected the PY. Herd, sire within herd and parity significantly affected DY. Among covariates, birth weight, square of birth weight and lactation length affected the DY. Lactation length was affected by herd, sire nested into herd and parity. Standard 305 d milk yield was affected positively by birth weight while increasing parity increased milk yield up to third parity. It is concluded that the milk production ability of dairy buffaloes improves by increasing the birth weight and maturity, while keeping the calving interval shorter and the parity up to third lactation.

Key Words: lactation, animal model, dairy buffalo

W193   Development of a Monte Carlo simulation model to quantify genetic progress from an emerging in vitro fertilized embryo transfer dairy reproduction system. K. Kaniyamattam*, J. Schneider, and A. De Vries, *University of Florida, Gainesville.*

Objective of this study was to develop a Markov chain Monte Carlo simulation model to quantify genetic progress from an emerging in vitro fertilized (IVF) embryo transfer dairy reproduction system. The hypothesis is that IVF coupled with genomic testing of calves will rapidly accelerate the genetic gain from the female side. The model simulated individual dairy young stock and cows day by day for 20 years into the future. Individual animal performance was modeled using functions for feed intake, milk production, reproduction, body weight, risk of culling and genetic merit. The model was parameterized to represent an average US Holstein dairy herd. Phenotypic milk production was dependent on genetic merit. All heifer calves born were assumed to be genomically tested and ranked based on a Net Merit index, drawn from a normal distribution. A fixed cow herd size was assumed. The extra heifer calves were sold and the bull calves were sold within 2 weeks after birth. The top 5% of heifers from 10 mo of age to 5 mo of pregnancy were used as oocyte donors. The donor list was updated each month. Oocytes were collected from each donor 4 times per month. The collected oocytes were in vitro fertilized. On average there were 5 transferable embryos per collection. All open eligible heifers and cows

were observed for estrus 3 d after giving prostaglandin. It was assumed that only 66% of eligible animals came into estrus. The recipients were randomly chosen. The recipients on d 6, 7, 8 of the estrus cycle were transferred with a d 7 embryo. Surplus embryos were frozen if there were not enough recipients available and AI was used if there were not enough embryos (fresh or frozen) available. The model was developed in JAVA. Preliminary results showed an increase in Net Merit of $30 per year based on selection on the female side. The model will be further used for evaluations and sensitivity analyses of management factors that affect genetic progress and profitability of this reproduction system such as genomic testing strategy and selection of recipients.

Key Words: in vitro fertilization, embryo transfer, genetic gain

W194   Heritability estimates of performance and health traits of Holstein calves. M. Mousa*[1,2], A. Seykora[2], H. Chester-Jones[3], D. Ziegler[3], and J. Cole[4], [1]*Department of Animal Production, Faculty of Agriculture, Assiut University, Assiut, Egypt, [2]Department of Animal Science, University of Minnesota, Saint Paul, [3]University of Minnesota, SORC, Waseca, [4]Animal Improvement Programs Laboratory, ARS-USDA, Beltsville, MD.*

The objective of this study was to estimate heritabilities of performance and health traits of Holstein calves. These traits were available on 6,390 AI sire-identified Holstein heifer calves reared at University of Minnesota, SROC facility. Calves were picked-up at 2 - 4 d old from 3 Minnesota commercial dairy farms during the period April 2003 to May 2012. Calves were removed from the data set if they were in sire progeny groups of less than 2, leaving 6,189 observations for analyses. Performance traits were BW (W56) and hip height (HH56) at 56d of age, BW (LBW) and hip height (LHH) at approximately 200d of age, daily gains in the nursery from arrival to weaning at 56d of age (WADG) and from arrival to 200d of age (LADG). Health traits were coded relative to number of incidences that required treatment during the first 56d of age (0, 1, 2 treatment incidences). The Proc MIXED procedure of SAS 9.1 was used to estimate variance components with sire fitted as a random variable. Significant fixed effects ($P < 0.01$) in the model were year of birth, month of birth, year of birth × month of birth, arrival BW and serum protein level fit as a covariate. Performance traits were moderately heritable, with estimates ranging from 0.25 to 0.37. Health traits had low heritabilities, ranging from 0.01 to 0.06. Results suggest that calf performance and health can be improved genetically.

Table 1. Performance and health traits

Performance trait	Average	SD	Sire variance	Residual	Heritability
W56 (kg)	74	9.38	2.5447	35.9814	0.26
HH56 (cm)	90	3.29	0.3357	5.128	0.25
LBW (kg)	206	21.90	29.9901	285.46	0.37
LHH (cm)	114	3.66	0.8692	8.9867	0.35
WADG (kg/d)	0.62	0.13	0.0008	0.0115	0.26
LADG (kg/d)	0.86	0.09	0.0004	0.0056	0.29

Health trait	Incidence occurrence (%)			Sire variance	Residual	Heritability
	0	1	2			
Scours	49.78	50.05	0.17	0.0034	0.2417	0.06
Respiratory	99.48	0.51	0.01	0.0005	0.0485	0.04
Navel	99.57	0.38	0.05	0.0002	0.0592	0.01

Key Words: heritability estimate, performance and health traits, Holstein calf

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