

Breeding and Genetics: Applications and methodology in animal breeding—Dairy

T86 Genetic and phenotypic trends for age at first calving and milk yield in daughters from imported and Thai Holstein sires.

Tawirat Konkrua¹, Skorn Koonawootrittriron*¹, Thanathip Suwanasopee¹, and Mauricio A. Elzo², ¹*Kasetsart University, Bangkok, Thailand*, ²*University of Florida, Gainesville, FL*.

Age at first calving (AFC) and milk yield (MY; accumulated 305-d milk yield) are important traits for the dairy cattle industry. To genetically improve these traits under tropical conditions in Thailand, both imported Holstein (IH) and Thai Holstein (TH; purebred and crossbred Holstein-Other Breeds) sires have been used for mating with Holstein purebred and Holstein-Other Breeds crossbred cows. The objective of this study was to compare genetic changes in AFC and MY from 1991 to 2014 in first-lactation daughters of IH and TH sires. The data set included AFC and first-lactation MY from 5,390 daughters of 507 IH and 232 TH sires that calved from 1991 to 2013 in 481 dairy farms. The bivariate animal model considered herd-year-season and Holstein fraction as fixed effects, and animal and residual as random effects. Variance components were estimated using an average information restricted maximum likelihood procedure. Variance component estimates were used to compute heritabilities and correlations. Mean estimated breeding value (EBV) for daughters of IH and TH sires were computed for each calving year. Regressions of mean EBV for AFC and MY on calving years were computed to assess genetic trends. Heritability estimates were 0.19 ± 0.04 for AFC and 0.13 ± 0.04 for MY. Near zero genetic (0.09 ± 0.18) and phenotypic (0.07 ± 0.02) correlations were estimated between AFC and MY. Overall genetic trends were negative for AFC (-0.013 ± 0.003 mo/yr; $P < 0.001$) and positive for MY (1.16 ± 0.30 kg/yr; $P < 0.001$). However, non-significant negative AFC genetic trends existed for daughters of IH sires (-0.006 ± 0.003 mo/yr; $P = 0.06$) and TH sires (-0.020 ± 0.004 mo/yr; $P < 0.001$). Conversely, significant positive MY genetic trends occurred for progeny of IH sires (1.14 ± 0.43 kg/yr; $P = 0.008$) and TH sires (4.40 ± 0.46 kg/yr; $P < 0.001$). These results indicated that there was genetic improvement in the appropriate direction (negative for AFC and positive for MY) in this Thai dairy population, and that TH sires brought larger changes than IH sires, primarily for MY.

Key Words: dairy, selection, tropics

T87 Genomic-polygenic evaluation for milk yield and fat yield in a multibreed dairy cattle population in central Thailand.

Bodin Wongpom¹, Skorn Koonawootrittriron*¹, Mauricio A. Elzo², and Thanathip Suwanasopee¹, ¹*Kasetsart University, Bangkok, Thailand*, ²*University of Florida, Gainesville, FL*.

Milk yield (MY) and fat yield (FY) are economically important traits for Thai dairy businesses. Genetic prediction for MY and FY in Thailand uses only pedigree and phenotypic information. Combining SNP genotypes of individual animals with pedigree and phenotypes would be expected to increase the accuracy of genetic predictions and speed up selection progress. The objectives of this study were to estimate the fraction of the genetic variance accounted for by 8,257 SNP from GeneSeek GGP-LD BeadChip and to compare the rankings of animals evaluated with a genomic-polygenic (GP), genomic (G), and polygenic (P) models for MY and FY. The data set consisted of first-lactation MY and FY records from 600 cows from 56 farms in Central Thailand collected from 2000 to 2013. The mixed model contained herd-year-season, Holstein fraction and age at first calving as fixed effects (all models).

Random effects were SNP genomic (GP and G), animal polygenic (GP and P) and residual. Variance components were estimated using GS3 software (option VCE; GP and P). Additive genetic predictions were computed with GS3 (option BLUP) for all models. The fraction of additive genetic variances explained by the 8,257 SNP from GGP-LD and computed with the GP model were 46% for MY and 45% for FY. Heritability estimates with the GP model were higher (0.37 for MY and 0.40 for FY) than those with the P model (0.28 for MY and 0.30 for FY). Rank correlations between GP and G models were the highest (0.99 for both MY and FY; $P < 0.0001$), followed by correlations between GP and P models (0.91 for MY and 0.75 for FY), and the lowest correlations were between G and P models (0.89 for MY and 0.73 for FY; $P < 0.0001$). Thus, SNP from GeneSeek GGP-LD not only accounted for a sizeable fraction of the additive genetic variance for MY and FY, but they also yielded animal genomic EBV whose ranking was highly correlated with rankings of both genomic-polygenic and polygenic EBV. These results indicated that utilization of GGP-LD, and perhaps higher density genotyping chips, would be advantageous for genomic-polygenic evaluation and selection in Central Thailand.

Key Words: dairy, genomic, tropics

T88 Genomic evaluation, breed identification, and population structure of North American, English and Island Guernsey dairy cattle.

Tabatha A. Cooper*¹, Sophie A. E. Eaglen², George R. Wiggans¹, Janez Jenko², Heather J. Huson³, David M. Morrice², Maurice Bichard⁴, William G. Luff⁵, John A. Woolliams², and Brian P. Van Doormaal⁷, ¹*Animal Genomic and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD*, ²*The Roslin Institute & R(D)SVS, University of Edinburgh, Easter Bush, United Kingdom*, ³*Department of Animal Science, Cornell University, Ithaca, NY*, ⁴*English Guernsey Cattle Society, Launceston, United Kingdom*, ⁵*World Guernsey Cattle Federation, Castel, Guernsey, United Kingdom*, ⁶*Select Sires, Plain City, OH*, ⁷*Canadian Dairy Network, Guelph, ON, Canada*.

