

807 Environmental modifications to address heat stress. M. J. Brouk*¹, J. P. Harner, III¹, J. F. Smith¹, and D. V. Armstrong², ¹*Kansas State University, Manhattan*, ²*University of Arizona, Tucson*.

Heat stress results in significant economic and production losses for dairy operations throughout the world each summer. Due to the continuous nature of dairy production, losses in the current lactation often result in losses in subsequent lactations or premature culling of animals. Reduction of losses due to heat stress represent an opportunity for dairy producers to gain a competitive edge. As a result, many producers have utilized different methods of heat abatement. In general these methods can be divided into two groups, those which enhance heat exchange between the cow and the environment or those which modify the environment to prevent or limit the degree of heat stress to which the animals are exposed. Increased heat exchange generally involves increasing heat loss from the body surface by enhancing heat loss mechanisms. The most common methods involve the addition of water to the hair coat and supplemental airflow to increase the rate of evaporation of the additional water and sweat enhancing heat exchange which reduces body temperature. Heat stress abatement with these systems is generally achieved by cooling heat stressed cattle. Environmental modifications attempt to reduce the potential for heat stress by lowering the temperature of the air around the cow. Evaporation of water into warm air reduces the temperature while increasing the relative humidity. Water evaporation can be achieved by high pressure fogging systems or by drawing warm air through evaporative pads. The challenge is to maintain an environment in which the temperature-humidity index is below the heat stress threshold for lactating dairy cattle. Critical factors for consideration when evaluating these systems is the air temperature and relative humidity of the environment. An inadequate or improperly designed system may actually increase the THI above the unmodified environment. When selecting a heat abatement system, one should consider production goals, facilities, environment, heat stress potential, water supply, and economic factors. In some very stressful environments, application of both environmental modifications and surface heat exchange may be beneficial.

Key Words: Cooling, Facilities, Environmental Stress

808 What we have learned about the genes involved in the response to heat stress. R. J. Collier* and R. P. Rhoads, *University of Arizona*.

Climate has profound effects on animal performance (i.e. growth, reproduction and lactation) and understanding the interaction between thermal environment and animal production has been the subject of intense research. Traditionally, examination of heat stress effects have focused on physiological and phenotypic changes, however, the development of molecular tools is allowing animal scientists to characterize transcriptional alterations across the genome and identify key cellular responses to heat stress. Gene expression changes associated with thermal environment may be grouped into 3 categories; acute, acclimatory and adaptive. Acute and acclimatory responses occur on a physiological and cellular level and decay with removal of the stress while adaptive responses involve short and long-term genetic alterations. At the systemic level, gene families associated with homeorhetic regulation of metabolism (growth hormone, prolactin, thyroxine, glucocorticoids) play an important role in heat stress acclimation. At the cellular level, thermal tolerance is maintained as long as heat shock family proteins are elevated and lost when expression of these genes declines in the face of continued stress. Cellular expression of heat shock proteins during thermal stress is altered by prolactin, IGF-I and prostaglandins E2 and A1. indicating that considerable opportunity may exist to improve thermotolerance. Evolutionary adaptation to heat stress involves genotypic differences associated with coat color, hair quality and density and sweat gland function which are related to inter-breed variation in heat gain and loss. Short-term genetic alterations involving epigenetic regulation of gene expression and thermal imprinting of the genome represent potentially promising but relatively unexplored areas in animal agriculture. Opportunities exist to improve thermal tolerance of animals by selection for specific hair coat characteristics, homeorhetic responses to thermal stress and improved heat shock response. The heat shock response opportunity is greatest during early embryonic development.

Key Words: Heat Stress, Gene Expression, Acclimation

Breeding and Genetics - Livestock and Poultry: Swine

809 Genetic factors affecting growth traits of Nili-Ravi Buffalo calves in Pakistan. P. Akhtar*, U. Kalsoom, S. Ali, M. Yaqoob, M. I. Mustafa, and J. I. Sultan, *Faculty of Animal Husbandry, University of Agriculture, Faisalabad, Punjab, Pakistan*.

Records on body weights at different ages of 624 Nili Ravi buffalo calves (from 1989 to 2002) kept at LES, Bahadurnagar, (Pakistan), were analyzed by computer programs LSMLMW and DFREML. Average weights at birth, weaning and yearling were 35.86±4.30, 66.12±9.16 and 145.82±19.50 kg. Pre-weaning average daily gain was 316 ± 88 gm, while post-weaning average daily gain was 301±29 gm. The ANOVA indicated that year and season of birth, age and weight of dam significantly effected the traits. Maximum weights were observed in spring season, while minimum gains were obtained in other seasons. Maximum heritability was 0.25±0.14 for birth weight, while minimum heritability was observed for weight at nine months of age that was 0.11±0.12 which indicates that growth traits were moderate to highly heritable suggesting that selection will be a best criteria for improvement. Among phenotypic correlations maximum correlation

was 0.90 that was between weaning weight and weight at six months of age whereas minimum correlation was observed in birth weight. Environmental, phenotypic and genetic correlations were fairly large and positive indicating that selection for the improvement of one trait will positively affect the other trait.

