Breeding and Genetics: Application and methods in animal breeding—Swine, poultry, and other species

M67 Accuracy of estimated breeding values for males and females with genomic information on males, females, or both: A broiler chicken example. Daniela A. L. Lourenco*[1], Breno O. Fragomeni[1], Shogo Tsuruta[1], Ignacio Aguilar[2], Birgit Zumbach[3], Rachel J. Hawken[3], Andres Legarra[4], and Ignacy Misztal[1], *[1]University of Georgia, Athens, GA, [2]INIA, Las Brujas, Uruguay, [3]Cobb-Vantress Inc., Siloam Springs, AR, [4]INRA, Castanet-Tolosan, France.*

Phenotypes were available on 4 production traits recorded for up to 196,613 broiler chickens. Heritabilities ranged from 0.22 to 0.49. Among all phenotyped birds, 15,723 were genotyped for 39,102 segregating SNP. Traditional and genomic evaluations were run in a multiple-trait model. Single-step genomic BLUP (ssGBLUP) was used for genomic evaluations with 3 different reference sets including only males (4648), only females (8100), and both sexes (12,748). Realized accuracy of genomic EBV (GEBV) was used to evaluate the inclusion of genotypes for different reference sets on predictive ability of young genotyped males (1501), females (1474), and both sexes (2975). Using male genotypes as reference, the average increase in accuracy of GEBV over EBV for males and females was 12 and 1 percentage point, respectively. When the reference population included only female genotypes, the increase for males and females was 1 and 18 percentage points, respectively. Using genotypes on both sexes as reference increased accuracies by 19 points for males and 20 points for females. Adding genotypes for females without phenotypes did not improve predictions. For one trait, EBV and GEBV accuracies for females were much lower than for males. For another trait with similar heritability, both accuracies were higher, and females had higher accuracy than males. For validation animals GEBV $\approx w_1$PA + w_2DGV, where PA is parent average, DGV is genomic prediction, and the w terms are the weights for each component. When the number of genotyped animals is high, the highest weight is for w_2. When an animal is genotyped, the increase in accuracy comes mainly from the DGV portion of GEBV and marginally from improved PA. For non-genotyped animals there is no improvement in accuracy due to DGV. Accuracies for animals of one sex increase with genotypes of the other sex when that sex has independent phenotypic information and when the evaluation methodology avoids double counting. Realized accuracies are biased down by selection, and analysis of realized accuracies can reveal different selection pressure for traits and sex.

Key Words: genomic prediction, genotyping strategy

M68 Genetic parameters for length of productive life and lifetime production traits of purebred Landrace and Yorkshire sows in northern Thailand. Udomsak Noppibool*[1,2], Skorn Koonawootrittriron[1], Mauricio A. Elzo[2], and Thanathip Suwanasopee[1], *[1]Kasetsart University, Chatuchak, Bangkok, Thailand, [2]University of Florida, Gainesville, FL.*

The objective of this research was to estimate genetic parameters and trends for length of productive life (LPL), lifetime piglets born alive (LBA), lifetime piglets weaned (LPW), lifetime piglets' birth weight (LBW), lifetime piglets' weaning weight (LWW) in a commercial swine farm in Northern Thailand. Phenotypic records came from 1,983 Landrace (L) and 745 Yorkshire sows (Y) collected from July 1989 to August 2013. Variance and covariance components, heritabilities and correlations were estimated using a multiple-trait AIREML procedure. The 5-trait mixed animal model contained the fixed effects of first farrowing year-season, breed group (L and Y), and age at first farrowing. Random effects were sow and residual. Medium heritabilities were estimated for all 5 traits (LPL = 0.16 ± 0.04; LBA = 0.18 ± 0.04; LPW = 0.22 ± 0.04, LBW 0.18 ± 0.04 and LWW = 0.22 ± 0.04). Genetic correlations among these traits were positive and favorable (greater than 0.91; $P <$ 0.05). Genetic correlation estimates were 0.94 ± 0.02 for LPL-LBA, 0.98 ± 0.03 for LPL-LPW, 0.92 ± 0.03 for LPL-LBW, 0.93 ± 0.02 for LPL-LWW, 0.96 ± 0.01 for LBA-LPW, 0.96 ± 0.01 for LBA-LBW, 0.93 ± 0.02 for LBA-LWW, 0.93 ± 0.02 for LPW-LBW, 0.97 ± 0.01 for LPW-LWW and 0.94 ± 0.02 for LBW-LWW. Dam genetic trends were positive, small and significant only for LBA (0.18 ± 0.05 piglets/yr; P = 0.0024), LPW (0.12 ± 0.05 piglets/yr; P = 0.0153), LBW (0.35 ± 0.09 kg/yr; P = 0.0009), and LWW (1.36 ± 0.40 kg/yr; P = 0.0024). Genetic trends for sows and sires were mostly small, negative and not significant for any trait. Thus, the selection program in this commercial herd was ineffective to improve LPL in sows, sires, and dams, and lifetime production traits in sows and sires. This program was only effective to improve lifetime productive traits in dams.