Genomic evaluations of dairy cattle in the United States have been available for Brown Swiss, Holstein, and Jersey since 2009 and for Ayrshire since 2013. As of February 2015, 2,281 Guernsey bulls and cows had genotypes from collaboration between the United States (USA), Canada (CAN), England (E), and the Island of Guernsey (I). The E/I contributions were made possible by the European Commission project, Gene2Farm. Of those genotyped, 431 were males with traditional evaluations. Evaluation accuracy was assessed using 4-fold cross-validation using males only. The cross-validation was repeated 10-fold and gains in reliability over parent average were averaged. Twenty-two traits were analyzed including 5 yield traits, 3 functional traits and 14 conformation traits. Mean gain in reliability over parent average for all traits was 13.8 percentage points. The highest gains were for strength (26.7), rump width (23.6), fore udder attachment (23.2) and fat percent (21.1). Traits with the lowest gains were daughter pregnancy rate (1.0) and somatic cell score (-0.9). The average 13.8-point gain for Guernsey can be compared with averages of 9, 24, 40, and 31 for Ayrshire, Brown Swiss, Holstein, and Jersey respectively. Twenty-one single nucleotide polymorphisms were useful for Guernsey breed determination and are used in routine genotype quality control to confirm breed and identify crossbreds. Genetic differences between E/I animals and USA/CAN

animals from an admixture study using principal component analysis will be presented. No haplotypes that affect fertility were identified from the current data set however; monthly assessments are conducted. These results are expected to lead to routine genomic evaluation of Guernseys in the USA and E/I.

Key Words: Guernsey, genomic evaluation, single nucleotide polymorphism

T89 Genetic relationship between final score and production traits in Brazilian Holstein cattle. Victor B. Pedrosa*¹, Pedro G. Ribas Neto², Silvano F. Valoto², Luis F. B. Pinto³, and Gabrieli S. Romano³, ¹*Universidade Estadual de Ponta Grossa, Ponta Grossa, Parana, Brazil*, ²*Associação Paranaense dos Criadores de Bovinos da Raca Holandesa, Curitiba, Parana, Brazil*, ³*Universidade Federal da Bahia, Salvador, Bahia, Brazil*.

Dairy cattle farmers seek to have animals that stay longer in the herd and still produce more milk and solids with each generation. In this regard, the final score has been used as a selection criterion to be related to many linear type traits and possibly present positive correlation with dairy yield traits. Thus, this study aimed to evaluate the genetic correlations between final score, milk, fat and protein yield and thus prove the positive relationship between them to better conduct dairy cattle programs in Brazil. The database contained information on 83,176 first lactation cows born between 1991 and 2011, with 148,534 records on pedigree file. The considered final score was 50 to 97, wherein the lower score represents a weak classification and the highest score excellent. Genetic parameters estimation were obtained based on the animal model using the VCE software. Analyses were performed considering the contemporary group (same herd-year) as fixed effect and the age of cow as a covariate. The average of final score and production of milk, fat, and protein were respectively 81.50 points, 8,531.50 kg, 287.90 kg, 270.74 kg. The genetic correlation between final score and production traits were 0.12, 0.02 and 0.14, respectively for milk, fat and protein. Hence, the correlation among milk and fat, milk and protein and lastly fat and protein were 0.49, 0.84 and 0.55, respectively. The results showed that there is a low, but positive correlation between final score and production traits, demonstrating that the selection for this type feature can improve dairy production. The results of relationship between production traits are consistent with findings in the literature in Holstein breed, in which the selection to increase milk or solids will benefit other production traits, specialty among milk and protein yields. Therefore, the final score should be included in the Brazilian Holstein breeding programs because it is widely known to be positive associated with legs, feet and udder, besides genetically contributing to increase dairy production.

Key Words: dairy cattle, linear type trait, milk yield

T90 Genetic trends in dairy production of Brazilian Holstein cow. Victor B. Pedrosa*¹, Altair A. Valloto², Jose A. Horst², Avelino M. Figueiredo², and Adriana S. Martins¹, ¹*Universidade Estadual de Ponta Grossa, Ponta Grossa, Parana, Brazil*, ²*Associação Paranaense dos Criadores de Bovinos da Raca Holandesa, Curitiba, Parana, Brazil*.

Production and pedigree monitoring in Holstein cattle is carried out for many years but a only a few farmers effectively use breeding programs in Brazil. In the year 2014, the Holstein Association of Paraná State in partnership with the State University of Ponta Grossa created the State breeding program of cows, to accelerate genetic progress and consequently increase dairy production. Therefore, this study aimed to

evaluate the genetic trend obtained in the last 10 years for milk, fat, and protein yield and thus increase the genetic evaluation of female population in the country. The database contained information on 54,224 first lactation cows born between 2001 and 2011, with 81,336 records on pedigree file. Genetic trends were estimated from the linear regression of annual averages of breeding values. Estimates of breeding values were obtained based on the methodology of mixed models through BLUP solutions using the PEST software. Analyses were performed considering the contemporary group (same herd-year) as fixed effect and the age of cow as a covariate. The average production of milk, fat, and protein were respectively 8,693.17 kg, 286.51 kg and 264.28 kg. The estimated genetic trend was 6.62 kg/yr for milk, 0.44 kg/yr for fat and 0.34 kg/yr for protein. The results show that even with low adherence to animal breeding programs by dairy farmers there was a significant genetic progress for the 3 studied traits. This result might be explained by the use of imported genetic material of quality bulls from markets such as the United States, Canada and the Netherlands. However, it is essential to mention the importance of the farmers to increase selection based on genetic values estimated in a national selection program, reducing possible negative effects caused by the use of imported genetic material, selected in a different environment. Thus, it is expected that the new breeding program of cows provide greater genetic and productive advances for Brazilian herds.

Key Words: breeding program, milk yield, selection

T91 Association between genomic SNPs and dairy production traits in Thai multibreed dairy cattle. Pimchanok Yodklaew¹, Skorn Koonawootrittriron*¹, Mauricio A. Elzo², and Thanathip Suwanasopee¹, ¹*Kasetsart University, Bangkok, Thailand*, ²*University of Florida, Gainesville, FL*.