Key Words: Genetic Factors, Growth, Buffalo Calves

810 Genetic analysis of ewe stayability and its association with lamb growth and adult body weight. R. C. Borg¹, D. R. Notter*¹, and R. W. Kott², ¹*Virginia Polytechnic Institute and State University, Blacksburg*, ²*Montana State University, Bozeman*.

Records from 2,525 adult Targhee ewes and 10,099 lambs were used to estimate genetic parameters in an animal model for ewe stayability (STAY), weaning weight (WW), adult weight (AW), and number of lamb born (NB). Weaning weights were recorded at approximately 120

d of age. Annual NB and AW were recorded at lambing and weaning, respectively. Stayability were analyzed as overall stayability (STAY_n|2) which indicated presence or absence of a ewe at n yr of age, given the ewe was present at 2 yr of age, or marginal stayability (STAY_n|n-1) recording the presences of a ewe at n yr of age, given the ewe was present in the previous year. Adjustments were made to WW for effects of age, type of birth and rearing, age of dam, and sex, and NB was adjusted for ewe age effects. Birth year was included as a fixed effect on all traits; additional fixed effects of management group on WW and ewe age and type of birth and rearing on AW were also included. Models for all traits included random direct additive genetic and residual effects. Uncorrelated random effects of the ewe were also included for AW and NB, and additive maternal and dam permanent environmental effects were included for WW. Additive variance in STAY was only present after 5 yr of age ($P < 0.05$), so only STAY₅|4 and STAY₆|2, with heritability estimates of 0.08 and 0.10, respectively, were used in multiple-trait analyses. All phenotypic correlations involving STAY were near zero, ranging from -0.04 to 0.03. Estimates of direct additive-maternal correlations of STAY₅|4 and STAY₆|2 with WW were positive (both 0.46; $P < 0.05$), suggesting that STAY and maternal effects on WW may both reflect genetic variation in ewe fitness characteristics. Genetic correlations between STAY₆|2 and WW, AW, and NB were all negative, with values of -0.17, -0.32 ($P < 0.05$) and -0.03, respectively, indicating a possible small antagonism between STAY and additive effects on body size.

Key Words: Sheep, Heritability, Stayability

811 Gene regulation in liver of cattle exposed to heat stress.

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Summer heat stress results annually in hundreds of million of dollars of lost productivity and impaired animal health. Cattle have reduced feed intake, lower growth and conception rates, panting activity, increased peripheral blood flow and sweating. Although these effects are well documented, the changes in cellular function and gene regulation are poorly understood. Liver is one of the major organs involved in the regulation of metabolism and heat production. The goal of this study is to investigate the changes in gene regulation in liver of cattle under long term mild heat stress. Angus steers (n=5) from the University of Missouri herd were housed in the Brody Environmental Center. Steers were maintained for 7 days at a temperature of $19.07 \pm 0.06^\circ\text{C}$ after which liver biopsies were obtained. Heat stress consisted of a 14 day exposure to a cycle of $27.39 \pm 0.15^\circ\text{C}$ nighttime low to $36.21 \pm 0.14^\circ\text{C}$ daytime high temperatures. Biopsies were again performed at the end of the heat stress period. RNA was extracted, labeled and hybridized to our cDNA bovine cDNA array. The microarrays were printed using PCR products amplified from 17,692 bovine cDNA clones. Normalization was accomplished by using a two-stage ANOVA analysis and a list of differentially expressed genes was obtained using the Fs statistic. A total of 100 differentially expressed genes were identified with at least a 40% up- or down-regulation and a false discovery rate of less than 0.05% (adjusted for multiple testing using permutations). Some genes involved in oxidative stress were down-regulated, such as Metallothionein 1, 2, and 3 (80%) and glutathione peroxidase (40%), while glutathione S-transferase was up-regulated by heat stress (240%). Insulin-like growth factor binding proteins 2 and 5 were up-regulated 200% and 160 %, respectively. Heat shock 70-kD protein 2 was up-regulated by 160%. Several genes involved in energy metabolism were differentially expressed, such as cytochrome

c oxidase subunit I and III, ATP synthase F0 subunit 8, and NADH dehydrogenase subunit 4L and 5. A number of genes involved in immune functions were also differentially expressed under heat stress.

