

Breeding and Genetics: Fertility and Early-Life Traits

M26 The relationship of herd-average conception rates and calving interval with sire predicted transmitting ability for three fertility traits. E. S. Benner and C. D. Dechow,* Penn State University, University Park.

The objective of this study was to determine the relationship of sire predicted transmitting ability (PTA) for fertility with reproductive performance in low and high fertility Holstein herds. First service conception rate (FSC; 42,389 records), services per conception (SPC; 29,924 records), and calving interval (CI; 28,113 records) were the herd fertility traits. Herds with a FSC of $\geq 28.4\%$ and a CI of ≤ 13.8 mo were classified as high fertility, whereas herds with $< 28.4\%$ FSC and > 13.8 mo CI were classified as low fertility. Records were further stratified into high genetic groups of daughter pregnancy rate (DPR) if sire DPR was ≥ -0.6 , high cow conception rate (CCR) if sire CCR was ≥ -0.7 , and high heifer conception rate (HCR) if sire HCR was ≥ -0.4 . Records with from cows with sire PTA below those levels were classified as belonging to the low genetic group for each trait. Fertility traits were evaluated in ASREML and the effect of DPR, CCR, and HCR genetic groups were evaluated separately. The model included fixed effects for lactation number, herd group (high or low fertility), genetic group (high or low sire PTA), and the interaction of herd and genetic groups. Age within lactation number, herd-calving-cluster, and error were the random effects. The effect of herd group was highly significant for all traits. The effect of DPR genetic group, CCR genetic group, and HCR genetic group was also significant for all traits ($P < 0.05$). FSC was 3.9% and 3.1% higher for the high CCR and DPR genetic groups, respectively, than the corresponding low genetic groups. SPC decreased by 0.07 services for the high HCR genetic group, 0.10 services for the high DPR genetic group, and 0.14 services for the high CCR genetic group. CI decreased from 1.6 d (HCR) to 5.1 d (DPR) in the high genetic groups. The interaction of DPR or CCR genetic group with herd fertility group was not significant for any trait. The interaction of HCR genetic group effect and herd fertility was significant for FSC ($P < 0.05$). FSC was 17% for both high and low HCR group in low fertility herds, but increased from 32% for low HCR group to 34% for the high HCR group in high fertility herds. In conclusion, this study provides evidence that selection for high fertility can improve reproductive performance in both favorable and adverse fertility herds.

Key Words: daughter pregnancy rate, conception rate, fertility

M27 Effect of body condition score at open period on reproductive traits of dairy cows in Hokkaido. J. Hirose,* Y. Masuda, and M. Suzuki, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido, Japan.

Body condition score (BCS) is a useful indicator for farmers to evaluate negative energy balance (NEB) of dairy cows. During postpartum period, severe NEB in a cow tends to lower reproductive performance. This suggests that if BCS is scored before conception farmers may be able to predict fertility. The objective of this study was to investigate the relationship between BCS at open period and fertility traits. Reproductive and lactation records collected by the Hokkaido Dairy Milk Recording and Testing Association, and type records collected by Holstein Cattle Association of Japan (Hokkaido Branch) were used. From this data set, only primiparous cows recorded between 2007 and 2009 were extracted. The fertility traits used were days open (DO), days from calving to first service (DFS), and number of services (NS). DO and DFS were analyzed using the GLM procedure of SAS and the LOGISTIC procedure of SAS

was used for NS analysis. BCS was scored on a scale of 1 to 9, where 1 = thin and 9 = fat. These scores were then divided into 5 classes: 1 to 3, 4, 5, 6, and 7 to 9. The months of calving were divided into 4 seasons: January to March = spring, April to June = summer, July to September = fall and October to December = winter. BCS, dairy milk yield, protein to fat ratio (P/F), the square of P/F, age of calving, and season were included as fixed effects in all models. As a result, individuals in BCS class 1 showed significantly delayed DO (+11.27 d) and DFS (+11.86 d) compared with BCS class 3 ($P < 0.05$). In contrast individuals in BCS class 4 and 5 were estimated to have a fewer NS (0.15 and 0.23 times) than BCS class 3. The optimal P/F range was found and it significantly decreased DO, DFS, and NS, but spring and summer had significantly adverse effects on these traits. Cows with a younger calving age had significantly shorter DO and DFS. The effects of calving seasons and milk production are associated with fertility traits; however, cows with a medium to high BCS also showed the same tendencies. The BCS at the open period may be an important indicator of when to start the reproductive cycle.

Key Words: body condition score, reproductive trait, dairy cows

M28 Cyclicity and fertility of Holstein, Jersey, and crossbred cows in a fall-calving, pasture-based dairy. K. Glosson* and S. Washburn, North Carolina State University, Raleigh.