Genomic chips containing large number of single nucleotide polymorphisms (SNPs) have been widely used to study marker-trait associations in dairy cattle. Identification of genes associated with economically relevant traits close to significant SNPs are subsequently identified in genomic databases. The objective of this study was to find significant SNPs and genes that were associated with milk yield (MY), initial yield (IY), peak yield (PY), day to peak (DP), persistency (PS) and age at first calving (AFC) in a Thai Holstein-Other multibreed dairy population. The data set contained 2,409 first-lactation records from 295 dairy farms located in Central, Northern, Western, and Southern Thailand that were collected between 1997 and 2014. Animals were genotyped with 1 of 4 GeneSeek Genomic Profiler BeadChips (9K, 20K, 26K, or 80K). Thus, a set of 7,357 SNPs from autosomes in common among the 4 chips were used in this study. Association between SNPs and traits were analyzed using QXPAK.5 software. The mixed model included herd-year-season, Holstein fraction, age at first calving and SNPs as fixed effects, and animal and residual as random effects. The number of significant SNPs associated with MY, IY, PY, DP, PS and AFC were 649, 491, 627, 477, 527, and 381 at $P < 0.05$, and 342, 225, 301, 215, 259 and 156 at $P < 0.01$, respectively. All significant SNPs were checked for their association to 5,320 genes in the NCBI database obtained using Map2NCBI (R package). No gene was related to all traits. However, 8 genes were associated with 5 traits (*C3H1orf87*, *LOC100848063*, *NR5A2*, *PCDH15*, *WWO30*, *NCAMI*, *GLI2* and *LOC784126*) at $P < 0.05$, and 7 genes were associated with 4 traits at $P < 0.01$ (*NR5A2*, *KCNIP1*, *INSC*, *LOC784126*, *EEF1E1*, *ATRNL1* and *LOC100294923*) at $P < 0.01$. Results from this research emphasized the need to validate SNP-dairy trait associations under Thai tropical environmental conditions to optimize the benefits of genomic selection.

Key Words: SNP, multibreed, tropics

T92 Accuracy of genomic prediction using principal component analysis on an imputed high-density SNP panel in Italian Holstein cattle. Antonio Puledda¹, Giustino Gaspa¹, Ezequiel L. Nicolazzi², Corrado Dimauro¹, Paolo Ajmone Marsan³, Alessio Valentini⁴, and Nicolo PP Macciotta*¹, ¹Dipartimento di Agraria, Università di Sassari, Sassari, Italy, ²Fondazione Parco Tecnologico Padano, Lodi, Italy, ³Istituto di Zootecnica, Università Cattolica del Sacro Cuore, Piacenza, Italy, ⁴Dipartimento per l'Innovazione dei sistemi biologici, agroalimentari e forestali, Università della Tuscia, Viterbo, Italy.

In this study, the effect of predictor dimensionality reduction using Principal Component analysis (PCA) on the accuracy of Direct Genomic Values (DGV) for of 2,822 Italian Holstein bulls was tested. A subset of animals (916) were genotyped with high density (HD, 800K) bead-chip; the remaining were imputed from medium density (MD, 50K) to HD. Several 617,166 markers were retained after data editing. A MD panel was simulated for all animals by merging the HD panel with the BovineSNP50v2. A total of 40,669 markers were retained for the analysis. PCA were carried out both genome and chromosome wide for the MD (MD_GW and MD_CHR respectively), only by chromosome for the HD (HD_CHR) panel. Several PC explaining 90% of the total variance was retained: 1,436 (MD_GW) 4,829 (MD_CHR) and 5,321 (HD_CHR) respectively. PC score effects for 32 productive, functional and conformation traits were estimated on 2,301 training bulls born before 2004. DGVs were computed for the remaining 521 validation bulls born after 2003. Accuracy of prediction (rDGV) was computed as correlation between DGVs and phenotypes. Average rDGV across 32 traits were 0.29 ± 0.13 , 0.31 ± 0.13 , 0.36 ± 0.14 for MD_GW, HD_CHR and MD_CHR, respectively. Such an increase may be explained by the reduction of asymmetry between the number of predictors and observations. In particular, the shrinkage of the total variance of different SNP panel size in a quite similar number of PCs occurring during PCs extraction, could be seen as possible explanation of a better repartition of variance that resulted in a gain of rDGV passing from genome to chromosome wide and from high to medium density. This research was supported by Italian Ministry of Agriculture, grant INNOVAGEN.

Key Words: genomic selection, principal component analysis, high-density SNP panel

T93 Estimation of genetic parameters for calving ease of Holstein cattle in Korea. Mahboob Alam, Kwang Hyeon Cho*, Tae Jeong Choi, Chung Il Cho, and Yun Ho Choy, *National Institute of Animal Science, Rural Development Administration, Cheonan-si, Chungcheongnam-do, Republic of Korea.*

Calving ease (CE) is a complex reproductive trait of economic importance for dairy cattle. This study was aimed to estimate the genetic parameters of CE for Holsteins in Korea. A total of 978,674 records of CE, collected from 1992 to 2014, from first 5 parities of Holstein cows were analyzed. Age of cows at first 5 parities were ranged within 18–42 mo, 30–54 mo, 42–66 mo, 54–78 mo, and 66–90 mo, respectively. Calving ease was recorded as ordered categories ranged from 1 to 5, indicating 1 = normal (not assisted), 2 = moderate assistance (extraction by 1 person), 3 = moderate assistance (extraction by 2/3 persons), 4 = difficult (extraction by > 3 persons), and 5 = surgical assistance calving. All CE categories were converted to a continuous scale through Snell score transformation procedure. The derived Snell scores for all parities were 0.01, 3.92, 6.288, 7.485, and 8.825 for category 1 through 5, respectively. A single trait sire-maternal grandsire model (S-MGS) was considered for ANOVA and covariance components from each parity