Key Words: genetic parameter, lifetime production trait, swine

M69 A study on *PIT1* gene polymorphism and its association with growth traits in pigs. S. Mohana Devi*[1], V. Balachandar[2], and I. H. Kim[1], *[1]Department of Animal Resource & Science, Dankook University, Cheonan, Chungnam, South Korea, [2]Department of Human Genetics and Molecular Biology, Bharathiar University, Coimbatore, Tamil Nadu, India.*

The pituitary transcription factor (PIT1) (or POU1F1) protein belongs to pituitary-specific transcription factors localized on chromosome 13 in porcine. The PIT1 gene was used as a candidate gene for selecting animals for growth and carcass traits. Thus, the aim of this study was to identify and compare the Rsa I polymorphism of the PIT1 gene in finishing pigs to evaluate mutations in the meat quality of porcine by screening to novel gene markers PIT-1 and to investigate the genotypic alteration of the pigs, which may help to locate the chromosomal regions that may be linked with candidate genes that are associated with pig muscle growth and pork quality. The genomic DNA from 460 pigs was extracted and the genotypes for polymorphism analysis were determined using PCR-RFLP. The PIT1 genotype frequencies analyzed were 42.39% for AA, 39.13% for AB and 18.48% for BB. Several significant associations of PIT1 gene polymorphisms with some of the growth traits were observed. The pigs with BB genotype showed the highest average daily gain. Several significant differences were observed in meat color (A, B and L*; $P < 0.05$). Meat carcass traits LMP and LMC seem to be lower in pigs with BB genotype compared with AA genotype animals. The AA finishers presented a lower level of back fat thickness compared with AB genotypes. The PIT1 are potential candidate genes, influencing quality traits as they encode proteins, which causes essential effects in its functions and the present study tries to confirm the association of its polymorphism with its economically important traits in pigs. Therefore the assumption that genetic unpredictability of the PIT1gene could be associated with swine population in commercial traits.

Key Words: *PIT1* gene, growth trait, pig

M70 Recombination rates in layer chickens. Zi-Qing Weng*[1], Anna Wolc[1,2], Rohan L. Fernando[1], Jack C. M. Dekkers[1], Jesus Arango[2], Petek Settar[2], Janet E. Fulton[2], Neil P. O'Sullivan[2], and Dorian J. Garrcik[1], *[1]Department of Animal Science, Iowa State University, Ames, IA, [2]Hy-Line International, Dallas Center, IA.*

Recombination events, which occur during meiosis, vary in frequency across chromosomes, and among individuals. Recombinations are more common in certain genomic locations known as hotspots and these are controlled by genes. The objective of this study was to assess recombination events across the genome, and identify quantitative trait loci (QTL) that influence recombination frequency in white and brown layer chickens. This study included 1,200 white layers hatched between 2006 and 2012, genotyped with a 600K single nucleotide polymorphisms (SNP) panel, and 5,108 brown layers hatched between 2003 and 2011, genotyped with a 40K SNP panel. FImpute was used to impute missing genotypes. After quality control, 173,224 and 23,098 segregating SNPs remained. There were 492 half-sib families in white layers averaging 3.0 ± 3.0 birds, and 1717 half-sib families averaging 5.4 ± 4.9 brown layer birds. Recombinations were identified within half-sib families using LINKPHASE. Total recombination rates within each 1-Mb window was calculated across 28 chromosomes (Chr). Windows with recombination rates greater than 0.03 (≥1.5 SD from the mean) were considered to be recombination hotspots, while those with no recombinations were cold-spots. Genome-wide recombination numbers of parents were analyzed in a weighted BayesB model. Windows that explained >1% genetic variance were considered to harbor QTL. There were 14,746, and 230,701 recombination events detected in white layers and brown layers, respectively. There were 163 and 281 windows with hotspots detected in white and brown layers, respectively, of which 66 were in common. There were 48 common cold-spots in these 2 breeds. Genome-wide recombination number (GRN) differed by breed and sex. White layers (10.9 ± 4.1) had smaller GRN than brown layers (24.1 ± 3.9). In white layers, females (13.6 ± 3.7) had higher GRN than males (9.3 ± 3.5) but in brown layers GRN were similar in females (24.2 ± 4.2) and males (23.9 ± 3.4). A total of 14 and 6 significant windows, which harbor candidate genes influencing genome-wide recombination, were detected in the 2 breeds. No common QTL windows were found in the 2 breeds. Sample size, marker density, inbreeding level and population structure lead to differences in detection of recombination events and QTL in the 2 breeds.

