0384 WS Influence of first calving date on stayability in *Bos indicus* crossbred cows. B. N. Engle*, C. A. Gill, J. O. Sanders, D. G. Riley, J. E. Sawyer, and A. D. Herring, *Department of Animal Science, Texas A&M University, College Station.*

Longevity is one of the most important, complex, and difficult to improve traits sought by cow-calf producers. Consequently, a measurement or tool that could be utilized early in a cow's life to predict her future reproductive performance would be advantageous to producers and researchers alike. In this study, we sought to determine the effect of first calving season period on stayability in Nellore-crossbred females through 5 yr, 6 yr, and 7 yr of age. Stayability through each age was scored as a binary trait, with 1 indicating the cow remained in the herd and 0 indicating she was culled, given either a perfect calving or weaning record. Each female was assigned a value of 1, 2, 3, or 4 corresponding to the respective 21-d period of her first calving season (for first, second, or third 21-d period, or > 63 d, respectively). Cow stayability models were evaluated through mixed model procedures (PROC MIXED in SAS). Of the cows with perfect calving records, more ($P < 0.05$) females that calved in the first 21-d period remained in the herd than those that calved in the second 21-d period through 5 yr (66.9% vs. 53.6%), 6 yr (60.0% vs. 45.9%), and 7 yr of age (56.7% vs. 39.3%). They also differed ($P < 0.005$) from females whose first calf was born 63 d or later into the calving season through ages 5 (66.9% vs. 36.0%), 6 (60.0% vs. 29.5%), and 7 (56.7% vs. 27.2%). Of the cows with a perfect weaning record, more ($P < 0.05$) of the females that calved in the first 21-d period of the calving season remained in the herd through 5 yr (56.1% vs. 31.0%) and 6 yr of age (48.3% vs. 26.0%) than heifers whose calf was born at the end of the calving season. These results document that regardless of the culling criteria, *Bos indicus* crossbred heifers that calve early in their first calving season are more likely to maintain a perfect calving or weaning record later in life than females that calve late in the first calving season. Consequently, there is potential that the heifer's first calving season period may be used as valuation or culling criteria when selecting for stayability and longevity, or when merchandizing beef replacements.

Key Words: beef cows, calving season, stayability

0385 Use of a threshold animal model to estimate calving ease and stillbirth (co)variance components for U.S. Holsteins. J. B. Cole*[1], D. J. Null[1], and S. Tsuruta[2], [1]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD,* [2]*University of Georgia, Athens.*

(Co)variance components for calving ease and stillbirth in U.S. Holsteins were estimated using a single-trait threshold animal model and two different sets of data edits. Six sets of approximately 250,000 records each were created by randomly selecting herd codes without replacement from the data used for the December 2015 national evaluations, and from a second extract using more stringent edits than the official run. The stricter edits required that records have a valid dam ID in addition to a known sire, cows have corresponding lactation records, and animals have a breed composition of at least 93.75% of the breed of evaluation. Calving ease was recorded on a five-point scale ranging from no assistance needed (most common) to extreme difficulty (least common). Stillbirth was coded as a binomial trait indicating whether or not the calf was alive 48 h postpartum. Gibbs sampling was used to estimate (co)variance components from each sample; 100,000 samples were drawn, the first 10,000 rounds were discarded as burn-in, and every fifth sample was retained. The model included fixed parity (1 through 5) and sex-of-calf effects, and random herd-year-season, animal (direct), maternal, maternal permanent environment, and residual error effects. (Co)variance components and heritabilities were averaged over the six replicates of each scenario for each trait and are shown (with standard errors). Direct animal effects in the animal model are comparable to sire calving ease and sire stillbirth in the sire-maternal grandsire (S-MGS) model, and heritabilities were similar for the S-MGS and animal models. Maternal heritabilties were slightly lower in the animal model. Heritability estimates were very similar between scenarios within traits, although maternal heritabilities were slightly higher using the new edits. These differences may be due in part to larger estimates of direct-maternal covariances than reported in previous studies, as well as stricter requirements for known parent IDs in the new edits. The implementation of an animal model for calving traits will provide direct estimates of genetic merit for all animals, not only males, and the adoption of stricter

Table 0385.

	Calving Ease		Stillbirth	
Component of variance	Official	New edits	Official	New edits
Herd-year-season	0.6312 (0.07)	0.7294 (0.14)	0.1064 (0.007)	0.0873 (0.005)
Direct genetic	0.2679 (0.02)	0.3233 (0.07)	0.0546 (0.002)	0.0370 (0.004)
Maternal genetic	0.0997 (0.02)	0.1118 (0.02)	0.0467 (0.002)	0.0572 (0.006)
Direct-maternal covariance	0.0387 (0.02)	0.0489 (0.04)	0.0083 (0.002)	0.0164 (0.002)
Maternal permanent environment	0.1604 (0.02)	0.2364 (0.06)	0.0731 (0.003)	0.0373 (0.007)
Residual	1.8558 (0.21)	2.0667 (0.32)	1.0000 (0.000)	1.0000 (0.000)
Direct heritability	0.09 (0.01)	0.09 (0.02)	0.03 (0.002)	0.03 (0.003)
Maternal heritability	0.03 (0.01)	0.04 (0.01)	0.04 (0.001)	0.05 (0.005)

edits will improve data quality without having large effects on the (co)variances used in the evaluation. It also is anticipated that such a change will increase correlations of U.S. evaluations with other Interbull participants for calving traits.