With the decline in fertility in dairy herds over many years, use of crossbreeding is one practice that may improve reproduction. At the Center for Environmental Farming Systems Dairy Unit in Goldsboro, North Carolina, 143 cows were studied in a fall-calving (Oct. to Jan.), pasture-based dairy. The 2010–2011 herd included 15 Jerseys (JJ), 12 Holsteins (HH), 37 crosses of JH or HJ (F1), 39 crosses $> 50\%$ Jersey (JX), and 40 crosses $> 50\%$ Holstein (HX). Milk samples collected at 10-d intervals around 30, 60, and 90 d postpartum were tested for progesterone, to determine cyclic status. Any milk sample with progesterone concentration at $> 1.0 \text{ ng/mL}$ or an observed estrus were used to confirm that a cow was cyclic. Cows were observed for estrus and inseminated via AI from Jan 1, 2011 through April 30, 2011. Data for percentages of cows cycling at 30, 60, and 90 d after calving and for those pregnant to first insemination and within the 120-d breeding season are included in the table as raw data means. More JJ, JX, and F1 cows were cyclic at 30 d postpartum compared with HX or HH. Differences in cyclic status were less at 60 d and all cows were cyclic by 90 d postpartum. Conception rates at first service and pregnancy percentages for the 120-d breeding season were generally higher for crossbred cows than for JJ and HH. However, the number of observations was low for both purebred groups. The data in this study are consistent with the potential for improved reproduction for crossbred dairy cows.

Table 1. Cyclicity and fertility of crossbred dairy cows

Item	Breed types				
	JJ	JX	F1	HX	HH
Number	15	39	37	40	12
Cyclic at 30 d (%)	60.0	59.0	62.2	35.0	41.7
Cyclic at 60 d (%)	100	97.4	89.2	72.5	91.6
Cyclic at 90 d (%)	100	100	100	100	100
Pregnant at 1st service (%)	33.3	46.2	56.8	50.0	41.7
Pregnant within 120-d season (%)	46.7	71.8	78.4	70.0	50.0

Key Words: fertility, progesterone, crossbred

M29 Genomic differences between highly fertile and sub-fertile Holstein dairy heifers. A. E. Navarrete^{*1}, C. A. Gill¹, T. E. Spencer², and T. R. Bilby^{1,3}, ¹Department of Animal Science, Texas A&M University, College Station, ²Department of Animal Sciences, Washington State University, Pullman, ³Texas Agrilife Research and Extension, Stephenville.

Reduced fertility in dairy cattle remains a major economic loss to dairy producers. Identifying dairy cattle with superior genetic potential for fertility would increase dairy farm profitability. Blood samples were taken and DNA extracted from dairy heifers ($n = 40$) on 2 commercial dairies in Texas. Heifers were classified into 2 groups based upon services per conception (SPC); those animals with a single SPC were determined to be highly fertile ($n = 20$) and heifers with greater than or equal to 4 SPC were classified as sub-fertile ($n = 20$), representing the 2 tails of the population distribution. Whole genome association analysis was performed utilizing a 777K high-density (HD) single nucleotide polymorphism (SNP) chip. Genomic data were evaluated utilizing a whole genome association analysis toolset (PLINK) and 570,620 SNP were available for analysis with a total of 39 samples being analyzed. Forty-four SNP were determined to be associated with fertility ($P \leq 10^{-5}$) and were located on *Bos taurus* chromosomes (BTA) 2, 4, 9, 19, and 26. The SNP and ranges between SNP were analyzed using BLAST-Like Alignment Tool (BLAT), and SNP were associated with 5 candidate genes for reproduction. The SNP on BTA 2 were located within the region coding for the non-imprinted Prader-Willi/Angelman syndrome 2 (NIPA2) gene and cytoplasmic fragile X mental retardation 1 (FMR1) interaction protein 1 (CYFIP1). In addition, 3 SNP on BTA 9 were located near monofunctional C1-tetrahydrofolate synthase (MTHFD1L). A difference in allele frequency was observed between the 2 groups for SNP located on BTA 19 in proximity to 2 genes, zinc finger 18 (ZNF18) and mitogen activated protein kinase 4 (MAP2K4). The SNP associated with 3 genes and one microRNA, which were significant but had no known role in reproduction, were elac homolog 2 (ELAC2), vacuolar protein sorting 41 homolog (VPS41), glutaredoxin 3 (GLRX3), and microRNA 744 (MIR744). The NIPA2, CYFIP1, MTHFD1L, ZNF18, and MAP2K4 genes have all been linked to reproduction in various species and may play a role in fertility in dairy cattle. Further studies are needed to ascertain the involvement of these and other genes related to fertility in dairy cattle.

Key Words: dairy, genomics, SNP

M30 The quality and yield of embryos from Holstein dairy cows in relation to inbreeding. J. Bezdicke^{*1}, A. Makarevich², R. Holasek², E. Kubovicova², Z. Hegedusova², and F. Louda², ¹Agroresearch Rapotin, Ltd., Vlkovice, Czech Republic, ²Research Institute for Cattle Breeding, Ltd., Vlkovice, Czech Republic.