Key Words: recombination, layer chicken

M71 Genetic selection tool for number born alive and stillbirth piglets in commercial Thai populations. Thanathip Suwanasopee*[1], Skorn Koonawootrittriron[1], and Mauricio A. Elzo[2], *[1]Department of Animal Science, Faculty of Agriculture, Kasetsart University, Bangkok, Thailand, [2]Department of Animal Sciences, University of Florida, Gainesville, FL.*

Genetic markers are widely used for selection and prediction in commercial pig populations. Number of piglets born alive (NBA) and stillborn piglets (STB) within litters have a major effect on overall economic returns. The aim of this study was to determine the association between estrogen receptor gene (*ESR*) and paternally expressed gene 1 (*PEG1*) and NBA and STB. The data set included information from 2 commercial pig populations, one in Northern Thailand (210 sows; 123 Landrace and 87 Yorkshire) and another one in Northeastern Thailand (130 sows; 70 Landrace and 60 Large White). Each population was analyzed separately using 2 models. Model 1 included farrowing year-season, parity, age at first farrowing and breed group as fixed effects, and animal and residual as random effects. Model 2 included all effects from model 1 plus genotypes for *ESR* (AA, AB, and BB) and *PEG1* (AA, GA, and GG) as fixed effects. Association between predicted EBV from models 1 and 2 were analyzed using Spearman rank correlations. Genotype frequencies were 0.67, 0.29 and 0.04 for ESR and 0.01, 0.40, and 0.59 for PEG1 in the Northern population, and 0.42, 0.34, and 0.24 for ESR and 0.05, 0.25, and 0.70 for PEG1 in the Northeastern population. The *ESR* genotype influenced the EBV of Yorkshire sows for NBA ($P < 0.05$) and STB ($P < 0.01$). Yorkshire *ESR* AA sows had the highest average EBV for NBA (0.16 ± 0.03 piglets), whereas Yorkshire *ESR* AB sows had the lowest average EBV for STB (−0.01 ± 0.01 piglets). The *PEG1* genotype affected the EBV of Landrace, Yorkshire and Large White sows for NBA and STB ($P < 0.05$). Large White *PEG1* GG sows had the highest average EBV for NBA (0.43 ± 0.06 piglets), and Landrace *PEG1* AA sows had the lowest average EBV for STB (−0.09 ± 0.09 piglets). Positive rank correlations between EBV from models 1 and 2 existed in the 2 populations for all breeds (0.41 to 0.63; $P < 0.01$), except for Landrace sows in the Northern population (−0.08; $P > 0.05$). These rank correlations indicated that selecting sows with higher NBA and lower STB by using EBV from models with and without *ESR* and *PEG1* marker effects would likely yield similar outcomes.

Key Words: pig, genetic marker, selection

M72 Genomic correlation between piglet preweaning mortality and individual birth weight using a bivariate threshold-linear maternal effect model. Shogo Tsuruta*[1], Ching-Yi Chen[2], William O. Herring[2], and Ignacy Misztal[1], *[1]University of Georgia, Athens, GA, [2]PIC North America, Hendersonville, TN.*

The objective of this study was to predict genomic breeding values for preweaning mortality and birth weight using a bivariate threshold-linear maternal effect model.

The data for preweaning mortality and birth weight, and genotypes were obtained from PIC North America and contained 123,163 phenotypic records and 135,530 animals in pedigree. The genotype file contained 42,787 single nucleotide polymorphism (SNP) markers for 13,566 pigs. Birth weight and preweaning mortality were recorded at piglet level. The model included fixed contemporary group, sex, parity, and number of total born per litter effects, random direct and maternal genetic effects, random maternal permanent environmental effects (MPE), and random residual effects (R). First, direct and maternal heritabilities for preweaning mortality and birth weight and genetic correlations were estimated with the Gibbs sampling THRGIBBS1F90 program. Second, genomic breeding values (GEBV) were predicted with the CBLUP90IOD program, which uses preconditioning conjugate gradients and iteration-on-data for a large number of categorical records, using a single-step genomic BLUP. Direct heritability estimates for preweaning mortality and birth weight were 5.4 and 14.0%, respectively. Maternal heritability estimates were 2.1 and 17.2%. Direct and maternal genetic correlations between the two traits were −0.18 and −0.63, respectively. Environmental correlations were also negative (−0.34 and −0.41 for MPE and R). Correlations of GEBV for 13,566 genotyped animals between the two traits were −0.17 and −0.84 for direct and maternal genomic effects, respectively. Preweaning mortality is negatively affected by birth weight especially through maternal genetic components.

Key Words: preweaning mortality, birth weight, genotype

M73 Genetic parameters of lifetime characteristics of pre-weaning production traits of landrace sows raised under tropical conditions. Teerapong Jaichansukkit[1], Thanathip Suwanasopee*[1], Skorn Koonawootrittriron[1], and Mauricio A. Elzo[2], *[1]Kasetsart University, Bangkok, Thailand, [2]University of Florida, Gainesville, FL.*

