760 Comparison of traditional vs. genomic, and single vs. multiple trait analyses of broiler chicken mortality. Xinyue Zhang*[1], Shogo Tsuruta[1], Daniela A. L. Lourenco[1], Robyn L. Sapp[2], and Rachel J. Hawken[2], *[1]University of Georgia, Athens, GA, [2]Cobb-Vantress Inc., Siloam Springs, GA.*

The purpose of this study was to determine whether broiler mortality is influenced by selection on correlated traits, determine the accuracy of genetic evaluation for mortality with traditional and genomic evaluations, and determine whether the use of the multi-trait model increases the accuracy of predictions. Phenotypes were available on 181,022 broilers for up to 8 traits, 4 linear and 4 categorical. Pedigree was available for 186,596 broilers and genotypes were available on 18,047 animals. For linear traits the model included the fixed effects of sex and contemporary group, random direct genetic, and maternal genetic effect for body weight. Contemporary group is the grouping of source, mini-generation and hatch. For categorical traits, the contemporary group was treated as random and a fixed effect of generation was added. (Co) variance components were estimated with a Gibbs sampling program THRGIBBS1F90 for threshold-linear models. A traditional BLUP using a pedigree relationship matrix and a genomic BLUP (ssGBLUP) using a combined pedigree-genomic relationship matrix were used to predict EBV and genomic EBV, respectively. Because few dead animals were genotyped, the traditional validation techniques did not apply. Subsequently models were compared using a data splitting technique based on the correlation of EBV from 2 non-overlapping samples, each one with one-half of the phenotypes selected across contemporary groups. The correlations were computed only for genotyped animals in the last generation and are measures of realized accuracy. The genetic correlation between mortality and the other traits were generally small (absolute value < 0.15), with notable differences for maternal body weight (−0.50) and Ascites (0.77); heritability for mortality was 13%. The correlations between independent samples in a univariate model for mortality were 0.59 for the non-genomic and 0.64 for the genomic model. In a multiple trait genomic model, the correlations increased by 0.09 over single trait genomic model. Results indicate mortality may be more affected by ascites and maternal growth compared with other traits under selection. Use of the genomic data increases the accuracy of genetic evaluation for mortality.

Key Words: mortality, broiler, threshold model

761 Polymorphisms in *CAST*, *TNNI1*, and *MYOG* genes and their relationship with pig carcass traits at different weight groups. Andrea Nyisalovits*[1], János Posta[2], Levente Czeglédi[2], Márta Horváth[1], and László Babinszky[1], *[1]Department of Feed- and Food Biotechnology, University of Debrecen, Debrecen, Hungary, [2]Department of Animal Breeding, University of Debrecen, Debrecen, Hungary.*

The aim of this study is to determine the relationship between 3 previously described polymorphisms (SNPs) located at 3 candidate genes (*CAST*, *TNNI1*, *MYOG*) and slaughter traits in different weight groups of commercially housed hybrid pigs. A total of 402 pigs [Large White × (Landrace × Duroc) sows line × Pietrain boar line] were tested using PCR-RFLP method. After 111 and 118 d in fattening (DF) their carcasses were qualified in a slaughterhouse where the hot weight (HW), backfat thickness (BF) and loin diameter (LD) were measured, lean meat % (LM %), live weight (LW) and average daily gain (ADG) were calculated. Because of the wide range of LW (82–144 kg) heterogeneity of experimental population had to be reduced, therefor animals were divided into 3 groups based on mean (116.1 kg) and SD (10.2 kg) of LW as follows: low (L) (<mean-1 SD, n = 63), medium (M) (mean ± 1 SD, n = 276) and high (H) (>mean+1 SD, n = 63). The effects of SNPs on carcass quality traits were analyzed in the 3 classes separately using the least square analysis of the GLM method with Tukey-Kramer correction (SAS 9.1) including sex and DF as fixed effects and LW as covariance factor. According to our results the examined SNPs show different effects on carcass quality at different weight. Pigs with the GG genotype of CAST (Ser66Asn) gene show the worst BF and LM % ($P < 0.05$) values in the L group, but no significant results were found in the other 2 groups. The TNNI1 gene has no significant effect on traits. The SNP in 3′ UTR region of MYOG gene influenced BF and LM % ($P < 0.05$) values, but only in the H group. The marker-assisted selection plays crucial role in animal husbandry, despite economically important traits show multifactorial inheritance with a strong environmental influence. Our results prove that the effect of polymorphisms depends on LW, moreover, the LW strongly influences the carcass quality traits, therefore if the test population shows a high degree of variability the use of weight categories should be considered.

