646 Large-scale single-step genomic BLUP evaluation for American Angus. Daniela A. L. Lourenco*[1], Shogo Tsuruta[1], Breno O. Fragomeni[1], Yutaka Masuda[1], Ignacio Aguilar[2], Andres Legarra[3], Joseph K. Bertrand[1], Tonya S. Amen[4], Lizhen Wang[4], Dan W. Moser[4], and Ignacy Misztal[1], *[1]University of Georgia, Athens, GA, [2]INIA, Las Brujas, Uruguay, [3]INRA, Castanet-Tolosan, France, [4]Angus Genetics Inc., St. Joseph, MO.*

This study aims to investigate the feasibility of single-step genomic BLUP (ssGBLUP) for American Angus evaluation. Over 6 million records were available on birth weight (BW) and weaning weight (WW), 3.4 million on post-weaning gain (PWG), and 1.3 million on calving ease (CE). Genomic information was available on 51,883 animals. Realized accuracies were based on a validation population of 18,721 young animals born in 2013. Traditional and genomic EBV were computed by BLUP and ssGBLUP, respectively, using a multiple-trait linear model for growth traits and a bivariate threshold-linear model for CE-BW. Additionally, 2 methods for handling a large number of genotyped animals were tested: indirect prediction (IND) based on SNP effects derived from ssGBLUP, and algorithm for proven and young (APY) that uses genomic recursions on a small subset of reference animals to invert the genomic relationship matrix (G). All ssGBLUP, IND_ssGBLUP, and APY_ssGBLUP were based on reference populations of about 2000 high accuracy sires and cows (2k), 2k + all genotyped ancestors of the validation population (8k), and 8k + all remaining genotyped individuals not in the validation (33k). With BLUP, realized accuracies were 0.48, 0.67, 0.52, and 0.29 for BW, WW, PWG, and CE, respectively. With ssGBLUP and the 2k (33k animals) reference population, the accuracies were 0.55, 0.71, 0.60, and 0.31 (0.62, 0.78, 0.65, and 0.31), respectively. Low accuracy for CE was due to many missing records and low incidence rate. With 8k reference population, index of indirect prediction with parent average was as accurate as prediction from regular ssGBLUP. With 33k reference population, indirect prediction alone was as accurate as prediction from regular ssGBLUP. APY with recursions on 4k (8k) animals reached 97% (99%) of regular ssGBLUP accuracy; the cost of APY inverse of G is 1% (4%) of the regular inverse. The genomic evaluation in beef cattle with ssGBLUP is feasible while keeping the same models already used in regular BLUP. Indirect predictions allow for low cost interim evaluations. Use of the APY allows for inclusion of large number of genotyped animals in the main evaluation.

Key Words: beef cattle, genomic selection

647 Assignment of polled status using single nucleotide polymorphism genotypes and predicted gene content. John B. Cole[1], Daniel J. Null*[1], Chuanyu Sun[2], and Paul M. VanRaden[1], *[1]Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, [2]Sexing Technologies, Navasota, TX.*