Lifetime preweaning production traits are important for increasing profitability in commercial swine operations. Sows with larger pre-weaning production from the first to the last parity in her lifetime are preferred. Thus, it is important to determine how heritable lifetime pre-weaning production traits are in swine populations under tropical conditions in Thailand. Consequently, the objective of this study was to estimate genetic parameters for characteristics of lifetime pre-weaning production traits of Landrace (L) sows raised in an open-house system in Thailand. The pre-weaning production traits were number of piglet born alive (NBA), number of piglets weaned (NPW), average weight of piglets at birth (ABW), and average weight of piglets at weaning (AWW). The characteristics considered for these traits were first-parity value (FPV), peak-parity value (PPV), number of parities from first-parity to peak-parity (P1P), and persistency from the third to the last parity (regression coefficient; P3L). The data set contained 6,075 performance records from 941 sows that farrowed from 2004 to 2012. Variance components for each characteristic were estimated separately for the 4 traits using an AI-REML procedure. The 4-trait animal model for each characteristic included first-farrowing year-season and age at first farrowing as fixed effects, and sow and residual as random effects. Heritability estimates ranged from 0.04 (NPW) to 0.10 (ABW) for FPV, 0.06 (NPW) to 0.20 (NBA) for PPV, 0.01 (NBA) to 0.04 (ABW) for P1P, and 0.03 (NPW) to 0.17 (ABW) for P3L. Genetic correlation estimates ranged from −0.47 (NPW-AWW) to 0.87 (ABW-AWW) for FPV, −0.10 (NPW-AWW) to 0.85 (ABW-AWW) for PPV, −0.73 (NBA-NPW) to 0.58 (NBA-AWW) for P1P, and −0.70 (NPW-AWW) to 0.13 (NPW-ABW). The low estimates of heritability for all characteristics in these 4 lifetime preweaning production traits indicated that genetic improvement for these characteristics in all these traits would either be slow or nonexistent in this Landrace population.

Key Words: pig, lifetime production, tropics

M74 General and specific combining abilities for reproductive and growth performance of three color variants of Nigerian indigenous turkeys. Matthew A. Adeleke*[1], Rasheed O. Ojo[1], Sunday O. Peters[2], and Michael O. Ozoje[1], *[1]Department of Animal Breeding and Genetics, Federal University of Agriculture, Abeokuta, Ogun State, Nigeria, [2]Department of Animal Science, Berry College, Mount Berry, GA.*

Assessment of combining abilities is important in evaluation of hybrid combinations for genetic improvement. Our objective in this study was to determine combining abilities of 3 color variants of Nigerian indigenous turkeys. Two hundred fifty poults consisting of 41 White × White (WW), 40 Black × Black (BB), 32 Lavender × Lavender (LL) purebreds; 26 White × Black (W×B), 24 Black × White (B×W), 22 White × Lavender (W×L), 20 Lavender × White (L×W), 23 Black × Lavender (B×L) and 22 Lavender x Black (L×B) crossbreds were generated from matings among White, Black and Lavender color types. The poults were raised from day-old to 20 weeks. A 3 × 3 diallel design was set up and data analyzed using SAS (2005) to estimate general combining ability (GCA) and specific combining ability (SCA) for fertility, hatchability, weak-in-shell, dead-in-shell, dead-in-germ, body weight, breast girth, body length and thigh length. The highest GCA was recorded for fertility (4.44), hatchability (5.39) and dead-in-shell (2.60) in BB, LL and WW respectively. SCA for fertility was the highest in W×B (0.07). W×L had highest SCA (3.28) for hatchability. Least SCA for weak-in-shell (−0.50), dead-in-germ (−2.87) and dead-in-shell (−47.17) were observed in W×L crossbred. The highest GCA for body weight at wk 20 was recorded for WW (90.83). The highest SCA for body weight at wk 20 was recorded in W×L (0.62). BB had highest GCA values for breast girth, body length and thigh length at wk 20 (1.46, 0.46 and 0.41 respectively). B×W recorded the highest SCA (0.94) for breast girth; W×L gave the highest SCA (2.34) for body length while the highest SCA (0.89) for thigh length was observed in B×L turkey genotype. Based on genetic parameter estimates, additive variance was more important for growth parameters, fertility and dead-in-germ while dominance variance was higher and more important in controlling hatchability, weak-in-shell and dead-in-shell than additive variance. Dams from B×W crossbred local turkey can be used to improve growth performance while W×L can be used to achieve best combiners for improvement of reproductive traits in Nigerian indigenous turkeys.

Key Words: combining ability, turkey, plumage color

M75 Association with disease resistance markers and economic traits in Korean native chickens. Boyeong Park*, Anh Duc Truong, Jihye Ban, and Yeong Ho Hong, *Chung-Ang University, Anseong, Gyeonggi, Korea.*