Key Words: carcass quality, pig, RFLP

762 Estimates of variance components for gilt retention traits. Matthew D. A. Morrison*[1], Kent A. Gray[2], Miles T. See[1], and Mark T. Knauer[1], *[1]North Carolina State University, Raleigh, NC, [2]Smithfield Premium Genetics, Rose Hill, NC.*

Numerous studies have been conducted on sow retention and longevity; however, less research has been completed on gilt retention. Increasing the percentage of gilts that farrow a litter would reduce gilt development costs, improve sow longevity, and enhance farmer profitability. Hence the purpose of this study was to estimate variance components for gilt retention traits. Data consisted of 6,282 commercial gilts from Large White dams and Landrace sires (Smithfield Premium Genetics, Rose Hill, NC). During development, gilts were reared in environmentally controlled facilities with slatted concrete flooring, natural ventilation and ad libitum access to feed and water. At an average age of 211 d (SD ± 41.5) females were moved to one of 11 sow farms in eastern North Carolina. Traits included successful gilt farrow event (STAY; success = 1, failure = 2) gilt culled for reproductive (REPRO; Yes = 1, no = 2), or non-reproductive reasons (OTHER, yes = 1, no = 2), age at first service (AFS), and age at first farrowing (AFF). Variance components were estimated using an animal model with THRGIBBS1F90 for categorical traits and AIREMLF90 for linear traits. All models contained a fixed effect of contemporary group (farm × year × month) and a random effect of animal. Of the gilts entering sow farms, 15.4% did not farrow a litter, 7.3% were culled for REPRO, and 8.1% were culled for OTHER. Average AFS and AFF were 262 d (SD ± 24.7) and 377 d (SD ± 24.9), respectively. Heritability estimates for STAY, REPRO, OTHER, AFS, and AFF were 0.15, 0.19, 0.05, 0.27, and 0.21, respectively. Phenotypic variance estimates for STAY, REPRO, OTHER, AFS, and AFF were 1.18, 1.24, 1.06, 356.2, and 386.2, respectively. Results suggest selection for increased gilt retention is possible.

Key Words: gilt, heritability, retention

763 Estimates of genetic parameters for sow body weight loss during lactation. Cassandra L. Ferring*[1], Dale Hentges[2], Clint Schwab[2], and Mark T. Knauer[1], *[1]North Carolina State University, Raleigh, NC, [2]The Maschhoffs, Carlyle, IL.*

The purpose of this study was to estimate genetic parameters for sow BW loss during lactation. Data and pedigree information were available for Landrace (n = 3,310), York (n = 827) and Landrace × York F_1 sows (n = 354) from The Maschhoffs (Carlyle, IL). Sows were housed in environmentally controlled facilities with slatted concrete flooring and had ad libitum access to water. Females were restricted fed during gestation based on a visual body condition score of 1 to 5 (1 = thin, 5 = fat). During lactation sows were fed ad libitum. Sow traits analyzed included body condition score at farrowing (FBCS), total number born (TNB), number born alive (NBA), litter birth weight (LBW), litter weaning weight (LWW), number weaned (NW), body condition score at weaning (WBCS), and sow BW loss during lactation (WTΔ). Variance components were estimated using ASReml. All models included fixed effects of genetic line, parity, and contemporary group and random effects of animal (sow) and permanent environment. Covariates were included for LBW (NBA), LWW (piglet age at weaning and number of piglets fostered), NW (number of piglets fostered), WBCS (lactation length) and WTΔ (lactation length). Heritability estimates for FBCS, TNB, NBA, LBW, LWW, NW, WBCS and WTΔ were 0.17, 0.15, 0.15, 0.25, 0.15, 0.11, 0.16, and 0.13 respectively. Permanent environment variance estimates for FBCS, TNB, NBA, LBW, LWW, NW, WBCS and WTΔ were 0.0007, 0.26, 0.20, 0.49, 2.65, 0.04, 0.0004 and 1.29 respectively. Phenotypic variance estimates for FBCS, TNB, NBA, LBW, LWW, NW, WBCS and WTΔ were 0.015, 11.50, 10.49, 5.66, 112.4, 4.35, 0.014 and 251.5 respectively. Genetic correlations between WTΔ with FBCS, TNB, NBA, LBW, LWW, NW and WBCS were −0.05, 0.01, −0.02, 0.50, 0.28, 0.05 and −0.19 respectively. Phenotypic correlations between WTΔ with FBCS, TNB, NBA, LBW, LWW, NW and WBCS were 0.10, 0.09, 0.08, 0.15, 0.20, 0.15 and −0.03 respectively. Selection for reduced BW loss during lactation appears possible and would have minimal effect on litter size.