There is growing interest in cattle that are naturally polled, but the polled allele has a very low frequency. The best way to increase its frequency is by index selection, which requires known polled status for all animals. Laboratory tests for polled are used as data, and US and Canadian bulls with ≥500 daughters and not designated as polled are assumed homozygous normal. Polled status is imputed for all other genotyped animals using these data. There are 2 mutations in the region around 1.7–1.9 Mb (UMD3.1) on BTA1 known to cause polled. The Celtic mutation is a deletion and an insertion, and the Friesian mutation a duplication. Both are located in a 75-marker window spanning 0.1–3.5 Mb on BTA1. An animal is heterozygous if it has either mutation, and is homozygous if both haplotypes contain polled, regardless of the mutation. This is consistent with -P and -PP coding in all breeds. Brown Swiss, Holstein, and Jersey polled haplotypes have frequencies of 0.41%, 0.93%, and 2.22%, respectively. The National Dairy Database has genotypes for only 678,848 of 39 million cows with records. Gene content (GC) for non-genotyped animals, the number of polled haplotypes in an animal's genotype, was computed using records from genotyped relatives. The GC are real-valued and range between 0 and 2. Prediction accuracy was checked by comparing polled status from recessive codes and animal names to GC for 1,615 non-genotyped Jerseys with known status. 97% (n = 675) of horned animals were correctly assigned GC near 0, and 3% (n = 19) were assigned GC near 1. Heterozygous polled animals had GC near 0 (52%, n = 474) and near 1 (47%; n = 433), although 3 animals were assigned a GC near 2. The expectation for GC is near 1 for heterozygotes, but can be lower if many polled ancestors have unknown status or when pedigree is unknown. In those cases GC may be set to twice the allele frequency, which is low. Some with -P in the name may actually be PP. All homozygous polled animals (n = 11) were assigned GC near 2. Polled status for non-genotyped animals can be accurately determined, and this method can be extended to other genes of interest.

Key Words: gene content, imputation, polled

648 Genetic analysis of hair coat shedding in beef cattle with data collection using a practical strategy. Trent Smith*[1], Michael D. MacNeil[2], and Joseph P. Cassady[3], *[1]Mississippi State University, Mississippi State, MS, [2]Delta G, Miles City, MT, [3]South Dakota State University, Brookings, SD.*

Hair coat characteristics can affect adaptability of beef cattle and performance in various environments. Objectives of this study were to examine the usefulness of an annual hair coat shedding score (HCS) during the spring transition period and determine its relationship with maternal productivity as indicated by weaning weight (WW). Data were collected on 5,294 purebred Angus cows in May of 2011 and 2012 from various herds throughout the Southeastern US, Missouri, and Texas. Measurements included a HCS (1–5) and BCS (1–9) scored independently by 2 trained technicians and averaged. The WW of calves were obtained from the breed association database. The data included 2,225 cows that were observed in both years. Two bivariate analyses were conducted to examine the relationships of HCS with BCS and WW. The same model was used to analyze HCS and BCS. It included fixed effects of contemporary group and age, and random direct genetic and permanent environmental effects due to animals. The model for WW included fixed effects of contemporary group, age of dam and sex, and a linear covariate for age of calf at weaning. Random effects in the model for WW were direct and maternal genetic effects, and a permanent environmental effect due to dams. Phenotypic correlations of HCS with BCS and WW were 0.17 and approximately zero, respectively. Heritability estimates for HCS and BCS were 0.42 ± 0.03 and 0.12 ± 0.03, with a genetic correlation of −0.25 ± 0.10. For WW, heritability estimates were 0.28 ± 0.05 for direct and 0.05 ± 0.04 for maternal effects. The genetic correlation for WW direct and maternal was −0.34 ± 0.24. Estimated genetic correlations of HCS with direct and maternal genetic effects on WW were 0.17 ± 0.22 and −0.30 ± 0.25, respectively. Results of this study suggest that HCS assessed once a year during a transitional period could be used in selection decisions if profitable in

certain environmental conditions. Associations of HCS with other traits of economic importance need to be explored further.

Key Words: genetic variances, hair shedding, beef cattle

649 An application of MeSH enrichment analysis in livestock. Gota Morota*[1], Francisco Peñagaricano[2,3], Jessica L. Petersen[1], Daniel C. Ciobanu[1], Koki Tsuyuzaki[4,5], and Itoshi Nikaido[5], *[1]University of Nebraska-Lincoln, Lincoln, NE, [2]University of Florida, Gainesville, FL, [3]University of Florida Genetics Institute, Gainesville, FL, [4]Tokyo University of Science, Noda, Chiba, Japan, [5]RIKEN, 2-1 Hirosawa, Wako, Saitama, Japan.*