Avian coccidiosis is a mucosal infectious disease that significantly impairs the growth and feed efficiency of chickens. There are associations between oocyst and body weight, the parameters of resistance to coccidiosis and SNPs in 2 genes [Myeloid leukemia factor 2 (*MLF2*), T cell receptor-β (*TCR-β*)] located on chromosome 1. A total of 5 SNPs of *MLF2* and *TCR-β* genes were assessed for genetic effects on disease resistance. The MLF2-SNP_892 (GG) is most significantly related to decreased oocyst shedding. Besides, a combination of SNPs is mostly associated with disease resistance. A total of 340 female chickens from 7 pure-bred chicken lines [Rhode Island Red (RIR) D line, Korean Native Chicken (KNC) gray, KNC black, KNC, Leghorn F, Leghorn K, and Ogey line] were used to genotype with real-time PCR (Light-Cycler 960). The SNP genotyping was carried out for each line using the High Resolution Melting Master (LightCycler 480) that represent melting curves after PCR amplification. Interestingly, their haplotype is significantly matched with their economic traits. Taken together, this new information will be a parameter that disease resistance markers related with phenotypes consist of body weight, weight of first egg and further study required to prove those marker's availability in poultry breeding industry

Key Words: chicken, disease resistance marker, high-resolution melting

M76 Breeding implications of heteroskedastic whole-genome prediction of genetic merit. Zhining Ou*[1], Robert J. Tempelman[2], Juan P. Steibel[2], Catherine W. Ernst[2], Ronald O. Bates[2], and Nora M. Bello[1], *[1]Kansas State University, Manhattan, KS, [2]Michigan State University, East Lansing, MI.*

Current breeding programs in animal production systems involve selection of candidate animals with superior genetic merit to serve as progenitors of the next generation. In this study, we predicted genomic breeding values (GEBV) for 2 quantitative traits from the Michigan State University Swine Resource Population using standard whole-genome prediction (WGP) models that assume homogeneous residual variance (i.e., RR-BLUP, BayesA, BayesB and BayesCπ) and their heteroskedastic counterparts. We divided the data into 5 mutu-

ally exclusive folds, such that 4 folds were alternatively used to train homoskedastic and heteroskedastic versions of each WGP model and then predict GEBV on animals on the remaining validation fold. The pseudo-Bayes factors indicated that heteroskedastic error WGP models improved model fit at all 5 crossvalidation folds. Within each fold, we then computed the Spearman rank correlation between homoskedastic- and heteroskedastic-based GEBV for top and bottom 10% individuals to compare their relative rankings. We noticed a considerable degree of re-ranking of animals with 10% top and bottom homoskedastic GEBV, particularly as the amount of residual heterogeneity in the data increased. For loin muscle pH at 45 min post-mortem, the median rank correlation of GEBV for top (bottom) 10% animals between heteroskedastic and homoskedastic models ranged from 0.52 to 0.70 (0.64 to 0.70) across data folds and WGP models. Similarly, for carcass temperature at 45 min post-mortem, the median rank correlation ranged from 0.05 to 0.38 (top 10%) and from 0.43 to 0.54 (bottom 10%). These results indicated non-negligible re-ranking of individuals with extreme genetic merit when heterogeneity of residual variances across environments is accounted for, thereby supporting potential practical implications for selection purposes in breeding programs.

Key Words: whole-genome prediction model, residual heteroskedasticity, re-ranking

M77 Co-association gene networks for meat quality and carcass traits in pigs and validating by transcription factors. Darlene A. S. Duarte*, Fabyano F. Silva, Renata Veroneze, Lucas L. Verardo, Ivan Carvalho Filho, Simone E. F. Guimarães, and Paulo S. Lopes, *Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

The aim of this study was perform genome association studies for meat quality and carcass traits and thereafter build gene network to improve the knowledge of genes, pathways and the physiological mechanisms that affect meat quality and carcass traits. In addition, the identification of transcriptional factors related to those genes was used to validate this network. We performed genome association studies for 12 traits (one trait at time) in a F_2 population (produced by crossing naturalized Brazilian breed Piau with commercial line) and we found 144 significant SNPs (p-value < 0.05). These SNPs were selected to build the Association Weight Matrix (AWM), which was used to investigate the genetic basis of these traits and generate gene network based on the co-association of pair-wise SNPs across phenotypes. Through this methodology, we found 45 genes that were used to build a gene network based on pair-wise correlations between them. We identified 25 transcription factors (TF) strongly related (p-value < 0.001) with genes in the network. The top 3 TF (Sox5, Nkx2–5 and T) were chosen for construction of a network with their pathways and gene ontology. The genes present in the network generated from AWM and also present in TF network were involved mainly in metabolism of adipose tissue and skeletal muscle. These results suggest that genes and TF identified here are important in the control of meat quality and carcass traits. However, further efforts should be made to study in more detail the new gene-gene interactions here identified, as well as, the key transcription factors and pathways involved in these traits.