Key Words: body weight, lactation, reproduction

764 Genetic selection for feed efficiency in crossbred animals. Rob Bergsma* and Egbert F. Knol, *Topigs Norsvin Research Centre B.V., Beuningen, the Netherlands.*

Worldwide, the majority of the commercial slaughter pigs are a cross of 3 or even 4 purebred lines. Although genetic selection takes place in purebred lines, the breeding goal should be directed toward crossbred performance. Applying a crossbred breeding goal is important if purebred traits show a genetic correlation significantly lower than 1.0 with their crossbred counterparts and/or when the genetic variation of purebred traits is different from those of crossbred traits. Recent research showed that this especially applies to feed intake and feed efficiency, while carcass composition in purebreds and crossbreds appeared to be more similar traits. The percentage of the genetic trend in purebred lines, expressed in crossbreds can be calculated as the ratio of the crossbred genetic standard deviation multiplied by the genetic correlation and the genetic purebred standard deviation. Our results show that of the genetic progress in purebreds 62, 52, 111 and 85% is expressed in crossbreds for daily gain, feed intake, back fat and loin depth, respectively. For feed efficiency this ratio depends on the trait considered. For feed conversion ratio, 60% of the genetic trend in purebreds was expressed in crossbreds, whereas for residual feed intake this ratio was only 41%. Feed intake (and thus feed efficiency) are traits that are not widely available on individual crossbred animals. The limited availability may also indicate that the crossbred/purebred phenotypes are confounded with their environment, given rise to a possible genotype by environment interaction. Another possible explanation is that dominance plays a larger role in feed intake and feed efficiency compared with other traits. And finally, genomic selection has been implemented for purebreds but when using crossbred animals as reference population we have to take into account that a QTL in breed A can behave different than in breed B. Current research focuses on partitioning the possible causes in explaining the lower expression of the genetic trend of purebreds in crossbred. Results will facilitate decisions on the most appropriate genetic model to include crossbred information in a combined crossbred purebred breeding program.

Key Words: pig breeding, crossbred performance, feed efficiency

765 Genomic regions associated with response to PRRSV and PCV2b co-infection in nursery pigs. Jenelle R. Dunkelberger*[1], Nick V. L. Serão[1], Maureen A. Kerrigan[2], Joan K. Lunney[3], Raymond R. R. Rowland[2], and Jack C. M. Dekkers[1], *[1]Department of Animal Science, Iowa State University, Ames, IA, [2]College of Veterinary Medicine, Kansas State University, Manhattan, KS, [3]USDA, ARS, BARC, APDL, Beltsville, MD.*