The effect of inbreeding depression on reproduction traits in livestock is very important. There are several reproduction traits that reveal inbreeding depression, such as service period and age at first calving. The aim of this study was to evaluate the effect of inbreeding level (F_X) on yield and quality of embryos from Holstein cows. The data involve cows used for embryo transfer in the years 2010–2011 at farms in the Czech Republic. The value of F_X ranged from 3.125 to 6.25%. In total, 648 embryos were recovered from 87 donors by flushing of the uterus with Complete flush solution. Of these donors, 21 were inbred (163 embryos collected) and 66 non-inbred cows (485 embryos collected). The data were analyzed using StatSoft Inc. Statistica 10 with descriptive statistics and *t*-tests. Of 485 embryos flushed from 66 non-inbred cows (4.9 embryos per flushing; $s_X = 4.5$) 322 embryos (66.4%) were transferred to recipients. The number of unfertilized embryos was 114

(23.5%) with average of 1.7 embryos per flushing ($s_X = 2.2$) and 49 embryos (10.1%) were degenerated with average of 0.7 embryos per flushing ($s_X = 1.3$). Of 163 embryos collected from 21 inbred cows 107 embryos were transferable (65.6%) with average of 5.1 embryos per flushing ($s_X = 5.2$), 39 embryos were unfertilized (23.9%) with average of 1.9 embryos per flushing ($s_X = 2.0$) and 17 embryos were degenerated (10.5%) with average of 0.8 embryos per flushing ($s_X = 1.7$). There were no statistically significant differences between the inbred and non-inbred cows (*t*-test), although in some cases the records from inbred cows were poorer (number of transferable embryos, unfertilized embryos, degenerated embryos). The significant (negative) correlation was found only between F_X and the total number of collected embryos ($r = -0.50$; $P < 0.05$). There was also non-significant correlation between F_X and number of embryos suitable for transfer (-0.41). In conclusion, the inbred cows with a lower degree of F_X showed insignificantly slightly poorer yield and quality of embryos.

Key Words: embryo transfer, inbreeding

M31 Antioxidants in bovine semen cryopreservation. M. F. Duarte-Junior, L. K. Hatamoto-Zervoudakis,^{*} J. T. Zervoudakis, P. P. Tsuneda, P. H. D. Gomes, F. M. Wingert, F. A. P. B. Arguello, and W. A. S. Marinho, *Federal University of Mato Grosso, Cuiabá, Mato Grosso, Brazil*.

The present study aimed to determine if the addition of vitamins E and C to bovine semen extender reduces damage caused by cryopreservation and oxidative stress, and preserves fertility after the freeze-thawing process. We used 16 Nelore bulls (*Bos taurus indicus*) aged between 2 and 3 years, with proven fertility and without pathology in the reproductive tract. Each ejaculate was split into 3 equal groups and diluted in Tris-based extender containing vitamin E (tocopherol acetate, 10 mmol), vitamin C (ascorbic acid, 0.45 mg/ml), and no additive (control). Diluted semen was chilled for 4 h to 4°C and placed into 0.5 mL chilled straws at a concentration of 25×10^6 sperm/straw. Straws were cooled for 10 min to -95°C in nitrogen vapor, followed by storage in liquid nitrogen until laboratory analysis. Frozen straws were then thawed individually at 37°C for 20 s in a water bath for the evaluation. Spermatic characteristics (motility, viability, abnormality and acrosomal integrity) and oxidative stress (lipid peroxidation) were assessed for each sample. No significant differences ($P > 0.10$) were observed in sperm motility, viability and abnormality, and oxidative stress among the groups. Addition of vitamin E to extender provided better acrosomal membrane integrity ($P < 0.10$) when compared with controls ($94.34\% \pm 0.57$ vs. $92.04\% \pm 2.69$), however the addition of vitamin C ($93.04\% \pm 2.98$) did not protect acrosomal membranes as compared with other groups. Extender supplemented with vitamin E protected acrosomal membranes against freeze-thaw-induced damages and improved measures of bovine semen quality. Further studies are required to obtain more concrete results on the determination of lipid peroxidation and antioxidant capacities of vitamin E in cryopreserved bovine semen.

Key Words: vitamin E, vitamin C, oxidative stress

M32 Extender supplementation with vitamin E and cryopreservation of bull sperm. P. P. Tsuneda, L. K. Hatamoto-Zervoudakis,^{*} J. T. Zervoudakis, L. C. M. Soares, M. F. Duarte-Junior, P. H. D. Gomes, and F. M. Wingert, *Federal University of Mato Grosso, Cuiabá, Mato Grosso, Brazil*.

The objective were evaluation of bovine semen extender supplementation with vitamin E improved viability and quality sperm. Were used

5 young Nelore bulls. Each ejaculate retreated 2 aliquots which were subsequently diluted with lactate extender (Lactato-based extender) and another Lactato extender supplemented with 50.0 mM of vitamin E in concentration of 100×10^6 /mL viable spermatozoa. The diluted aliquots were chilled to 5°C for 4 h, then packaged into 0.5-mL straws and maintained for 20 min up to 5 cm in nitrogen vapor and after immersed in liquid nitrogen. Thawing was performed at 36°C for 30 s, immediately after thawing were evaluated sperm motility, sperm viability and oxidative stress (lipid peroxidation). There was no statistical effect in spermatozoa motility and viability ($P = 0.2133$, $P = 0.3696$, respectively). The supplementation of extender with vitamin E increased oxidative stress ($P = 0.0001$) suffered by spermatocytic cell during the process of freezing and thawing. Spermatozoa cryopreserved in a medium not supplemented showed a less oxidative stress (180.362 ± 64.858 ng/mL) compared with spermatocytic cells cryopreserved in extender supplemented (736.851 ± 112.662 ng/mL). It is concluded that extender supplementation with 50 mmol of vitamin E was not effective in protecting spermatocytic cell against damage caused by freezing and thawing processes.