Key Words: genome association studies, gene network, pig

M78 An improved approach for swine SNP genotyping using Genotyping-by-Sequencing. Cheng Tan*[1], Jiangli Ren[1], Zhuolin Huang[1], Yiqiang Zhao[1], Yang Da[2], and Xiaoxiang Hu[1], *[1]State Key Laboratory for Agrobiotechnology, China Agricultural University, Beijing, China, [2]Department of Animal Science, University of Minnesota, Saint Paul, MN.*

Genotyping-by-sequencing (GBS) technology has a capacity for delivering large numbers of single nucleotide polymorphism (SNP) marker genotypes with potentially lower cost than SNP chips. To achieve stable genotyping results, we selected the *Eco*RI-*Msp*I enzyme from a large number of candidate enzymes, and used the magnet beads-based purification method to stably and simply recapture GBS tags. Genomic DNA samples from 192 Duroc pigs were digested with *Eco*RI-*Msp*I enzyme, ligated to adapters containing unique barcode, and sequenced on the Illumina NextSeq 500 system with 75bp single-end sequencing. The results showed that all 192 barcoded DNA samples were represented evenly, and that on average 4 million reads per animal were produced. From these samples, about 450,000 unique sequence tags per sample containing 55,843 SNPs were identified through TASSEL4.0 analysis package requiring a minimum of 10 times that a tag must be present, which covered about 1% of the whole genome. The average call rate per individual was more than 94.6%. By repeating GBS genotyping on 2 different samples with 96 pigs in each sample performed by different technicians, 88.5% of the 55,843 SNPs had the same genomic locations from both samples. The cost of the 55,843 SNPs per sample was under $50 per animal. These results showed that our improved GBS technique is sufficiently high-throughput, economical and provides an acceptable marker density for genomic selection or genome-wide association studies.

Key Words: genotyping-by-sequencing, swine, SNP

M80 Growth curve analyses of three turkey genotypes in the hot humid tropics using a Bayesian mixed model approach. Michael O. Ozoje*[1], Sunday O. Peters[2], Kyle C. Caires[2], and Kadir Kizilkaya[3], *[1]Federal University of Agriculture, Abeokuta, Ogun State, Nigeria, [2]Berry College, Mount Berry, GA, [3]Adnan Menderes University, Aydin, Turkey,.*

Growth curves are critical for the understanding and formulation of breeding plans because they shift in response to selection. Nonlinear functions have been used extensively to represent changes in sizes with age, so that the genetic potentials of animals for growth can be evaluated. This study was undertaken to apply the nonlinear Bayesian mixed effect model to examine the changes in the growth pattern of 3 Turkey genotypes in Nigeria. Growth data of 435 turkey poults over a 20-wk period were evaluated using Logistic, von Bertalanffy and Gompertz growth models with normally or Student's-t distributed error. The parameter estimates were significantly different in the models by sexes and genotypes. However, the estimates of parameters were similar except for the differences observed among the local turkey genotypes whose values decreased significantly under the Student's-t distribution. The estimate of the average mature weight (A) in the von Bertalanffy model was the closest to the observed average. The estimate of constant B ranged from 15.62 to 22.17 under the Logistic model but significantly dropped to a range of 0.78 to 4.19 with Gompertz and von Bertalanffy models. The estimate of the rate of maturing (k) varied from 0.06 in von Bertalanffy to 0.26 in the Logistic model. Large estimates of A were generally associated with smaller estimates of k in the von Bertalanffy model. Evaluation of the goodness of fit based on the Deviance Information Criteria showed that the von Bertalanffy model was superior. The differences between functions with respect to average life time absolute growth rate, absolute maturing rate and relative growth rate reflect differences in rate of growth and maturing throughout the growing and maturing phases. In general, these differences are indicative of the

differences that exist among the functions with respect to their abilities to fit the actual growth curve of these turkey genotypes and their sexes.

Key Words: turkey, growth curve, nonlinear function

M81 Inferring the causal effect of number of lambs born on milk yield in dairy sheep using propensity score methods. Vera C. Ferreira*, Bruno D. Valente, David L. Thomas, and Guilherme J. M. Rosa, *University of Wisconsin-Madison, Madison, WI.*

Assigning causal interpretation to associations obtained from observational data is challenging as they are prone to confounding. Number of lambs born (prolificacy) in sheep may be considered as a potential factor contributing to milk yield (MY). However, inferring this effect using traditional regression or ANOVA techniques can generate spurious results whenever there are confounder variables that influence both the outcome (i.e., MY) and treatment (i.e., prolificacy). Propensity score (PS) methods tackle this issue by balancing baseline covariate distributions between treatment levels, allowing unbiased inference of marginal effects. This method belongs to the framework of causal models dealing with potential outcomes. It intends to mimic aspects of randomized trials, for which comparison of treatment groups is causally meaningful. Our goal was to infer the causal effect of ewe prolificacy on her subsequent MY using PS based on Matched Samples. Data comprised 4,319 records from 1,534 crossbred dairy ewes. The set of potential confounder variables was composed by lactation number (1st, 2nd, and 3rd – 6th) and dairy breed composition (<0.5, 0.5-0.75 and >0.75 of East Friesian or Lacaune). For the treatment variable, single lamb birth was assigned to Group 0, while multiple birth (2, 3 or 4 lambs) was assigned to Group 1. MY represented the volume of milk produced for the whole lactation (mean = 268.5 L and SD = 116.4 L). The analysis was conducted using the R package "nonrandom." A total of 1,166 pairs of treated/nontreated individuals with similar PS values were formed. The criterion for similarity was defined by a caliper size equal to 20% of the sd in the PS logit (0.13) and a ratio of treated/untreated = 1. Standardized differences were chosen as the statistical test for the hypothesis of PS balance, and all covariates were deemed balanced after matching (cutoff for standardized bias = 0.2). The estimated causal effect of prolificacy on MY was 20.52 L, SE = 3.77 L, 95% CI = 13.13–27.91 L. Hence, results indicate that ewes that gave birth to a single lamb would be expected to have MY increased by 20.52 L if they had given birth to multiple lambs and all other variables were held constant.