The objective of this study was to identify genomic regions associated with porcine reproductive and respiratory syndrome (PRRS) viral load (VL), porcine circovirus type-2b (PCV2b) VL, and weight gain (WG) in nursery pigs co-infected with PRRS virus (PRRSV) and PCV2b. Two PRRS Host Genetics Consortium trials were conducted using commercial crossbred pigs (n = 400) pre-selected (50% AA and 50% AB) for the WUR single nucleotide polymorphism (SNP) on chromosome (SSC) 4 that is associated with response to PRRS. Half of the pigs received a PRRS modified live vaccine and all pigs were co-infected with PRRSV and PCV2b 28 d later. For the genome-wide association studies (GWAS), 61,730 SNPs were fitted simultaneously using the BayesB method with $\pi = 0.994$. For analysis of PCV2b VL, trial, WUR, vaccination (Vx), WUR×Vx, weight at Vx, age at Vx, PRRS viremia at 0 dpi, PCV2b viremia at 0 dpi, and pen were fitted as fixed effects. For analysis of WG and PRRS VL, trial×Vx replaced WUR×Vx. Marker-based heritability estimates were 0.33, 0.34, and 0.14 for WG, PCV2b VL, and PRRS VL, respectively. Compared with AA pigs, AB pigs did not significantly differ ($P = 0.70$) in WG but had lower PRRS VL ($P < 0.0001$) and, in the vaccinated group, lower PCV2b VL ($P = 0.09$). Sizable genetic associations were identified for the GWAS of WG and PCV2b VL, but not for PRRS VL. A 2-Mb window on SSC9, at 27–28 Mb, explained 7.7% of genetic variance in WG, which has been associated with growth of nursery pigs across multiple breeds. For PCV2b VL, 1-Mb windows on SSC1 (162 Mb), SSC5 (102 Mb), and SSC7 (41 Mb) explained 1.4, 1.1, and 1.0% of genetic variance, respectively. Thus, the AB WUR genotype was associated with reduced PRRS VL and with reduced PCV2b VL in vaccinated pigs, following co-infection with PRRSV and PCV2b. Genomic regions associated with WG and PCV2b VL were identified, regions for the latter trait being novel. These results suggest the possibility of selectively breeding pigs, based on these regions, for improved host response to PRRSV/PCV2b co-infection. This work was supported by the USDA ARS NIFA awards 2012–38420–19286 and 2013–68004–20362.

Key Words: genetic susceptibility, GWAS, swine

766 Genetic and economic effects of incorporating genomic predictions on health in swine breeding schemes. Chandraratne M. B. Dematawewa*[1], Anna Grosse Holthaus[2], Henner Simianer[2], and Jack C. M. Dekkers[1], *[1]Iowa State University, Ames, IA, [2]University of Göttingen, Göttingen, Germany.*

A study was conducted to determine the effect of inclusion of genomic evaluations for health (GE-health) on improvements in health, the overall breeding goal (ΔH) and discounted profit (ΔΩ) in commercial cross breeding schemes. A 3-way cross breeding scheme with 2 maternal lines [female: Yorkshire (YS); male: Landrace (LR)] and a terminal sire line (Duroc, DU) was deterministically simulated using the ZPLAN+ software. The YS nucleus consisted of 50 boars and 1000 sows, while LR and DU nuclei had 100 boars and 800 sows each. Productive life of nucleus and multiplier (n = 2400) animals was 1 year, while F_1 crossbred sows were kept for 2 years to produce 532,400 commercial piglets/year. Days to market (DY), backfat thickness (BF), and litter weight at 21 d (LW; for YS and LR only) were considered with heritabilities (h^2) of 0.4, 0.5, and 0.09. The traits were standardized to genetic SD = 1. A health trait (HL) was simulated with $h^2 = 0.05$ and genetic SD = 1, with positive genetic (0.2) and phenotypic (0.3) correlations with DY and BF, and zero correlations with LW. HL was recorded from 80 commercial halfsibs/animal. Economic weights ($) for DY, BF, LW and HL were −1.86, −1.82, 5.35, and 1.86 per genetic SD, respectively. Planning horizon was 10 years (discount rate = 0.05). Costs for high and low density genotyping and health recording were $100, $40 and $10 per animal, respectively. Accuracy of GE-health ($r_{MG\text{-}HEALTH}$) was varied from 0 to 1.0 and 0.7 for the other traits. Inclusion of GE-health for both sires and dams increased both ΔH and ΔΩ as $r_{MG\text{-}HEALTH}$ increased, mainly due to greater genetic gain in HEALTH. At $r_{MG\text{-}HEALTH} = 0.8$, extra response in ΔH and ΔΩ for were 6.25% and $0.55 per animal in the breeding program, compared with having no GE-health. The corresponding values were higher (7.06% and $1.34, respectively) when HEALTH phenotypes were not recorded, partly due to lower initial response. The benefit of health recording diminished when $r_{MG\text{-}HEALTH}$ increased. These results show economic feasibility for implementing GE-health in commercial swine breeding. Funded by Genome Canada.