Key Words: fertility, spermatozoa, antioxidant

M33 Multibreed genetic evaluation of calving ease and birth weight using a threshold-linear model in Brangus. S. Tsuruta,* A. H. Nelson, J. K. Bertrand, and I. Misztal, *University of Georgia, Athens.*

Multibreed genetic evaluation (MBE) was implemented for calving ease (CE) and birth weight (BW) using a threshold-linear model applied to data from the International Brangus Breeders Association. Data included 60,586 CE records with 2 categories (1: easy; 2: difficult) and 500,278 BW records from 1975 to 2011. The pedigree file contained 735,925 animals. Calving ease priors for heterosis and unknown parent group within breeds (breed effects) were obtained by scaling the BW heterosis and breed effects 2%; however, external EPD for CE were not available. External BW EPD priors from the American Angus Association for Angus sires were fit in the analysis. (Co)variance components and MBE for CE and BW were estimated with a threshold-linear model. The model included fixed effects of contemporary group (age-sex-herd), age of dam and heterosis breed contribution, and direct and maternal genetic random effects. The EPDs were compared with those from the current (C-) MBE for BW in Brangus. Of all CE records, 94.5% indicated easy calving. Direct and maternal heritability estimates were 0.23 and 0.18 for CE and 0.46 and 0.16 for BW, respectively. Genetic correlations between CE and BW were 0.87 for direct effects and 0.45 for maternal effects. Genetic correlations between direct and maternal effects were -0.19 for CE and -0.50 for BW. By setting the oldest age group for Angus breed as the mean base in MBE (87.5% in probability scale), predicted breeding values for CE were converted to a probability scale. The EPD was calculated as a deviation from the mean. For 17,847 sires with at least one progeny for birth weight, the correlation of direct EPD between BW in this study and in the C-MBE was 0.96. The correlation between BW in the C-MBE and CE in this study was -0.85. The correlation between BW and CE in this study was -0.90. For maternal EPD, the correlation between BW in this study and in the C-MBE was 0.87. The correlation between BW in the C-MBE and CE in this study was -0.18. The correlation between BW and CE in this study was -0.08.

Key Words: multibreed evaluation, calving ease, Brangus

M34 Expression profiling of testicular sense and antisense RNA transcripts of Brahman bulls. K. K. Adams^{*1}, L. R. Chenault¹, J. Valenta¹, R. N. Vaughn¹, A. K. Torres¹, K. J. Kochan¹, T. H. Welsh Jr.¹, R. D. Randel², F. M. Rouquette Jr.², A. D. Herring¹, and P. K. Riggs¹, ¹Texas A&M University, College Station, ²Texas AgriLife Research, Overton.

This study was designed to identify the extent to which both sense and antisense RNA transcripts were expressed in testis from postpubertal *Bos indicus* bulls as part of a bovine epigenetics project. Concurrent incidences of sense and antisense gene transcription were investigated by microarray analysis. Total RNA was extracted from testicular parenchymal tissue of sixteen 18-mo-old Brahman bulls immediately after slaughter at the departmental abattoir. A random subset of 4 of the 16 RNA samples was used in a microarray experiment. Expression microarrays were designed to assess transcription across the whole bovine genome without emphasis on known gene loci. Therefore, the 60-mer oligo probe-set from a commercial bovine whole-genome comparative genomic hybridization array was printed in expression format (Agilent Technologies, Santa Clara, CA). A total of 171,533 unique probes distributed approximately evenly across the genome were printed on the array (slide A). A second array was designed in which the reverse complement of each of the 171,353 probes was printed (slide B). Cy3-labeled cRNA from each of 4 bulls was hybridized to 4 pairs of microarrays. Expression was detected for 16,738 probes on slide A, and 20,853 probes on slide B. Transcription was detected in both directions for 2,229 unique oligo sequences. To confirm the microarray results for sequences expressed as both sense and antisense transcripts, nested primers were used to directly prime reverse transcription reactions and amplify PCR products so that sense and antisense transcription could be compared for 8 genes by quantitative real-time RT-PCR (qRT-PCR). Gene expression was measured by qRT-PCR of RNA from tissue from all 16 bulls. By relative quantification analysis, similar patterns of expression were observed across animals for a given gene. The relative abundance of sense to antisense transcript quantity was gene dependent, and appeared to be differentially expressed within genes, but not across animals. In summary, we observed that approximately 10% of expressed transcripts in testis are expressed bi-directionally. These data provide a foundation for examining how non-coding transcripts attenuate and regulate gene expression in the bovine testis.