Key Words: Heat Stress, Microarray, Liver

812 Differential gene expression profiling of malignant melanoma in Sinclair swine. M. A. Okomo-Adhiambo¹, A. Rink², W. Rauw¹, C. W. Beattie³, and L. Gomez-Raya*¹, ¹*University of Nevada, Reno*, ²*Animal Disease and Food Safety Laboratory, Reno, NV*, ³*University of Illinois, Chicago.*

The miniature strain of Sinclair swine develops an aggressive form of malignant melanoma, which in many cases spontaneously regresses after a complete metastatic phase. We used Affymetrix GeneChip[®] Porcine Genome Array consisting of 24,123 transcripts to compare gene expression profiles of blood and visceral tissues harvested from a Sinclair piglet afflicted by melanoma at birth and exhibiting metastatic lesions at weaning (6 weeks), with those from a full sibling piglet that showed no incidence of melanoma at birth and at weaning. Between 2% (in spleen) to 14% (in liver) of analyzed transcripts were significantly up-regulated (fold change in gene expression ≥ 2.0 and t-test p-values ≤ 0.05) in tissues sampled from the melanoma pig compared to those sampled from the normal pig, while 3% (in blood) to 15% (in inguinal lymph node) were significantly down-regulated. Among the modulated transcripts were genes directly involved in melanoma development and progression, as well as genes generally associated with cancer pathogenesis including oncogenes, transcription factors, cell cycle regulators and apoptosis related genes. These results suggest that significant changes in gene expression occur during the progression and metastasis of malignant melanoma in the Sinclair pig model, facilitating further analysis for discovery of candidate genes and transcriptional pathways that can be utilized in the development of novel intervention and diagnostic strategies for malignant melanoma.

Key Words: Malignant Melanoma, Sinclair Swine, Oligonucleotide Microarrays

813 Genetic parameter estimates for growth, carcass composition, and meat quality traits in Duroc swine. C. R. Schwab*, R. Tait, and T. J. Baas, *Iowa State University, Ames.*

The objective of this study was to estimate genetic parameters for growth, carcass composition, and meat quality traits in Duroc swine. Five generations of data from a project involving selection for increased intramuscular fat (IMF) using real-time ultrasound were analyzed. Within each generation, off-test ultrasonic measures (n = 3885) were collected on all three genders. Loin samples from all available barrows and randomly selected gilts (n = 847) were collected at a commercial abattoir for carcass composition and further meat quality assessment. Genetic parameters were estimated using MTDFREML procedures applied to a two-trait animal model that included fixed effects of sex and contemporary group along with a random effect for permanent environment of the litter. A covariate of BW was included for traits measured at off-test, and a covariate of carcass weight was included for composition traits measured on the carcass. Average heritability values across all two-trait analyses for IMF and ultrasonically predicted

intramuscular fat (PFAT) were 0.56 and 0.30, respectively, and their mutual genetic correlation was 0.87. The table shows estimated heritabilities and genetic correlations of IMF and PFAT with selected growth, carcass composition, and meat quality traits. The estimated genetic parameters further validate the use of ultrasound measurements in breeding programs aimed at meat quality improvement.

Table 1. Heritability and genetic correlation estimates of growth, carcass composition, and meat quality traits in Duroc swine

Trait	h ²	Genetic Correlation	
		IMF	PFAT
Weight per day of age	0.32	-0.08	0.18
Ultrasonic 10th rib backfat	0.57	0.46	0.52
Ultrasonic loin muscle area	0.55	-0.25	-0.30
Carcass 10th rib backfat	0.41	0.52	0.42
Carcass loin muscle area	0.59	-0.71	-0.45
24 hr pH	0.32	-0.04	-0.05
24 hr Minolta reflectance	0.26	0.72	0.54
Percent cooking loss	0.06	0.01	0.08
Instron tenderness	0.16	-0.30	-0.10

Key Words: Genetic Parameters, Heritability, Swine

814 Doe reproductive and fitness traits among three meat goat breeds semi-intensively managed in the southeastern US. R. Browning, Jr.*, M. L. Leite-Browning, B. Donnelly, and M. Byars, *Tennessee State University, Nashville.*