Key Words: genomic selection, health, swine breeding

767 Exploring causal networks underlying fat deposition and muscularity in pigs through the integration of phenotypic, genotypic and transcriptomic data. Francisco Peñagaricano*[1,2], Bruno D. Valente[1], Juan P. Steibel[3], Ronald O. Bates[3], Cathy W. Ernst[3], Hasan Khatib[1], and Guilherme J. M. Rosa[1], *[1]University of Wisconsin-Madison, Madison, WI, [2]University of Florida, Gainesville, FL, [3]Michigan State University, East Lansing, MI.*

Joint modeling and analysis of phenotypic, genotypic and transcriptomic data have the potential to uncover the genetic control of gene activity and phenotypic variation, as well as shed light on the manner and extent of connectedness among these variables. Current studies mainly report associations; that is, undirected connections among variables without causal interpretation. Knowledge regarding causal relationships among genes and phenotypes can be used to predict the behavior of complex systems, as well as to optimize management practices and selection strategies. Here, we performed a multistep procedure for inferring causal networks underlying carcass fat deposition and muscularity in pigs using multi-omics data obtained from an F_2 Duroc × Pietrain resource pig population. The data set included several carcass and meat quality phenotypes, genotypic information spanning the whole swine genome, and gene expression data from loin muscle for a total of 171 F_2 individuals. We initially explored marginal associations between genotypes and phenotypic and expression traits through whole-genome scans, and then, in genomic regions with multiple significant hits, we assessed gene-phenotype network reconstruction using causal structural learning algorithms. One genomic region in SSC6 showed significant associations with 3 relevant phenotypes, midline 10th-rib backfat thickness, loin muscle weight, and average intramuscular fat percentage, and also with the expression of 7 genes, including *ZNF24*, *SSX2IP*, and *AKR7A2*. The inferred network indicated that the genotype affects the 3 phenotypes mainly through the expression of several genes. Among the phenotypes, fat deposition traits negatively affected loin muscle weight. Overall, our findings shed light on the antagonist relationship between carcass fat deposition and meat lean content in pigs. In addition, the procedure described in this study has the potential to unravel gene-phenotype networks underlying complex phenotypes.

Key Words: causal inference, complex trait, systems genetics

768 Genomic prediction accuracy of porcine respiratory and reproductive syndrome (PRRS) antibody response in commercial gilts and sows. Nick V. L. Serão*[1], Robert A. Kemp[2], Benny E. Mote[3], John C. S. Harding[4], Philip Willson[4], Stephen C. Bishop[5], Graham S. Plastow[6], and Jack C. M. Dekkers[1], *[1]Iowa State University, Ames, IA, [2]Genesus, Oakville, ON, Canada, [3]Fast Genetics, Saskatoon, SK, Canada, [4]University of Saskatchewan, Saskatoon, SK, Canada, [5]The Roslin Institute, Easter Bush, Midlothian, UK, [6]University of Alberta, Edmonton, AB, Canada.*