Key Words: antisense RNA, *Bos indicus*, testis

M35 Model comparison for genetic parameter estimation of birth and weaning weight traits in beef cattle. S. O. Peters^{*1,5}, K. Kizilkaya^{2,3}, D. J. Garrick², R. L. Fernando², E. J. Pollak⁴, M. De Donato^{1,6}, E. Chaffee¹, T. Hussain⁷, and I. G. Imumorin¹, ¹Cornell University, Ithaca, NY, ²Iowa State University, Ames, ³Adnan Menderes University, Aydin, Turkey, ⁴US Meat Animal Research Center, Clay Center, NE, ⁵Federal University of Agriculture, Abeokuta, Nigeria, ⁶Universidad de Oriente, Cumana, Venezuela, ⁷University of Veterinary and Animal Sciences, Lahore, Pakistan.

Assumptions of normality in most animal breeding applications may make inferences vulnerable to the presence of outliers. Heavy-tail densities are viable alternatives to normal distribution and provide robustness against unusual or outlying observations when used to model the densities of residual effects. Our objective is to compare estimates of genetic parameters of fitting normal with heavy-tail distributions (Student's *t* and Slash) for residuals in univariate data of birth and weaning traits in beef cattle. A total of 17,019 birth and weaning weight records from 1998 through 2010 at the Rex Ranch were analyzed. Models included fixed effects of contemporary group and sire breed, while animal and

maternal effects were random. The posterior mean and median estimates of the 2 heritabilities, and the genetic correlation using the Markov Chain Monte Carlo algorithms were similar to each other across models, implying that the posterior densities were symmetric and unimodal. Results revealed that posterior means for degrees of freedom were 6.78 and 4.89 in Student's *t* error model and 2.23 and 1.80 in slash error model for birth and weaning weight. Posterior means of direct and maternal heritabilities for birth weight were slightly smaller in Student's *t* when compared with the Normal model. The smallest values were found in the Slash model. For weaning weight, posterior means of direct and maternal heritabilities were highest in Normal models, followed by Slash and the least values were found in Student's *t* error model. Evaluation of 95% posterior probability interval showed that the genetic correlation between additive and maternal effects were not significant for birth weight but they were significant for weaning weight.

Key Words: genetic parameters, robust models, heavy-tailed distributions

M36 Genetic parameters of the reproductive traits in Nelore beef cattle. C. C. P. Paz^{*1,2}, H. L. Moreira², M. E. Buzanskas³, L. El Faro¹, R. B. Lôbo^{2,4}, and D. P. Munari³, ¹SAA/APTA, Ribeirão Preto, SP, Brazil, ²USP/FMMP, Ribeirão Preto, SP, Brazil, ³UNESP/FCAV, Jaboticabal, SP Brazil, ⁴ANCP, Ribeirão Preto, SP, Brazil.

The scrotal circumference (SC) and age at first calving (AFC) are traits easily measured and the most important as indicative of precocity in bovine. Genetic parameters for birth weight (BW), age at first calving (AFC), gestation length (GL) and scrotal circumference (SC) were estimated using records of the 109,185 animals of the Nelore breed participating in a cattle breeding program of the Brazil. The gestation length was analyzed as cow trait (GLcow) and as calf trait (GLcalf). Estimation of genetic parameters was performed using the restricted maximum likelihood method (REML) for animal models, using the WOMBAT software. The mixed model used for BW and GLcalf was $y = Xb + Z1a + Z2m + e$, in which y is the vector of the dependent variable; X is the incidence matrix for fixed effects, thereby associating the elements of b and y ; b is the fixed-effects vector (contemporary group); $Z1$ and $Z2$ is the incidence matrix for direct and maternal random effects, thereby associating the elements of a and y ; a is the random-effects vector for direct additive genetic effects; m is the random-effects vector for maternal genetic effect and e is the residual-effects vector. For SC, AFC and GLcow, the maternal genetic effect was not included in the mixed model. For BW and GL, a linear and quadratic effect of the covariate dam age was considered. Heritability estimates were moderate for BW (0.30 ± 0.02), AFC (0.20 ± 0.02), GLcow (0.20 ± 0.01), GLcalf (0.49 ± 0.05) and SC (0.41 ± 0.02). Genetic correlation estimates between BW and AFC, GLcow, GLcalf, SC were $0.36, 0.31, 0.13, 0.07$ respectively, between AFC and GLcow, GLcalf, SC were $0.19, 0.28, -0.40$, respectively, between GLcow and SC was 0.02 and between GLcalf and SC was -0.21 . These results suggest that selection for AFC and GL could improve female reproductive efficiency. The direct selection for SC and GLcalf could be better than the selection for AFC due to higher heritability estimate. The gestation length analyzed as calf trait (GLcalf) could be included in the selection index of the Nelore Brazil Program.

Key Words: genetic associations, heritability, precocity

M37 Genetic trends for growth-related traits and calving ease

of Simmental beef cattle. H. M. Saad^{*1}, W. Shafer², and R. M. Enns¹, ¹Department of Animal Sciences, Colorado State University, Fort Collins, ²American Simmental Association, Bozeman, MT.