cows using ASREML 3.0 software package. Age at calving was fitted as fixed covariate, and herd-year-season, sire and maternal grandsires of the recorded cows were fitted as random effects in the S-MGS model. Estimated direct heritabilities for parity 1 through 5 were 0.06 ± 0.01 , 0.08 ± 0.01 , 0.10 ± 0.01 , 0.07 ± 0.01 , and 0.06 ± 0.02 , respectively. Maternal heritabilities from the models were 0.02 ± 0.01 , 0.04 ± 0.02 , 0.03 ± 0.01 , 0.01 ± 0.01 , and 0.04 ± 0.01 , respectively. Genetic correlations between direct and maternal genetic components were moderately to strongly negative for first 5 parities, such as -0.51 ± 0.15 , -0.50 ± 0.16 , -0.89 ± 0.10 , -0.97 ± 0.30 , and -0.81 ± 0.17 , respectively. This study being the first report on CE of Korean Holsteins, we expect that the estimated genetic parameters derived in the study would be valuable for their calving ease improvement.

Key Words: calving ease, genetic parameter, Holstein cattle

T94 Modeling for estimation of genetic parameters of milk production traits using random regression models in Korean Holstein cattle. Chung Il Cho, Tae Jeong Choi*, Kwang Hyeon Cho, Mahboob Alam, Yun Ho Choi, and Jae Gu Lee, *National Institute of Animal Science, Rural Development Administration, Cheonan-si, Chungcheongnam-do, Republic of Korea.*

The study was aimed to estimate genetic parameters for milk production traits of Holstein using random regression models (RRM), and compare the goodness of various RRM with homogeneous and heterogeneous residual variances. A total of 126,980 test-day milk production records of the first parity Holstein cows between 2007 and 2014, from the Dairy Cattle Improvement Center of National Agricultural Cooperative Federation in South Korea, were used in this purpose. These records were milk yield (MILK), fat yield (FAT), protein yield (PROT) and solids-not-fat yield (SNF). The statistical models included random effects of genetic and permanent environments using Legendre polynomials of third to fifth order (L3-L5), fixed effects of herd-test day, and year-season at calving and, a fixed regression for the test-day record (third to fifth order). The residual variances in the models were either homogeneous (HOM) or heterogeneous (15 classes, HET15; 60 classes, HET60). Total 9 models (3 orders of polynomials \times 3 types of residual variance) such as L3-HOM, L3-HET15, L3-HET60, L4-HOM, L4-HET15, L4-HET60, L5-HOM, L5-HET15, and L5-HET60 were compared using AIC and/or BIC statistic to find the best fitted model(s) for particular traits. The AIC and BIC estimates were different among models for traits. The lowest BIC value was observed for the model L5-HET15 (MILK; PROT; SNF), and L4-HET15 (FAT), and those fitted the best. The BIC value of HET15 model for a particular polynomial order was lower than that of HET60 model in most cases. The estimated heritabilities from the best-fitted models in the study ranged from 0.08 to 0.15 for MILK, 0.06 to 0.14 for FAT, 0.08 to 0.12 for PROT, and 0.07 to 0.13 for SNF according to days in milk of first lactation. Genetic variances for studied traits tend to decrease at earlier stage of lactation, which then followed by an increase in the middle, and a further decrease at the end of lactation. Estimated RRM parameters can be used in Korean national genetic evaluation system instead of lactation models.

Key Words: random regression model, milk production trait, heritability

T95 Estimation of genetic trends and profitability of dairy herds using different reproductive and genetic culling strategies with a stochastic simulation model which includes multitrait genetics. K. Kaniyamattam* and A. De Vries, *University of Florida, Gainesville, FL.*

The objective of the study was to estimate the genetic and phenotypic performance of the herd when voluntary culling of heifers was based on estimated breeding value (EBV) of milk (1st criteria) or Net Merit (NM\$) (2nd criteria). A daily dynamic stochastic model that simulates 5000 milking dairy cows, heifers and embryos over time and which included multitrait genetics was used. Heifers were inseminated with conventional (CS) or sexed semen (SS). Surplus dairy cows were culled based on the same criteria used to rank heifers. Genetic and economic changes were measured by the changes in true breeding values (TBV) of milk and NM\$, as well as actual phenotypic milk production and profit in a decade. Each of 5 experiment was run 5 times. In the first set of experiments, only CS was used with criteria 1 and 2. The increases in mean \pm SE of TBV of milk in first parity cows were 1,243 \pm 9 and 1,223 \pm 12 kg for criteria 1 and 2 respectively. The corresponding increases in annual milk yield/milking cow were 1,628 \pm 31 and 1,607 \pm 41 kg. The increases in mean \pm SE of TBV of NM\$ in first parity cows were \$925 \pm 10 and \$951 \pm 6 for criteria 1 and 2, respectively. The corresponding increases in profit/milking cow/yr were \$752 and \$763. In the second set of 3 experiments SS was used in the first 2 inseminations in heifers with culling of the lowest 20%, 30% and 40% heifers ranked on EBV for DPR. The increases in mean \pm SE of TBV of milk in first parity cows were 1090 \pm 11, 1084 \pm 15 and 1060 \pm 4 kg for the 3 heifer cull rates respectively. The corresponding increases in annual milk yield were 1245 \pm 44, 1197 \pm 42 and 1087 \pm 30 kg. The increases in mean \pm SE of TBV of NM\$ in first parity cows were \$975 \pm 6, \$980 \pm 3 and \$974 \pm 6 for the 3 heifer cull rates respectively. The corresponding increases in profit/milking cow were \$680, \$685 and \$618. In conclusion, the results showed that genetic trends and profitability depended on the genetic culling and reproductive strategies. Future studies will determine optimal combinations of genetic selection and reproductive strategies.

