

Breeding and Genetics: Beef and meat species

646 Large-scale single-step genomic BLUP evaluation for American Angus. Daniela A. L. Lourenco*¹, Shogo Tsuruta¹, Breno O. Fragomeni¹, Yutaka Masuda¹, Ignacio Aguilar², Andres Legarra³, Joseph K. Bertrand¹, Tonya S. Amen⁴, Lizhen Wang⁴, Dan W. Moser⁴, and Ignacy Misztal¹, ¹University of Georgia, Athens, GA, ²INIA, Las Brujas, Uruguay, ³INRA, Castanet-Tolosan, France, ⁴Angus 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. Cole¹, Daniel J. Null*¹, Chuanyu Sun², and Paul M. VanRaden¹, ¹Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, ²Sexing 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. MacNeil², and Joseph P. Cassady³, ¹Mississippi State University, Mississippi State, MS, ²Delta G, Miles City, MT, ³South 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