Key Words: causal inference, milk yield, prolificacy

M82 Comparative whole-genome analysis of CpG islands in camelid and selected mammalian genomes. Arsalan Barazandeh[1,2], Mohammadreza Mohammadabadi[2], Ikhide G. Imumorin[3], Sunday O. Peters*[4], Bolaji N. Thomas[5], Mostafa Ghaderi-Zefrehei[6], and Hossein Nezamabadi-Pour[1], *[1]Shahid Bahonar University of Kerman, Kerman, Iran, [2]Jiroft University, Jiroft, Iran, [3]Cornell University, Ithaca, NY, [4]Berry College, Rome, GA, [5]Rochester Institute of Technology, Rochester, NY, [6]University of Yasousj, Yasousj, Iran.*

Camels are dromedaries found in extreme desert environments of Africa and Asia with adaptations to arid conditions of temperatures exceeding 40°C, water losses greater than 25% of total body weight, and the ability to survive up to 14 d without water. Camels are important as beasts of burden for transport and as sources of meat, milk and wool in many desert countries. Therefore, camel could be very useful in the weather extremes precipitated by global climate change. Recent sequences of camelidae genomes [wild bactrian camel (*Camelus bactrianus ferus*), bactrian camel (*Camelus bactrianus*), dromedary (*Camelus dromedaries*) and alpaca (*Vicugna pacos*)] provides the opportunity to better understand the genomic architecture of this unique group of animals. CpG island (CGIs) sequence patterns in complex genomes typically consists of high-frequency of CpG dinucleoetides associated with promoter regions of about 70% of all genes, found in almost all housekeeping genes and in about half of tissue-specific genes. CGIs play important roles in the regulation of gene expression including X-chromosome inactivation, imprinting, silencing of intragenic parasites and are extensively linked to the epigenetic causes of cancer. We used newly available genomic sequence to perform comparative large-scale whole-genome analysis of CGIs for the first time in Camelidae using 5 different CGI detection algorithms. These algorithms detected different numbers of CGIs, CGI density and CGI length distribution in Camelidae. All algorithms agreed on the alpaca genome as having the largest number of CGIs, CGI density and average length of CGIs. When compared with other mammalian genomes of human, mouse, dog, horse and cow, CGIs features in cow genome was the most similar with camelid genomes. These results contribute to better understanding of the evolutionary genetics of camelid genomes in comparison with other livestock species. Further analysis of camelid genomes may shed more light on molecular origins and mechanisms of heat adaptation in these extreme heat-adapted animals.

Key Words: Camelidae, genome, CpG island

M83 Genome-wide association study of mandibular inferior in multiple breeds of sheep. Michelle R. Mousel*[1], Stephen N. White[1,2], J. Bret Taylor[3], and Donald P. Knowles[1,2], *[1]USDA-ARS, Animal Disease Research Unit, Pullman, WA, [2]Department of Veterinary Microbiology and Pathology, Pullman, WA, [3]USDA-ARS, Range Sheep Production Efficiency Research Unit, Dubois, ID.*

Misalignment of the jaw in sheep, which has long been considered a genetic condition, occurs in most sheep breeds, and culling of affected animals is recommended. Severe mandibular inferior, where the mandible is shorter than the maxillary, can lead to premature death due to starvation. A German breeding trial of affected sheep produced greater than 60% affected lambs and they estimated jaw misalignments were due to dominant and recessive gene effects. A genome wide association study was conducted using the OvineSNP50 marker set to genotype ewes that either produced unaffected lambs (n = 712) or at least 1 affected (n = 252) lamb during their lifetime. Large numbers of animals from multiple breeds improves the odds for detecting true positively associated genomic regions in multiple genetic backgrounds. Jaw misalignment was categorized as severe, greater than 1.3 cm longer maxillary, moderate, between 0.3 and 1.3 cm longer maxillary, mild, between 0.05 and 0.29 cm longer maxillary, and normal, no misalignment within 24 h of birth. Ewes were Rambouillet, Polypay, and Columbia breeds which produced a total of 8321 purebred and crossbred lambs over 13 y with 3.9% of lambs presented with mandibular inferior. Year of lamb birth was significant ($P < 0.01$) with lambs born in 2009 having more misaligned jaws compared with all other years. Sex of lamb was significant ($P < 0.01$) with a greater frequency of misaligned jaws in male lambs. Breed of lamb sire ($P > 0.52$), ewe age ($P > 0.32$), and breed of ewe ($P > 0.08$) did not affect lamb jaw alignment. A recessive model accounting for breed, population cluster, and minor allele frequency identified 2 genomic regions that were significantly (Bonferroni-corrected $P < 0.03$) and 2 genomic regions that were suggestively (unadjusted $P < 2.3 \times 10^{-6}$) associated with mandibular inferior. The 2 significant markers were located on chromosome 2, near a gene which affects growth, and chromosome 22 near a gene that plays a role in membrane trafficking.