Key Words: multitrait genetics, phenotype, profit

T97 Genetic parameters and trends for dairy traits in Holstein Friesian under North African conditions. Salem Abdalla-Bozrayda¹, Emhimad A. E. Abdalla¹, and Mauricio A. Elzo^{*2}, ¹*University of Benghazi, Benghazi, Libya*, ²*University of Florida, Gainesville, FL.*

Few studies have investigated the performance of Holstein Friesian cattle under North African conditions. Thus, the objectives of this research were to estimate genetic parameters for milk yield (MY, kg), true herd life (THL, d), and age at first calving (AFC, mo), and to compute genetic and environmental trends for MY using information from the Ghot Al-Sultan dairy farm near Benghazi, Libya. The data set contained MY, THL, and AFC records from 1,968 Holstein Friesian first-lactation cows collected from 1986 to 2002. There were 96 sires and 1,511 dams represented in the data set. Genetic parameters were estimated using restricted maximum likelihood procedures using a 3-trait mixed model. Fixed effects were year-season (all traits) and the covariates of age at first calving (MY, THL) and lactation period (MY). Random effects were cow and residual. The relationship matrix included 2,935 animals. Computations were carried out using the AIREMLF90 program. Milk yield genetic trends for cows, sires, and dams were estimated using means of breeding values for cows, sires and dams per year as regressions of average cow, sire, and dam mean breeding values on years. The estimates of heritability for MY (0.17 \pm 0.04) and AFC (0.14 \pm 0.03)

were low, whereas the value for THL (0.05 \pm 0.04) was close to zero. The estimates of genetic correlations between MY and THL (0.22 \pm 0.01), and between MY and AFC (0.19 \pm 0.04) were low, and the correlation between THL and AFC was near zero (0.07 \pm 0.04). The MY genetic trends were 4.11 \pm 0.92 kg/yr for cows, 5.70 \pm 1.12 kg/yr for sires, and 2.32 \pm 0.81 kg/yr for dams. Although low, the positive MY genetic trends for cows, sires and dams suggested the existence of an effective selection program and utilization of sires with superior breeding values under Libyan conditions. Conversely, environmental trends were negative for cows, sires, and dams suggesting deterioration of nutrition and management practices during the period covered in this study.

Key Words: dairy cattle, genetic trends, North Africa

T98 Genetic parameters for production traits and age at first calving in Gyr dairy cattle. Marco Prata^{*1,2}, Francesca Malchiodi², Filippo Miglior^{3,2}, Lenira El Faro⁴, Aníbal Vercesi Filho⁵, and Vera Cardoso¹, ¹*Departament of Genetics, Ribeirão Preto Medical School, University of São Paulo, Ribeirão Preto, SP, Brazil.*, ²*Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada*, ³*Canadian Dairy Network, Guelph, ON, Canada*, ⁴*Centro Avançado de Pesquisa Tecnológica do Agronegócio de Bovinos de Corte, Instituto de Zootecnia, Sertãozinho, SP, Brazil*, ⁵*Centro Avançado de Pesquisa Tecnológica do Agronegócio de Bovinos de Leite, Instituto de Zootecnia, Nova Odessa, SP, Brazil.*

The selection of Gyr cattle in Brazil has been focused mostly on improving milk yield. However, after the implementation of the Brazilian Agriculture Ministry regulation policies in 2002, which established new parameters for milk quality, producers have shown an interest in increasing fat and protein yield, as well as fat and protein content of milk. Other traits of interest for producers included age at first calving, known to be elevated in Gyr cattle, and which has an important economic impact on dairy farms. The objective of this study was to estimate genetic parameters for 305d milk, fat and protein yield, fat and protein content, and age at first calving for Gyr dairy cattle. The data set consisted of 10,977 records from 8,571 Gyr dairy cows in 245 herds in Brazil. Production traits were analyzed through a linear animal model including the fixed effects of contemporary groups (herd - calving year - calving season - parity) and age at calving as covariable (linear and quadratic effects). Direct additive genetic and permanent environmental effects were included as random effects. The model for age at first calving included the effect of contemporary group (herd - year and season of birth). Estimated heritabilities (SE) for milk, fat and protein yield were 0.23 (0.02), 0.18 (0.04), and 0.13 (0.07), respectively. Fat and protein content showed heritabilities of 0.12 (0.05) and 0.08 (0.07) respectively. Furthermore, the estimated heritability of age at first calving was 0.14 (0.02). The results indicated that the selection for these traits is possible in Brazilian Gyr. However, the low heritability values suggest that environmental factors (i.e., management strategies) could have the highest potential impact on the improvement of these traits. Further analysis should be performed to build a multi-trait selection index for Gyr dairy cattle breeding program in Brazil, to obtain desirable genetic gain for these traits.

Key Words: Gyr cattle milk, production, age at first calving

T99 Evaluation of genetic diversity of three indigenous Russian cattle breeds using whole-genome scanning. Elena A. Gladyr¹, Alexander A. Sermyagin^{*1}, Tatiana E. Deniskova¹, Alexey A. Traspov¹, Veronika R. Kharsinova¹, Gottfried Brem², Natalia A. Zinovieva¹, and Alexey V. Shakhin¹, ¹*L.K.Ernst Institute of Animal*

Husbandry, Dubrovitsy, Moscow, Russia, ²Institute of animal breeding and genetics, University of Veterinary Medicine, Vienna, Austria.