The objective of this study was to assess the genomic prediction accuracy (GPA) of antibody response to PRRS in purebred sows and crossbred gilts. Data on 2,180 commercial crossbred gilts (CrossData), from 7 breeding companies, and 512 purebred multiplier Landrace sows (PureData), from one breeding company, were used to assess the ability to predict PRRS antibody response, measured as sample-to-positive (S/P) ratio, using 38,191 single nucleotide polymorphisms (SNPs). S/P ratio was measured in the CrossData at 40.7 ± 16 d after gilts entered commercial herds with a history of health problems, whereas in the PureData, S/P ratio was measured 46 d after a natural PRRS outbreak. Two prediction strategies were used: 1) CrossData was used for training and PureData for validation; 2) 7-fold cross-validation using the CrossData. Previous results showed that S/P ratio is mainly controlled by 2 regions on chromosome 7 (SSC7), at 24–31 Mb and 128–131 Mb. Therefore, different sets of SNPs were used for prediction: all SNPs (All_SNP), SNPs on SSC7 24–31 Mb (QTL1_SNP), SNPs on SSC7 128–131 Mb (QTL2_SNP), SNPs on both regions (SSC7_SNP), all SNPs except those on the SSC7 regions (Not7_SNP). GPA was measured as the correlation between genomic estimated breeding values and pre-adjusted phenotypes, divided by square root of heritability. Heritability estimates were 0.46 (PureData) and 0.31(CrossData). When training using the CrossData and validating on PureData, GPAs were 0.49 (All_SNP), 0.55 (QTL1_SNP), 0.30 (QTL2_SNP), 0.63 (SSC7_SNP), and 0.15 (Not7_SNP). GPAs were slightly lower using from cross-validation in the CrossData: when averaging across folds: 0.32 (All_SNP), 0.30 (QTL1_SNP), 0.27 (QTL2_SNP), 0.39 (SSC7_SNP), and 0.1 (Not7_SNP). The highest and lowest GPA from individual folds were −0.14 (Not7_SNP) and 0.60 (SSC7_All). These results show that S/P ratio can be accurately predicted using SNPs in pure and crossbred female pigs. In addition, greater accuracy can be obtained using the 2 QTL on SSC7 than the whole genome. Financial support from Genome Canada, the Canadian Swine Health Board, and PigGen Canada.

Key Words: SNP, host genetics, cross-validation

769 Genetic analysis and whole-genome wide association for feeding behavior traits in Duroc pigs. Shihui Jiao*[1], Christian Maltecca[1], Yijian Huang[2], and Kent A. Gray[2], *[1]North Carolina State University, Raleigh, NC, [2]Smithfield Premium Genetics, Rose Hill, NC.*

This study was aimed at estimating genetic parameters for feeding behavior and production traits and identifying genomic regions influencing those behavior traits in a Duroc population. Feed intake and related measures were collected from 2004 to 2013 for 14,869 boars with 4,940,348 visits. Several 7,319 pigs were genotyped with 35,700 SNP available for analysis. Traits included 4 production traits; average daily feed intake, average daily gain, off-test body weight and backfat thickness and 12 feeding behavior traits include; daily occupation time (OTD), number of visits (NVD), feeding rate (DFR), feed intake per visit (FIV), occupation time per visit (OTV), standard deviation (SD) of feed intake per visit (ASDFIV), SD of occupation time per visit (ASDOTV), SD of feeding rate per visit (ASDFRV), SD of daily feed intake (SDFI), SD of daily occupation time (SOTD), SD of number of visits (SDNVD) and SD of feeding rate (SDFR). Except for SDFI and SDFR, all behavior traits were moderately heritable with estimates ranging from 0.32 ± 0.03 (SOTD) to 0.68 ± 0.03 (FIV). Genomic heritability estimates using single-step methods incorporating genotypes were slightly lower than those obtained using pedigree by 0.10 ± 0.09 averaged across all behavior traits. Genetic correlation of behavior traits with production traits varied (ranging from −0.481 to 0.618). Single trait association analyses for behavior traits for 1,541 boars were performed using mixed linear models. Significance of marker was declared with a p-value less than 1.40×10^{-6} (Bonferroni correction). A total of 35 significant markers on SSC 2, 7, 8, 9 and 18 associated with NVD, OTV, ASDFRV and SOTD were identified and putative genes included *NCR3* (involving in natural killer cell mediated cytotoxicity and associated with obesity in human), *CLPS* (activating in digestion of dietary lipid and absorption) and *PPARD* (regulator of lipid metabolism). In conclusion, feeding behaviors were moderately heritable and we have identified several genomic regions associated with traits affecting feeding behaviors that may help us understand the genetic mechanism controlling the traits.