Further evaluation of these genomic regions is required to identify underlying causal mutations, which would be useful in marker-assisted selection for sheep producers.

Key Words: sheep, mandibular inferior, genome-wide association study

M84 Integration of haplotype analysis of functional genomic information with single SNP analysis improved accuracy of genomic prediction. Cheng Tan*[1,2], Dzianis Prakapenka[1], Chunkao Wang[1], Li Ma[3], John R. Garbe[4], Xiaoxiang Hu[2], and Yang Da[1], *[1]Department of Animal Science, University of Minnesota, Saint Paul, Minnesota, [2]State Key Laboratory of Agrobiotechnology, China Agricultural University, Beijing, China, [3]Department of Animal and Avian Sciences, University of Maryland, College Park, MD, [4]Minnesota Supercomputer Institute, University of Minnesota, Minneapolis, MN.*

We compared 3 methods of genomic prediction using additive and dominance effects of single SNPs and haplotype blocks. Method I was single SNP analysis of 423,131 SNPs covering all human autosomes from the Framingham Heart Study with over 6000 individuals. The next 2 methods add haplotype analysis of functional information to the single SNP analysis, i.e., Method II adds haplotype analysis of 595 "cholesterol-related genes" with 8,674 SNPs (2% of autosomes); Method III adds haplotype analysis of 9821 genes with 184,686 SNPs (36% of autosomes) after removing tiny genes without at least 2 SNPs. The results from 4 to 8 validation samples showed that adding haplotype analysis to single SNP analysis improved the prediction accuracy in most cases. Method II with cholesterol-related genes had the best prediction accuracy for total cholesterol with 4.78% increase in accuracy over single SNP analysis, and had stable accuracy increases across validation samples for all cholesterol phenotypes. Method III using all autosomal genes had the best accuracy for triglyceride with 17.75% increase in accuracy over single SNP analysis and tended to have the best performance across different phenotypes, but had larger variations than Method II across validation samples for cholesterol phenotypes. Results were also obtained from one validation sample for adding 3 other haplotype analyses to single SNP analysis: ChIPseq sites with 375,924 SNPs and average block size of 115.8Kb; non-hotspot blocks with each block between 2 crossover hotspots with 422,695 SNPs and average block size of 65Kb, and evenly divided blocks with block size of 100Kb of 422,814 SNPs. All 3 methods improved the prediction accuracy for most phenotypes but ChIPseq blocks mostly had better prediction accuracy than the other 2 methods, indicating that ChIPseq sites likely contained useful functional information not present in anonymous blocks. The results in this tudy tend to conclude that the integration of haplotype analysis of functional genomic information with single SNP analysis may improve the accuracy of genomic prediction for some phenotypes.

Key Words: haplotype, genomic selection, SNP

M85 Preliminary study of *DMRT3* variation and association with performance gait for American Saddlebred horses. Inaê C. Regatieri*[1], John E. Eberth[2], Fred Sarver[3], and Ernest Bailey[2], *[1]Faculdade de Ciências Agrárias e Veterinárias, UNESP – Univ Estadual Paulista, Jaboticabal, São Paulo, Brazil, [2]Department of Veterinary Science, University of Kentucky, Lexington, KY, [3]Cornerstone Farm, Carlisle, KY.*

The Doublesex and Mab-3 Related Transcription Factor 3 (*DMRT3*) gene encodes an important transcription factor in the setting of spinal cord circuits controlling movement in vertebrates. The SNP g.22999655C>A of the *DMRT3* gene was significantly associated with performance of 4-beat gaits in horses, such as the running walk and the amble American Saddlebreds ridden and shown under saddle seat in both 3-gaited (walk, trot, and canter) or 5-gaited classes (walk, trot, slow gate, rack, and canter). We investigated whether SNP g.22999655C>A of *DMRT3* was more prevalent among 5-gaited horses than among the random population of Saddlebred horses. The genotyping of the SNP of the DMRT3 gene was performed by PCR-RFLP using the restriction enzyme *Dde*I. The frequency of the *A* allele among 37 randomly selected Saddlebreds was 0.28. This is in agreement with results from a previous study in which the prevalence of the *A* allele in American Saddlebred horses was 27.5. Only 3 of the horses in our study had been shown as 5-gaited horses and all 3 had the genotype *A/C*. Although consistent with the hypothesis that the *A* allele is more prevalent among for 5-gaited horses, the numbers are too small for any conclusion. Additional Saddlebred horses, and especially 5-gaited horses, will be tested and results reported allowing determination of statistical significance.

Key Words: equine, genomics, genetics