Whole-genome analysis opens the new possibilities to characterize the genetic structure of population and to evaluate the biodiversity in agriculture animal species. The aim of our study was to investigate genetic diversity for local cattle breeds from Central and Northeast European parts of Russia and Siberia in comparison with dairy cattle breeds using the whole-genome SNP data. The total of 57 animals from 5 different breeds were genotyped by 50K Illumina BeadChip including Yaroslavlskaya (n = 5), Kholmogorskaya (n = 8) and Yakutian cattle (n = 7) as well as widespread Russian Black-and-White (n = 6) and Holstein (n = 30). Quality control and analysis was performed using PLINK (1.07), while 1119 loci with > 10% of missing data were excluded, 7069 SNPs failed test frequency minor alleles (MAF < 0.01) and one bull was removed with missingness rate > 10%. 46596 SNPs were left for further analysis. A total of 2660 heterozygous haploid genotypes with the genotyping rate 0.992 were revealed. All local breeds characterized by deficient of SNP heterozygotes. Values of index fixation (F) were positive and ranged from 0.57% in the Russian Black-and-White breed to 17.56% in the Yakutian cattle. The genomic inbreeding coefficient was 3.99%, 4.17% and 10.39% for Holstein, Kholmogorskaya and Yaroslavlskaya breeds, respectively. Runs of homozygosity (ROH) in all investigated animals were 7.64Mb in average wherein minimal ROH was observed for Kholmogorskaya, Yakutian and Yaroslavlskaya breeds (6,65Mb, 7.25Mb and 7.39Mb, respectively) while for Holsteins and Russian Black-and-Whites were characterized by the maximum value of ROH in 7.97–8.00Mb. Linkage disequilibrium in the data set was $r^2 = 0.40$. The principal component analysis based on pairwise identity-by-state distances confirmed that there was the clear clusterisation among animals of Russian local cattle breeds and the group of Black-and-White and Holstein breeds. The greatest genetic difference was shown between Yakutian, Yaroslavlskaya, and Kholmogorskaya breeds as well as between Yakutian and the populations, which were assigned to branch of Holstein cattle. Supported by the Federal Agency for Scientific Organizations, Theme number 19.3 and Russian Scientific Foundation, project number 14–36–00039.

Key Words: cattle, biodiversity, whole-genome analysis

T100 Exploring methodology for application of genomic information in South African dairy breeds. Bernice E. Mostert¹, Robert R. Van der Westhuizen², Este Van Marle-Köster*¹, and Brian Van Doormaal³, ¹Department of Animal and Wildlife Sciences, University of Pretoria, Pretoria, South Africa, ²SA Stud Book and Animal Improvement Association, Bloemfontein, South Africa, ³Canadian Dairy Network, Guelph, ON, Canada.

The establishment of reference populations for genomic selection for Holstein and Jersey breeds in South Africa (SA) is underway. SA breeders have been using direct genomic values (DGVs) based on foreign reference populations, depending on base year definitions and units of measurement of foreign countries to make within herd selection decisions. Due to extensive linkage with international dairy populations, potential exists for utilizing DGVs originating from foreign reference populations to provide SA breeders with genomic information, comparable to SA breeding values. International collaboration was sought for foreign genomic profiles. Genomic profiles of SA Holstein and Jersey animals were generated based on either the GGPHD78K or GGPLD23K chips and DGV on the Canadian scale were estimated, using the North American Consortium's reference population. These were converted to the SA scale using Interbull conversion equations and blended with the SA Parent Averages (PAs), based on performance of

SA cows. This blending was done according to weightings determined by the reliabilities of the DGV and SA PAs. To account for genotype × environmental interactions between Canada and SA, the reliability of the DGV was multiplied by the correlation coefficient between SA and Canada for the specific trait, thereby ensuring that DGV from traits with lower correlations received less weight in the blending with local estimated breeding values (EBV). The weighting for the blending was determined as: EBV weight = EBV reliability/(EBV reliability + DGV reliability). These blended EBVs have been released as genomically enhanced breeding values (GEBVs) and serves as the official breeding values for these animals in the genetic evaluation, which are directly comparable to EBVs of the same breed in SA. Significant increases in the reliability with implementation of this methodology have been observed, with an average increase of 27% for milk yield and 23% for functional herd life. This approach has resulted in the release of GEBVs for production, udder health, fertility, longevity and conformation traits for SA Holstein and Jersey breeders.

Key Words: dairy, genomic information, reliability

T101 Genetic parameters of fertility indicators in Holstein.

Dianelys Gonzalez-Pena*¹, Pablo J. Pinedo², Jose E. P. Santos³, Gustavo M. Schuenemann⁴, Guilherme J. M. Rosa⁵, Robert Gilbert⁶, Rodrigo C. Bicalho⁶, Ricardo C. Chebel³, Klíbs N. Galvão³, Christopher M. Seabury², John Fetrow⁷, William W. Thatcher³, and Sandra L. Rodriguez-Zas¹, ¹University of Illinois at Urbana-Champaign, Urbana, IL, ²Texas A&M University, College Station, TX, ³University of Florida, Gainesville, FL, ⁴The Ohio State University, Columbus, OH, ⁵University of Wisconsin, Madison, WI, ⁶Cornell University, Ithaca, NY, ⁷University of Minnesota, Saint Paul, MN.

Reproductive performance of lactating dairy cows influences the annual calving frequency, replacement heifers available, and milk yield. The goal of this study was to estimate the genetic parameters of fertility indicators in dairy cattle. Measurements from 953 Holstein cows from one farm in Texas across 2 calving years were analyzed. Three fertility indicators were evaluated: probability of cycling at d45 post-calving (Pr_Cyc), probability of disease diagnosis at 45d post-calving (Pr_Sck), and probability of pregnancy after 2 AIs (Pr_Prg). These indicators were estimated using a logistic model including the covariables: dystocia, retained placenta, body condition score at 7d and 35d post-calving (BCS7 and BCS35, respectively), and blood β -hydroxybutyrate (BHBA) indication of subclinical ketosis. Univariate sire models including the effects of contemporary group and lactation number were used to estimate the genetic parameters of days open (DO), BCS7, BCS35, Pr_Cyc, Pr_Sck, and Pr_Prg. The percentage of cows cycling, diagnosed with a disease, and pregnant after 2 AIs were 69.7%, 14.9%, and 64.6%, respectively. The marginal probabilities indicated that cows diagnosed with dystocia, retained placenta, metritis, and mastitis were 1.7%, 6.0%, 11.4%, and 7.3% less likely to be cycling than healthy cows, respectively. Cows were 2.7% and 4% less likely to be cycling per unit increase in mucus score and BHBA, respectively. The heritability estimates (and standard errors) for Pr_Cyc, Pr_Sck, Pr_Prg, DO, BCS7, and BCS35 were 0.23 (0.15), 0.29(0.17), 0.58(0.19), 0.19(0.13), 0.25(0.16), and 0.25(0.18), respectively. Our results indicate that the fertility traits considered in this study have an important genetic component and that they could be used as effective indicators of fertility in breeding and management decisions. These findings could be the foundation to develop novel fertility indices that combine the fertility indicators hereby studied to improve the accuracy of pregnancy prediction and selection for improved fertility in dairy production. These findings contribute to

a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Key Words: heritability, fertility, dairy cattle