Genetic change in a trait, over time, is primarily driven by the genetic variability, accuracy of selection, generation interval, and selection intensity and, in multiple trait selection programs, by genetic correlations with other traits of interest. Given modern genetic evaluation tools, and reproductive tools such as artificial insemination, selection intensity is a primary driver of genetic improvement. The main goal of this study was to quantify the selection pressure placed on growth and calving ease in the American Simmental Association (ASA) registry as part of a larger project to evaluate birth weight or calving ease EPD in selection programs. Data consisted of 2,540,928 records, from 1980 to 2011, from ASA. Data included maternal calving ease EPDs (CEM) and direct EPDs and accuracies for birth weight (BW), weaning weight (WW), yearling weight (YW), and calving ease (CED). To compare genetic trends on an equal scale, mean EPDs by year were converted to standard deviation units (sdu). Based on preliminary analysis indicating a change in selection pressure since the importation of Simmental genetics, genetic trend for all studied traits can be divided into 2 parts, that occurring from 1980 to 1991 (period 1) and that from 1992 to 2011 (period 2). Results show that mean EPDs for BW in period 1 increased by 0.017 ± 0.0004 sdu/year, which indicates that breeders put more emphasis on growth and correspondingly experienced increasing birth weight. During this period, mean EPDs for CED showed little change (0.0017 ± 0.0003 sdu/year), while mean EPDs for CEM increased by 0.023 ± 0.001 sdu/year. During period 2, the rate of genetic change of mean EPDs for BW dropped dramatically (-0.024 ± 0.001 sdu/year) while mean EPDs for CED increased by 0.019 ± 0.0007 sdu/year. As result, the rate of increase in mean EPDs for YW slowed (0.007 ± 0.0006 sdu/year) while that for WW did not show any change (0.00016 ± 0.0007 sdu/year). These results suggest selection emphasis differed between periods, with breeders selecting against BW in period 2 which resulted in a slower genetic change in growth-related traits compared with what they selected directly for calving ease.

Key Words: Simmental, genetic trend, calving ease

M38 Estimates of genetic parameters for female fertility traits

of Canadian Simmentals. J. Jamrozik^{*1}, S. McGrath², R. A. Kemp², B. Holmquist³, and S. P. Miller¹, ¹CGIL, Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, ²RAK Genetic Consulting Ltd., Lethbridge, AB, Canada, ³Canadian Simmental Association, Calgary, AB, Canada.

Calving to first insemination (CFI) (probability that a cow will successfully produce a calf from her first service) and days to calving (DC; interval between the first exposure to the bull and calving) defined separately for heifers and multi-parity cows were analyzed with a 4-trait linear animal model. The data were 108,206 records on 56,879 Canadian Simmental females with AI and Natural Service breeding records collected from 1974 to 2010. The model included fixed effects of year-season of breeding, age of cow by season of breeding, and age of cow's dam. Random effects were contemporary group, service sire by year of breeding (for CFI only), animal genetic, and cow permanent environmental (PE) effects for repeated records of multi-parity cows.

Bayesian methods were used to estimate posterior distributions of covariance components and genetic parameters. Estimates (SD) of heritability were low, ranging from 1.8% (0.29) for CFI in heifers to 3.7% (0.44) for DC in multi-parity cows. Interval trait (DC) had slightly higher heritabilities compared with CFI; both traits expressed in older cows were more heritable than corresponding traits for heifers. Contemporary group contributed up to 56% of the total variance for DC in heifers. Service sire and the PE were relatively larger (smaller) sources of variation compared with additive genetic (contemporary group) effects. All traits were highly genetically correlated: from 0.68 for CFI in heifers and multi-parity cows to 0.91 for DC in heifers and multi-parity cows. Environmental correlations ranged from -0.72 between CFI and DC in heifers to 0.91 for DC in heifers and multi-parity cows. Correlations smaller than 1 and heterogeneous variances indicated that CFI and DC expressed different aspects of female fertility in beef cattle, and fertility of heifers and multi-parity cows seemed to be different traits genetically. All 4 traits could be used in a form of selection index in Canadian Simmentals to breed for better fertility. Genetic progress, however, would be challenging given low values of heritability, and accurate EPD of bulls would require large numbers of progeny.

Key Words: female fertility, beef cattle, genetic parameters

M39 Polymorphisms in FSH- β ESR and BF genes and their relationship with reproductive traits in Yorkshire pigs. C. Liu¹, J. Shen¹, S. Zhu¹, W. Shi², and Y. Yu^{*1}, ¹*China Agricultural University, Beijing, China*, ²*Animal Husbandry and Veterinary Station of Beijing, Beijing, China*.