It is an integral part of functional genomics studies to assess the enrichment of specific biological terms in gene lists found to be playing an important role in biological phenomena. Contrasting the observed frequency of annotated terms with those of the background is at the core of over-representation analysis (ORA). Gene Ontology (GO) is a means to consistently classify and annotate gene products and has become a mainstay in ORA. Alternatively, Medical Subject Headings (MeSH) offers a comprehensive life science vocabulary including additional categories that are not covered by GO. Although MeSH is predominantly applied in human and model organism research, its full potential in livestock genetics is yet to be explored. MeSH ORA was evaluated to discern biological properties of the identified genes and contrasted with the results obtained from GO enrichment analysis. Three published data sets were employed for this purpose representing a gene expression study in dairy cattle, the use of SNPs for genome-wide prediction in swine, and the identification of genomic regions targeted by selection in horses. We found that several over-represented MeSH annotations linked to these gene sets share similar concepts with those of GO terms. Moreover, MeSH yielded unique annotations, which are not directly provided by GO terms, suggesting that MeSH has the potential to refine the representation of biological knowledge. We demonstrated that MeSH can be regarded as another choice of annotation to draw biological inferences from genes identified via experimental analyses. When used in combination with GO terms, our results indicate that MeSH can enhance our functional interpretations for specific biological conditions or the genetic basis of complex traits in livestock species.

Key Words: MeSH, enrichment analysis, annotation

650 Use of partial least squares regression to predict individual milk coagulation properties and cheese yield from Fourier transform infrared spectra in Sarda dairy sheep. Maria Grazia Manca[1], Jessica Serdino[1], Massimo Cellesi[1], Paolo Urgeghe[1], Ignazio Ibba[2], Marino Contu[2], and Nicolo P. P. Macciotta*[1], *[1]Dipartimento di Agraria, Università di Sassari, Sassari, Italy, [2]Associazione Regionale Allevatori della Sardegna, Cagliari, Italy.*

Milk coagulation properties (MCP) are popular indicators of milk cheese making ability. They are measured as rennet coagulation time (RCT, min), curd firming time (k_{20}, min) and curd firmness (a_{30}, mm). The potential cheese yield of milk could be also be assessed by individual cheese micro-manufacturing experiments (ILCY). However, the routine measure of these traits appears to be rather problematic in terms of costs and logistics. In this work, partial least squares regression (PLSR) is used to predict individual MCP and cheese yield of 965 Sarda breed ewes located in 47 flocks. MCP were measured using the Formagraph, and cheese yield was assessed by ILCY. Mid infrared spectra was obtained by Milkoscan (Foss Electric). Animals were split into 2 data sets: (1) training (700 ewes) that was used to estimate the PLS model and (2) validation (265 ewes), that was used to validate PLS predictions. One hundred replicates were performed, randomly assigning animals to training and validation sets. Goodness of predictions was assessed by calculating the determination coefficient (R^2), the residual mean squared error of prediction (RMSEP), the regression slope ($b_{obs,pred}$) and intercept ($a_{obs,pred}$) (Table 1).The R^2 indicates an accurate prediction for RCT and, to a lesser extent, a30, and very poor for k20. Also for ILCY the prediction was quite accurate. These figures were confirmed also by values of RMSEP and of regression parameters. The PLSR yielded prediction results of moderate accuracy for RCT and ILCY using mid-infrared spectral data as predictors and it could represent a valuable tool for the recording of these phenotypes for management and breeding purposes. Research supported by the regione Autonoma della Sardegna, project "Il latte Ovino della Sardegna".