Key Words: genomics, feeding behavior

770 Genomic mitigation of seasonality effect on carcass weight in commercial pigs. Breno D. Fragomeni*[1], Shogo Tsuruta[1], Daniela A.L. Lourenco[1], Kent Gray[2], Yijian Huang[2], and Ignacy Misztal[1], *[1]Department of Animal and Dairy Science, University of Georgia, Athens, GA, [2]Smithfield Premium Genetics, Rose Hill, NC.*

The purpose of this study was to determine the effect of heat stress on carcass weight in a commercial pig population. Phenotypes included hot carcass weight records on 227,043 commercial pigs collected from 2 packing plants located in the states of North Carolina and Missouri; the pigs were a cross between purebred Duroc sires and F1 Landrace x Large White dams. The pedigree file included 553,442 animals, and 60k SNP genotypes were available for 8,232 sires. Weather information was collected from airport weather stations within 100 miles distance from the finishing farms. Average temperature humidity index (THI) was calculated for a period of 70 d before each HCW was collected. The THI measurement was classified as heat stress (THI > 78, n = 32,783) or comfort conditions (THI = < 78, n = 194,260). Analyses were done with an animal model as either a single-trait or 2-trait model using records identified as heat stress and comfort conditions treated as separate traits. Variance components were estimated with AIREML, and traditional and genomic (G) EBV were computed either with BLUP or single-step genomic BLUP (ssGBLUP). Validations were computed for 94 animals from the last generation using the forward prediction method, and reliability of (G)EBV was calculated as R^2 of predictions based on the training population (all except the last generation) on progeny yield deviations of the last generation. The heritability estimate for hot carcass weight in the single-trait model was 0.20. In the multiple trait model, the heritability estimate was 0.20 under comfort conditions and 0.25 under heat stress, with a genetic correlation of 0.62. Under comfort conditions and heat stress, reliabilities in traditional EBV were 0.22 and 0.14 whereas reliabilities in GEBV were 0.38 and 0.19, respectively. The heritability of carcass weight is higher under heat stress. Use of ssGBLUP increases reliabilities of carcass weight under both heat stress and comfort conditions. Effects of seasonality on carcass weight can be mitigated by genetic selection, especially with the genomic information.

Key Words: heat stress, genotype × environment interaction, genomic selection

771 Effect of divergent selection for residual feed intake in finishing pigs on juvenile IGF-I. Emily D. Mauch*[1], Nick V. L. Serão[1], Joel R. Steckelberg[1], Anna Wolc[1,2], and Jack C. M. Dekkers[1], *[1]Department of Animal Science, Iowa State University, Ames, IA, [2]Hy-Line International, Dallas Center, IA.*

Since 2001, purebred Yorkshire pigs at Iowa State University have been divergently selected for increased (Low RFI) and decreased (High RFI) feed efficiency based on single trait selection for residual feed intake (RFI). Using data from generations 2–5 (G2–5), Bunter et al. (2010) found that serum insulin-like growth factor-I (IGF-I) concentration in young pigs (33–42 d) was lower in the Low RFI line, and had a high genetic correlation (0.63) with RFI, suggesting that it could be used as an indicator trait for RFI. The objective here was to validate these findings in G10 of the RFI lines. IGF-I concentration was measured by Rivalea Ltd. (Australia) using the Primegro assay on blood samples collected from 35 to 42 d of age on 377 piglets from G10. IGF-I data were analyzed in ASREML with a univariate sire model and a bivariate animal model with RFI data on 2,370 pigs from G1–10. Both models for IGF-I included the fixed effects of line, sex and contemporary group, covariates of age at blood collection and interval from weaning to blood collection, and random effects of litter, and sire (no pedigree) or animal (with complete pedigree). The concentration of IGF-I (ng/mL) was estimated to be 55.7 (±19.1) and 53.4 (±44.2) lower in the Low RFI line compared with the High RFI line based on the sire ($P = 0.01$) and animal ($P = 0.3$) models, respectively. Bunter et al. (2010) reported a similar line difference of 47.0 ng/mL in G5. The estimated genetic correlation between RFI and IGF-I was 0.68 (±0.38), similar to Bunter et al. (2010). In conclusion, lower juvenile IGF-I concentration was validated to be associated with pigs selected for increased feed efficiency based on RFI and, therefore, may serve as an early blood indicator to select for feed efficiency. However, when considering the full pedigree, the line difference was not significant. Funding provided by AFRI-NIFA grant #2011–68004–30336 and by Rivalea Ltd. (Australia).

Key Words: swine, genetic parameter, residual feed intake