The objectives were to provide the molecular basic information of sow reproduction traits for a Yorkshire breeding farm in Beijing, China. We investigated 3 SNPs in swine follicle stimulating hormone β (FSH- β ; Zhao et al., 1999), estrogen receptor (ESR; Rothschild et al., 1996) and properdin (BF; Chen et al., 2009) genes and analyzed their relationship with reproductive traits in the Yorkshire population. A total of 251 Yorkshire sows were randomly selected from the breeding farm in Beijing suburb, China. High quality genomic DNA were extracted from the hair follicles for each pig. PCR-RFLP procedure was used for genotyping of the 3 genes. Associations of the SNPs with 3 reproductive traits, total number born (TNB), number born alive (NBA), and litter birth weight (LBW), were analyzed with mixed GLM model (SAS 9.1). The effects of parity, season, herd, and genotype were included in the model. The dominant genotype for FSH- β , ESR, and BF in the population were BB, AB and CC, respectively. Parity, season, and genotypes significantly affected the reproductive traits of the sows. At the first parity, the sows with AB genotype in FSH- β gene had significantly higher NBA and LBW than AA ($P < 0.05$), and significantly higher NBA than BB genotype ($P < 0.05$). The sows with CC genotype of BF gene were 1.70 kg higher in LBW than the CT sows ($P < 0.05$). The sows with combined genotype of AB-BB-CC for FSH- β , ESR, and BF genes was found significantly higher TNB, NBA and BLW than the AB-AA-CT sows ($P < 0.01$). As for the multiparity, the sows with AB and BB genotypes of FSH- β gene showed significantly higher LBW than the AA sows ($P < 0.05$). The key reproductive traits of the Yorkshire population were significantly influenced by single gene effect of FSH- β . Combined effects of multigenes should be considered in the association study on pig reproduction traits.

Key Words: BF, ESR and FSH- β , pig reproduction traits

M40 Genetic parameters for lifetime number of piglets born alive and length of productive life using a linear censored model. C. Y. Chen^{*1}, A. C. Clutter², and S. Tsuruta³, ¹*Newsham Choice Genetics, Chesterfield, MO*, ²*Agricultural Research Division, University of Nebraska, Lincoln*, ³*Department of Animal and Dairy Science, University of Georgia, Athens*.

The objective of this study was to estimate genetic parameters for lifetime number of piglets born alive (LNBA) and length of productive life (LPL) using a single-trait linear model accounting for censoring. Records of 8,899 Large White females from a single farm collected between 2003 and 2011 were used. LNBA was defined as the number of piglets born alive produced during the lifetime of the sow. LPL was defined as the number of days from first farrowing to last farrowing in natural logarithm scale. Censored records represented 25% of the data. The average number of litters per sow was 5.0. Analyses were carried out with 3 approaches: a linear model excluding censored data (M1), a linear model ignoring censoring (M2), and a linear censored model (M3). Fixed effects included year_quarter based on entry date as contemporary group. Random effects were animal additive genetic effects. The effect of the 3 approaches on EBVs were evaluated for sows with parity < 4 (n = 3,391) and sows with parity > = 4 (n = 5,508). For LNBA, estimates of heritability were 0.13, 0.18, and 0.12 for models 1, 2, and 3. For LPL, estimates of heritability were 0.05, 0.07, and 0.07. Correlations between EBVs for LNBA were 0.97 for M1-2, 0.94 for M1-3, and 0.97 for M2-3 for sows with parity < 4. The same estimates were 0.94, 0.93, and 0.98 for sows with parity > = 4. For LPL, correlations were 0.95, 0.94, and 0.99 for M1-2, M1-3, and M2-3 for sows with parity < 4 and 0.94, 0.94, and 0.99 for sows with parity > = 4. Analysis accounting for censoring has lowest heritability due to increased residual variance and decreased genetic variance for LNBA whereas analysis excluding censored data has lowest estimate of heritability for LPL. Excluding censored data seemed to have larger effects on the estimation of breeding values than ignoring censoring. The effect of model choice on estimation of breeding values for LNBA was larger for sows with larger parity.

Key Words: censored data, genetic parameter, lifetime prolificacy, pigs

M41 Genome-wide association study of age at puberty in swine. J. F. Schneider,* D. J. Nonneman, R. T. Wiedmann, and G. A. Rohrer, *USDA, ARS, U. S. Meat Animal Research Center, Clay Center, NE*.

Age at puberty (AP) is an economically important trait in swine production. Reducing AP provides opportunities to lower the cost of gilt development, reduce age at first farrowing, increase litter size, and improve sow longevity. This analysis was designed to identify quantitative trait loci (QTL) associated with AP. Heat detection with boar contact began at 140 d of age and ended at 230 d of age. Seven hundred 50 7 gilts representing generations 5–8 of a Landrace-Duroc-Yorkshire cross reached puberty during 7 breeding seasons and were genotyped using a 60k chip. SNP were removed that met criteria including minor allele frequency <0.05, call rates <0.95, and unknown location. Five animals were removed with call rates <0.95 or that failed a Mendelian test. Bayesian methods were used to analyze 41,848 SNP. Prior estimates of variances were taken from MTDFREML with heritability = 0.32. The genomic variance priors were estimated by a preliminary run of BayesC using estimates from MTDFREML as priors. A previous

estimate of $P_i = 0.99$ was confirmed by BayesCPi. Final BayesCPi using a burnin of 1000 iterations and a total chain length of 51,000 produced an estimate of 0.16 for the proportion of phenotypic variances explained by genetic markers (genomic heritability). A total of 94 QTL (5 consecutive SNP) were selected for statistical testing based on QTL variance. Testing identified 72 significant QTL including 25 at $P < 0.001$, 32 at $P < 0.005$, and 15 at the $P < 0.01$ level. QTL were found on all chromosomes analyzed (SSC) except 17. Chromosome 2 (SSC2) contained the most QTL with 9, followed by SSC1, SSC3, and SSC7 with 6, and SSC6, SSC10, SSC12, and SSC15 with 5 QTL each. These regions correspond to previously identified QTL (<http://www.animalgenome.org/cgi-bin/QTLD/SS/index> accessed 2/06/2012). The results of this analysis demonstrate that opportunities exist to introduce QTL into genetic improvement programs designed to reduce AP. USDA is an equal opportunity provider and employer.