Table 1 (Abstr. 650). Statistics of PLS prediction for MCP and ILCY in the validation data set

	Mean obs	Mean pred	R^2	RMSEP	$b_{obs,pred}$	$a_{obs,pred}$
RCT (min)	15.25 ± 6.62	15.20 ± 5.82	0.71 ± 0.05	3.57 ± 0.35	0.97 ± 0.08	0.57 ± 1.17
k_{20} (min)	1.53 ± 0.85	1.55 ± 0.38	0.07 ± 0.03	0.83 ± 0.05	0.60 ± 0.17	0.60 ± 0.27
a_{30} (mm)	49.8 ± 20.2	49.8 ± 15.9	0.55 ± 0.05	13.5 ± 0.8	0.95 ± 0.08	2.5 ± 4.4
ILCY (%)	36.3 ± 9.3	36.3 ± 7.7	0.63 ± 0.06	5.7 ± 0.5	0.95 ± 0.06	1.7 ± 1.93

Key Words: milk coagulation properties, sheep, partial least squares regression

651 *MUC1* gene polymorphism in Murrah water buffaloes and its association with milk production traits. Fernanda da Rosa*[1], Carla Moreira[2], Marina Mortati[3], Gregorio M. Camargo[3], Henrique Oliveira[3], Rusbel Borquis[3], Arione Boligon[2], Humberto Tonhati[3], Heden Moreira[2], and Fabio Souza[2], *[1]Oregon State University, Corvallis, OR, [2]Universidade Federal de Pelotas, Pelotas, RS, Brazil, [3]Universidade Estadual Paulista "Júlio de Mesquita Filho," UNESP, Jaboticabal, SP, Brazil.*

MUC1 is a glycoprotein mucin expressed in apical mammalian epithelial tissues, such as mammalian gland, which the main function is protect the cell surface from the environment microorganisms. Hence, *MUC1* gene is a candidate gene to mastitis resistance. The MUC1 molecule is well defined in bovines, which has been associated with a highly polymorphic variable number of tandem repeats region (VNTR), which are highly conserved. However, there is no information about MUC1 for water buffaloes (*Bubalis bubalis*). Thus, the aim of this study was to identify the VNTR polymorphism of MUC1 gene in water buffaloes of Murrah breed and evaluated the polymorphism associations with economical traits and mastitis resistance. 200 animals from the experimental farm of State University of Sao Paulo (Brazil) were used. Genotyping was performed by the polymerase chain reaction (PCR). The amplified fragments were separated by electrophoresis on 1.5% agarose gel. The length of the alleles was estimated using the GeneRuler plus molecular weight marker. The traits evaluated were: somatic cell count (SCC), fat percentage (%F), age at first calving (AFC), calving interval (CI), fat yield (FY), protein percentage (%P), protein yield (PY) and milk production (MP). The analyses were performed using the PROC MIXED procedure of the SAS program to evaluate the effect of the presence/absence of the *MUC1* alleles on each trait. Differences with $P < 0.05$ were considered significant. Three alleles of different lengths were amplified and named allele 1, 2 and 3. Allele 2 was the predominant with a frequency of 0.56. Genotype 2/3 was the most frequent in all animals with a frequency of 0.41.The statistical analysis considering the presence/absence of the MUC1 alleles revealed that the alleles 1 and 3 were associated with some economic traits. A significant effect for the

allele 1 was observed for higher means for SCC (7.52) and %P (4.39). The absence of allele 3 was significantly associated with higher means for PY (82.45) and AFC (862.12). The allele 1 effect for SCC persisted significant after the Bonferroni adjustment. Our data indicate MUC1 gene association with traits related to mastitis resistance like SCC and with economic traits like %P.

Key Words: buffaloes, mastitis, mucin1

652 The effects of sire breed on reproductive and progeny performance in Kiko meat goats. Henry J. Henderson* and Chukwuemeka Okere, *Tuskegee University, Tuskegee Institute, AL.*