Key Words: animal model, calving traits, (co)variance components

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0386 Genetic parameters for production traits and heifer pregnancy in Red Angus cattle.

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Heifer pregnancy (HPG) is a prediction of the probability that a female will conceive during her first breeding season, typically at a year of age. An inherent issue in the genetic prediction of HPG is that phenotypes can only be collected on females, which limits the amount of information available. To overcome this, inclusion of correlated traits that can be recorded on both sexes, or fertility traits recorded on males could be used to improve accuracy of HPG predictions. Therefore, the objective of this study was to estimate genetic parameters for HPG, 205-d weight (WW), 160-d post weaning gain (PWG), 365-d weight (YW), and scrotal circumference (SC). The project included records on 142,146 animals from the Red Angus Association of America. (Co)Variance parameters were estimated using multiple, two trait animal models and a REML procedure. Heritability and genetic correlations between HPG and production traits were then calculated. Contemporary group was included as a fixed effect for all analyses, additionally, sex and age of dam were included for BW, WW, PWG, and YW analyses, and the linear effect of age was fit for HPG. The random effect of animal was used to estimate additive genetic effects for all analyses, the random effect of dam was fit for the WW and YW analyses to estimate maternal effects, and a random, maternal permanent environment effect was included for WW. Heritability estimates were 0.58 ± 0.01, 0.27 ± 0.01, 0.22 ± 0.01, 0.29 ± 0.01, 0.45 ± 0.02, and 0.12 for BW, WW, PWG, YW, SC, and HPG (averaged across all analyses on the underlying scale), respectively. Genetic correlations between HPG and BW (−0.06 ± 0.05), SC (−0.08 ± 0.09), WW maternal (−0.02 ± 0.09), PWG (0.06 ± 0.07), YW maternal (0.00 ± 0.11), had confidence intervals that included or were near zero, suggesting minimal genetic relationship between the traits. Correlations were highest between HPG and WW direct (0.29 ± 0.08) and YW direct (0.21 ± 0.07). These results suggest that Red Angus females with high genetic potential for weight at 205 d and 365 d have an increased probability of becoming pregnant during their first breeding season. Additionally, the traits WW or YW could be used to help improve accuracy of HPG genetic predictions.

Key Words: beef cattle, genetic correlation, growth, heifer pregnancy

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0387 Daily rumination time in Italian Holstein cows: Heritability and correlation with milk production.

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The aim of the study was to investigate the genetic variation of daily rumination time (min) and its correlation with test-day milk production (kg). Data for the analysis consisted of 91,589 records for rumination time and milk yield from 398 cows (age: 43.21 ± 16.11 mo), collected from September 2014 to October 2015 in two Italian Holstein herds (TAD and MIL). There were 493 calvings, and data distribution across parities was 46.4%, 26.7% and 26.7% for first, second and later parities, respectively. DIM classes were defined as one class for every 30 d, resulting in 11 classes, and there were a total of 378 herd-test-day contemporary groups. The average rumination time was 513.51 ± 115.84 min, and the average milk yield was 33.59 ± 9.18 kg.

Pedigree information was available for 11,634 animals. A Repeatability Animal Model was fitted using the AIREMLF90 software. Herd, yr/mo of calving, and DIM classes within parity were treated as fixed effects, while herd-test-day, permanent environmental, and the additive genetic cow effects were treated as random. Rumination time was longer in pluriparous than in primiparous cows and showed a decreasing trend across DIM. On average, at the beginning of the lactation, pluriparous cows ruminated 75 min longer than primiparous. As expected, pluriparous cows had a higher production levels across DIM than primiparous, with a peak around DIM class 2 and 3 (i.e., 60–90 d). The herd with the highest daily rumination time had the lowest milk production yield: the fixed effects solutions were 569.5 min and 25.8 kg (Herd TAD; rumination time and milk yield, respectively) and 446.4 min and 31.9 kg (Herd MIL; rumination time and milk yield, respectively). The heritabilities for test-day milk yield and daily rumination time were 0.13 (SE = 0.06) and 0.32 (SE = 0.09), respectively. Although the negative phenotypic correlation observed, genetic correlation between the two traits was 0.38 (SE = 0.47); this high standard error is possibly the consequence of the dataset dimension. So far, rumination time has been used as a key monitor of dairy cow health at farm level. Investigating its genetics aspect and the relationship with other important yields and health traits may turn this management tool in a new informative selection criterion for