Key Words: puberty, swine, QTL

M42 Survival in crossbred lambs: Individual, maternal, heterosis, and breed effects. V. C. Ferreira^{*1,2}, D. L. Thomas¹, and G. J. M. Rosa¹, ¹University of Wisconsin-Madison, Madison, ²Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil.

Early mortality in lambs causes substantial economic loss and animal welfare concerns and it is considered a major production limitation. The present study was a genetic analysis of lamb survival from a crossbred population involving 14 breeds to assess factors affecting death of lambs in 5 different periods of life. Data from 7,990 lambs, defined as a binary trait (dead or alive) in 5 different periods (until 1 d, 2 to 30 d, 2 to 60 d, 2 to 90 d and 2 to 120 d of age) were analyzed with a logistic version of the Dickerson full genetic model. Factors considered in the model predictor included sex of lamb, birth type (1, 2, ..., 5), birth month, dam age, individual and maternal breed composition, individual and maternal heterosis (assuming the same magnitude for all pairwise combinations of breeds), and the random individual and maternal additive genetic effects. Results revealed that the effect of F1 individual heterosis resulted in a significant reduction in the probability of death in all 5 periods of life: $-3.71\% (P = 0.08)$, $-6.12\% (P = 0.01)$, $-7.28\% (P = 0.02)$, $-8.24\% (P = 0.01)$ and $-11.26\% (P = 0.002)$. These results suggest the importance of using crossbred animals for increased survival. Maternal heterosis did not have a significant effect in survival in most periods (except the 2 to 30 d period), probably because all animals in the study were artificially raised on milk replacer. The East Friesian maternal effect caused a significant increase in the probability of death in all periods from 2 to 120 d of age (ranging from 11.29 to 14.45%). These results highlight the importance of splitting maternal and heterosis effects from the effect of breed itself when analyzing survival data. All individual breeds with a significant effect on survival caused a decrease in the

probability of death relative to the Lacaune breed, but the size of this decrease varied greatly among breeds and periods. Heritability for lamb survival tended to be low in all periods ranging from 0.04 to 0.13 and the maternal component was almost null (<0.04).

Key Words: crossbred, lamb, survival

M43 Efficiency of breeding Pantaneiro bulls by libido test. J. R. B. Sereno^{*1}, V. G. Ueno², C. H. Bucher³, U. G. P. Abreu⁴, R. S. Juliano⁴, and J. V. Malaquias¹, ¹Embrapa Cerrados, Planaltina, DF, Brazil, ²Centro Paula Souza, Adamantina, SP, Brazil, ³Med. Vet. Autônomo, Campo de Goytacazes, RJ, Brazil, ⁴Embrapa Pantanal, Corumbá, MS, Brazil.

Pantaneiro cattle have been a genetic resource of the Brazilian Pantanal region for nearly 3 centuries. They are well adapted to the soil and climate of the region, reproducing naturally. However, with the arrival of zebu cattle in the region in the 1930s, breeders began indiscriminately crossbreeding these 2 breeds and attributed the merit only for zebu cattle. Currently, the Pantaneiro population is threatened in the region by substitution from zebu cattle. However, Pantaneiro bulls are well known for high libido, showing optimal reproductive performance in natural mating. This study aimed to evaluate potential breeding efficiency of Pantaneiro bulls using libido tests, to characterize the breed with the hopes of its conservation. We used 6 adult bulls aged 3–8 years, who underwent libido tests lasting 20 min/test, using 3 females in a prostaglandin-induced heat in each test. Each bull was tested 6 to 11 times, totaling 56 libido tests with 18.6 h of observation. During the libido test, all sexual behaviors of interest were noted. Scoring was from 0 to 10 where zero = bull showed no sexual interest in females and 10 = the bull made 2 or more services, followed by sexual interest, including mounts, attempted mounts, and services. The results showed that all 6 bulls evaluated had grade 10. All bulls showed interest in a female within 17 s and the first service occurred within 5 min. During the 20 min test the following behaviors were observed: smelling/licking of the vulva (8×), Flehmen Reflex (3.5×), mounting tentative with hands suspended (7×), active pursuit (7×), complete mount (1.5×), exposure of the penis (9×), and sexual interest in more than one female (6.5×). These were all behaviors associated with full mounting. These bulls were shown to be direct in their approaches to mounting and held 2 mounts ($n = 2$), 4 mounts ($n = 3$), or 5 mounts ($n = 1$) during 20 min of observation. These results suggest that Pantaneiro bulls have a high libido and that breeding efficiency would be high if this excellent performance is also carried out in natural matings in the field during the breeding season.

Key Words: animal conservation, beef cattle, animal genetic resource

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