The aim of genetic selection in meat goat is to improve performance by incorporating the beneficial traits from a breed type. The primary objective of this study was to examine the effects of different sire types (Boer vs. Kiko) on reproduction and progeny performance of purebred Kiko does as well as growth and health performance of their offspring. Doe performance was analyzed by evaluating prolificacy (litter size), fecundity (fertility x prolificacy), and birth types (single, twins, or triplets). Doe and progeny performance were analyzed by evaluating prolificacy and pre-weaning growth and survival. A total number of 19 Kiko does were used in this study, 11 of which were bred to a Kiko buck and 8 to a Boer buck. Results revealed individual breed combination prolificacy values (1.9 and 1.75 kids/doe) for the Kiko Sired Group and Boer Sired group respectively. There were non-significant sire differences for gestation length (150 ± 2.66 vs. 148 ± 3.11 d, $P = 0.06$) for Boer and Kiko respectively. Weights of Kiko dams assigned to Boer and Kiko sires at breeding were similar (45.63 ± 10.17 vs. 42.39 ± 6.91, kg, $P = 0.41$). At weaning, weights of dams bred to Boer and Kiko sire were not significantly different (52.77 ± 14.64 and 42.76 ± 7.13, kg, $P = 0.10$). Litter size at birth and at weaning did not differ among sire breed (1.75 ± 0.46, $P = 0.37$ vs. 1.90 ± 0.30 and 1.50 ± 0.53 vs. 1.75 ± 0.46, $P = 0.33$) respectively. Boers sired kids were significantly heavier at birth but not at weaning (3.41 ± 0.48 vs. 2.78 ± 0.53 kg, $P = 0.001$ and 13.82 ± 2.78 vs. 12.43 ± 3.47 kg, $P = 0.26$). This suggests a growth-improvement potential for progeny when utilizing Boer sires. Non- significant differences were observed for ADG (0.15 ± 0.03 vs. 0.13 ± 0.03 kg/d) for Boer and Kiko sired kids respectively. Overall, results showed no consistent differences in reproduction and progeny performance traits between the main sire types used in this project.

Key Words: sire, prolificacy, progeny

653 Comparison of zinc finger sequences of hybrid sterility gene *Prdm9* between yaks, cattle, and their sterile hybrids. Xiaoqin Ma[1], Qin Zeng[1], Juming Zhong[2], Wenjing Liu[3], Lin Huang[1], Suyu Jin[1], and Yucai Zheng*[1], *[1]Southwest University for Nationalities, Chengdu, Sichuan Province, China, [2]Auburn University, Auburn, AL, [3]Southwest University of Science and Technology, Mianyang, Sichuan Province, China.*

Prdm9 (PR domain containing 9) is the first hybrid sterility gene reported in vertebrates, it is a meiosis-specific gene and possibly related to male infertility. The objective of this study was to compare the *Prdm9* zinc fingers of yaks (*Bos grunniens*, n = 33), Yellow cattle (*Bos taurus*, n = 6) and their sterile male hybrids (i.e., cattle-yaks, n = 7). Genomic DNA was extracted from muscle or testis tissues of the experimental animals, and PCR was performed to amplify zinc finger sequences of *Prdm9*. The PCR products were gel-purified and sequenced from both strands. The zinc finger sequence of yak *Prdm9* is highly conserved, the deduced Prdm9 protein consists of 5 C_2H_2 type zinc fingers, which share identical sequences among 3 yak breeds or individuals. However, Yellow cattle *Prdm9* showed variations in both sequence and numbers of zinc fingers among the 6 individuals, with zinc finger numbers of 5, 7 and 8 (5 in 4 cattle, 7 and 8 in 2 cattle). Amino acid sequence comparison of corresponding zinc fingers between yak and cattle revealed 6 polymorphisms and 9 mutations, and 7 of the mutations are located at the positive selection sites. These results indicate that the zinc fingers of *Prdm9* gene evolves much faster in cattle than in yak. Further analysis of the zinc finger sequences of *Prdm9* in sterile cattle-yaks showed that cattle-yaks carry heterozygous *Prdm9* alleles, 4 of which contain alleles with different numbers of zinc fingers. Cattle-yak exhibits higher body size, milk and meat yields than those of yak, but F1 to F3 male sterility. We propose that the differences of Prdm9 zinc fingers at the positive selection sites as well as the numbers of zinc fingers between yak and cattle might be closely associated with the sterility of male cattle-yak.

Key Words: yak, *Prdm9* gene, hybrid sterility