T102 Selection signature analysis in Holstein cattle identified genes known to affect reproduction. Li Ma¹, Tad, S. Sonstegard², Curtis Van Tassel², John B. Cole², George R. Wiggans², Brian A. Crooker³, F. Abel Ponce de Leon³, and Yang Da^{*3}, ¹*Department of Animal and Avian Sciences, University of Maryland, College Park, MD*, ²*Animal Genomics and Improvement Laboratory, ARS-USDA, Beltsville, MD*, ³*Department of Animal Science, University of Minnesota, Saint Paul, MN*.

Using direct comparison of 45,878 SNPs between a group of Holstein cattle unselected since 1964 and contemporary Holsteins that on average take 30 d longer for successful conception than the 1964 Holsteins, we conducted selection signature analyses to identify genome regions associated with dairy fertility. Several genes known to affect reproduction were located in or near genome regions with strong selection signals. These genes include the fibroblast growth factor 1 gene (*FGF1*) on Chr07; the follicle stimulating hormone receptor gene (*FSHR*) and the luteinizing hormone choriogonadotropin receptor gene (*LHCGR*) on Chr11; the KIT ligand gene (*KITLG* or *KITL*), the fibroblast growth factor 6 and 23 genes (*FGF6* and *FGF23*) and the cyclin D2 gene (*CCND2*) on Chr05; the placental growth factor gene (*PGF* or *PLGF*) and the estrogen-related receptor β gene (*ESRRB*) 2Mb downstream of *PGF* on Chr10; and the prolactin receptor gene (*PRLR*) on Chr20. The selection signal for the region containing *FGF1* was among the strongest selection signals we observed. According to the literature on these genes, *FGF1* is involved in broad mitogenic and cell survival activities including embryonic development, *PGF* plays a key role in embryogenesis, *ESRRB* plays an essential role in placenta development, *FSHR* is necessary for follicular development and is expressed on the granulosa cells that are closely associated with the developing female gamete in the ovary of mammals, and *LHCGR* is necessary for follicular maturation and ovulation. Mouse knockout models showed that *FSHR*, *KITLG*, *CCNG2*, and *PRLR* were involved in female fertility proteins. These known gene functions related to reproduction and the fact that these genes were in or near chromosome regions with strong selection signals indicate that these genes could be involved in the vast difference in fertility between contemporary Holsteins and the 1964 Holsteins.

Key Words: fertility, selection signature, Holstein

T103 Genetic interactions for heat stress and herd yield level: predicting foreign genetic merit from domestic data. Janice R. Wright* and Paul M. VanRaden, *Animal Genomics and Improvement Laboratory, Agricultural Research Service, US Department of Agriculture, Beltsville, MD*.

Genetic-by-environmental interactions were estimated from national data by separately adding random regressions for heat stress (HS) and herd yield level (HL) to the US all-breed animal model to improve predictions of future records and genetic rankings in other climates and production situations. Yield data included 79 million lactation records of 40 million cows; somatic cell score, productive life, and daughter pregnancy rate were also tested but had fewer records. Coefficients for HS were the state's July average temperature-humidity index; coefficients for HL were management-level weighted means for energy-corrected milk (ECM) divided by breed-year mean ECM. Coefficients were standardized to a mean of 0 and variance of 1. Predictions of current

(August 2014) from historical (August 2011) records were tested with a model that included herd management group (absorbed), sire estimated breeding value (EBV), dam EBV, and an interaction term (HS or HL) from the truncated data; records were weighted by lactation length for records in progress and by herd heritability using the same weights as in national evaluations. Estimated regression coefficients for sire EBV and dam EBV were always near their expected values of 0.5 and did not change when HS or HL interactions were added to the model. Estimated regressions for interaction terms, expected to be near 1, were 0.80 to 0.93 for HS and 0.61 to 0.72 for HL in yield traits. Squared correlations increased by < 0.0003 for both HS and HL; increases for nonyield traits were even smaller. An additional test used multitrait across-country EBV to predict rankings of the same bulls in the United States and 14 other countries with somewhat different environments. The HS coefficient was significant ($P < 0.05$) in 9 of 14 countries for milk and protein and in 10 for fat; the HL coefficient was significant in 8 countries for milk, 5 for protein, and 1 for fat. Squared correlations after adding an interaction term increased by < 0.004 for HL and < 0.01 for HS. The small changes in rank and correlation gains when HS and HL interactions were included in national evaluations indicate that current genetic predictions perform very well in a variety of environments.

Key Words: heat stress, environmental interaction, random regression

T104 Application of milk mid-infrared (MIR) spectrometry in the dairy cattle industry in Canada. Saranya Gunasegaram^{*1}, Allison Fleming¹, Astrid Koeck¹, Francesca Malchiodi¹, Mehdi Sargolzaei^{1,2}, Milena Corredig^{3,4}, Flavio Schenkel¹, Bonnie Mallard⁵, Ayesha Ali⁷, and Filippo Miglior^{1,7}, ¹*CGIL, University of Guelph, Guelph, ON, Canada*, ²*Semex Alliance, Guelph, ON, Canada*, ³*Gay Lea, Guelph, ON, Canada*, ⁴*Department of Food Science, University of Guelph, Guelph, ON, Canada*, ⁵*Department of Pathobiology, OVC, University of Guelph, Guelph, ON, Canada*, ⁶*Department of Mathematics and Statistics, University of Guelph, Guelph, ON, Canada*, ⁷*Canadian Dairy Network, Guelph, ON, Canada*.

In Canada, many projects are aiming to integrate milk MIR spectra to develop predictions of milk components and cow status. A proportion of milk spectral data from FOSS MIR machines at Canadian DHI partners, CanWest DHI (Guelph, ON) and Valacta (Sainte-Anne-de-Bellevue, QC), have been saved and transferred to the Canadian Dairy Network, since early 2013. With addition of roughly 60,000 milk spectra every month; from approximately 700,000 cows enrolled in milk recording programs in Canada; the database is nearing 1.8 million. These spectra will be merged with recorded cow reproduction and health events (including hoof health). Currently, University of Guelph is analyzing approximately 2,000 milk samples for their fatty acid profile, milk fat globule and casein micelle size, lactoferrin, calcium, casein, and phospholipid content to use as a reference for developing MIR prediction equations. Genetic and genomic evaluation of Canadian dairy cows and bulls will be done using these MIR predicted milk component traits, with the objective of improving the nutritional value of milk and milk products for human consumption. Use of milk MIR spectra will be incorporated in a pending Canadian project, measuring feed efficiency and methane emissions in dairy cattle as a possible means for prediction. Information available to improve both cow management and genetic evaluation in Canadian dairy industry will be increased with the implementation of MIR prediction of a variety of new milk component and cow traits.

Key Words: milk infrared spectra, genomic, dairy cattle

T105 Development of a daily stochastic dynamic dairy simulation model including the 12 traits in the Net Merit Index. K.

Kaniyamattam*, M. A. Elzo, and A. De Vries, *University of Florida, Gainesville, FL.*

We are interested in predicting changes in genetics and profitability of dairy herds when different reproductive strategies are combined with genetic selection. Our objective was to incorporate 12 correlated genetic traits included in Net Merit Index in a dynamic, stochastic model. An existing dynamic, stochastic model that mimics the biology and management of a herd of individual young stock and cows over time was adapted as follows. A true breeding value (TBV) for each trait was calculated as the average of the sire's and dam's TBV, plus a fraction of the inbreeding and Mendelian sampling. TBV were calculated from the Cholesky decomposed genetic covariance matrix of an average unselected Holstein population given as input, multiplied with by a 12×1 matrix of standard normal deviates. Similarly, an environmental component for each trait was calculated based on the Cholesky decomposition of the environmental covariance matrix of the same population. The environmental component was partitioned into a permanent and a daily temporary effect. The combined effect of TBV and the environmental component was converted into an effect on the phenotypic performance of each animal for 6 of the 12 traits, for example effects on milk production, fertility, and risk of culling. Hence, genetics and phenotypic performance were associated. Estimated breeding values (EBV) were calculated using a normal inverse function based on correlated random numbers, the animal's TBV and a standard deviation depending on the reliability of the estimate. The EBV were updated 3 times a year, with reliabilities depending on the age of animals. Complete technical and economic measures were calculated by the model over a period of time. Preliminary validation resulted in similar genetic changes per decade as predicted by USDA-AGIL when using the Net Merit index. The model is suitable to estimate the economic and genetic effects from using different reproductive strategies in dairy herds.

Key Words: multitrait genetics, stochastic modelling

T106 Genetic correlations between days open and milk, fat, and protein yields for the Uruguayan Holstein. Nicolas Frioni*¹,

Jorge I. Urioste¹, Ignacio Aguilar², and Gabriel Rovere¹, ¹*Facultad de Agronomía Universidad de la República, Montevideo, Montevideo, Uruguay,* ²*Instituto Nacional de Investigación Agropecuaria Las Brujas, Rincon de Colorado, Canelones, Uruguay.*

This study aims to estimate the additive genetic correlations (RA) among days open (DO), milk (MY), fat (FY) and protein yield (PY) in lactations 1 to 3 of Holstein herds on pastures-based production systems.

The database used had 546,659; 367,774 and 247,158 observations for 1st, 2nd, and 3rd lactation. Data were edited to set records to DO greater than 42 d. Traits for each lactation were considered different and they were analyzed using 6-variate models, with DO and a production trait. The fixed effects were the age at calving and the combined effect of the herd-year-season and the random additive genetic effect of the animal. Estimations were obtained via Gibbs sampling with Gibbs2f90 program. Heritabilities obtained for each lactation of DO ranged from 0.04 to 0.06, for MY the range was 0.23 to 0.22, for PY from 0.09 to 0.28 and for FY from 0.06 to 0.28. The RA between DO ranged from 0.68 to 0.96, although they were different from 1, most of the values were very high to consider them as different traits. The RA between DO and production traits is presented in Table 1. Results suggest that DO can be considered as one trait, adjusting the model with a fixed effect accounting for different lactations. Unfavorable relationship between DO and production traits may be confirmed, thus is necessary the inclusion of fertility in selection programs, and further estimation of RA analyzing all traits together with a repeatability model.

Table 1 (Abstr. T106). Additive genetic correlations among days open, milk yield (MY), fat yield (FY), and protein yield (PY) in lactations 1 to 3 of Holstein herds

		Days open		
		1	2	3
MY	1	0.39 (0.0375)	0.56 (0.0338)	0.51 (0.0638)
	2	0.49 (0.0357)	0.58 (0.0314)	0.59 (0.0640)
	3	0.40 (0.0335)	0.54 (0.0393)	0.63 (0.0581)
PY	1	0.43 (0.0456)	0.53 (0.0471)	0.78 (0.0282)
	2	0.44 (0.0425)	0.53 (0.0375)	0.69 (0.0372)
	3	0.46 (0.0601)	0.55 (0.0535)	0.67 (0.0543)
FY	1	0.41 (0.0751)	0.51 (0.0907)	0.69 (0.0565)
	2	0.54 (0.0604)	0.66 (0.0434)	0.80 (0.0345)
	3	0.34 (0.0620)	0.46 (0.0520)	0.63 (0.0493)

Key Words: fertility, heritability, dairy cattle