In the fall of 2003-2005, Boer (BR; n = 81), Kiko (KK; n = 64), and Spanish (SP; n = 59) straightbred does were exposed to Boer, Kiko, and Spanish bucks in a complete 3-breed diallel mating scheme to assess doe reproductive performance on southeastern US pastures. Does were managed together in a semi-intensive manner. This 3-yr dataset represents 157 BR, 152 KK, and 150 SP doe exposures. The proportion of exposed does delivering at least one live kid was lower ($P < 0.01$) for BR (82%) than for SP (93%) and KK (96 ± 3%). Litter size (1.9 kids) and litter weight (6.03 kg) at birth were not affected by breed of dam. By weaning at 3 mo, the proportion of exposed does weaning at least one kid was lower ($P < 0.01$) for BR (72%) than for KK and SP does (88 ± 4% each). Litter size at weaning was smaller ($P < 0.01$) for BR (1.55 kids) than for SP dams (1.8 ± 0.06 kids); KK were intermediate with 1.65 kids. Litter weight at weaning was lightest ($P < 0.01$) for BR (25.7 kg) than for KK dams (29.5 ± 1 kg); SP dams were intermediate (28.2 kg). The efficiency ratio of litter weight to dam weight at weaning was greater ($P < 0.01$) for SP and KK (67 and 61 ± 2%, respectively) compared to BR dams (52 ± 2%), SP and KK tended to differ ($P = 0.1$). As measures of whole herd performance based on all does exposed to bucks, BR does weaned a lower ($P < 0.01$) kid crop percent and litter weight (112%, 18.5 kg) compared to KK (144%, 25.8 kg) and SP (157 ± 9%, 24.5 ± 1.5 kg). Annual doe treatment rates for lameness and internal parasitism and attrition rates were higher ($P < 0.01$) for BR (71, 50, and 21%) than for SP (39, 24, and 8%) and KK does (31 ± 5%, 17 ± 5%, and 7 ± 4%). Fecal parasite egg counts differed ($P < 0.01$) among each of the three dam breeds: BR = 523, KK = 331, and SP = 233 ± 45 eggs/g. Results at this point of the study indicate that significant differences exist among meat goat breeds for doe performance on southeastern pastures.

Key Words: Meat Goat, Breed, Reproduction

815 Measures of libido and their relation to testicular hypertrophy and fertilizing competence in boars. D. O. Umeshiobi*, *Central University of Technology, Bloemfontein, Free State, South Africa.*

The aim of this study was to determine whether the testicular hypertrophy and reproductive competence in boars could be evaluated by selected measures of libido. Twenty-four (12 months old) Large White boars were randomly selected using standard tests for libido: reaction time (RT). Eight boars were assigned to each of the three treatment combinations involving 0, 5 and 10 minutes of sexual restraint (R). Semen was collected using gloved hand device following sexual stimulation and analyzed for quantitative and qualitative parameter using standard methodology. Sperm cells from each boar were used to artificially inseminate (AI) 10 oestrus-synchronized gilts (twice), 12 and 24 hours after the onset of oestrus. Boars were hemi-orchidectomised after 16 weeks of the experimental period. Sexual excitement of boars at 5 and 10R caused the weight of the testis to hypertrophise by 220.2% and 501.6%, respectively, as compared to the unexcited control (38.5%) boars. Total daily sperm production per testis (TDSP) increased to 160.3% and 328%, respectively, with this increase being dramatic (328%) in the 10R boars. Sexual excitement of boars at 10R resulted in the highest testicular traits, number of mounts (10.4 ± 1.6 per 30 min), ejaculation rates (4.1 ± 0.9 per 30 min, total sperm count (92.1 ± 3.1 × 10⁹), sperm motility (89.7 ± 1.4%) and normal acrosome morphology (94.4 ± 2.6%), with the shortest RT (1.5 ± 0.5 min). Gilts artificially inseminated with sperm cells from 10R boars exhibited significant improvements than the 5R boars, in NRR (91.5 ± 6.7 vs. 50.8 ± 13.3%), farrowing rate (88.3 ± 5.5 vs. 53.1 ± 9.2%), total piglets born (12.0 ± 0.4 vs. 5.5 ± 0.8) and live piglets (11.4 ± 0.2 vs. 3.5 ± 0.6). Results suggest that sexual excitement of boars induces testicular hypertrophy, leading to significant improvement in the fertilizing competence of boars.

Key Words: Boar Sexual Drive, Testicular Traits, Sow Fertility

816 Comparison of pure Berkshire, Landrace, and the reciprocal crosses at two market endpoints. K. M. Brueggemeier*, A. C. Naber, S. J. Moeller, H. N. Zerby, and K. M. Irvin, *The Ohio State University, Columbus.*

The objective of the study was to assess differences of two divergent breeds, using pure Berkshire (BB), Landrace (LL) and their reciprocal crosses (BL and LB; sire represented as the first letter) for carcass and pork quality traits at two market endpoints. The study was conducted in two seasons (n = 74 and 79) with approximately equal representation of the four combinations in each season. Pigs of each combination were harvested at two end-points: harvest 1 (H1; average weight 105 kg, 151 d) and harvest 2 (H2; average weight 123 kg, 178 d). Tenth rib backfat (BF), loin muscle area (LMA), Minolta L* (L), visual marbling score (MARB), and pH were assessed at 24 h postmortem with Warner-Bratzler Shear force assessed after aging for 7 d. Data were analyzed using a mixed model within a harvest endpoint. Fixed effects were breed combination, sex, and breed x sex interaction, with a random sire within breed combination effect, and live weight was included as a linear covariate for carcass traits. The only differences observed for BF occurred in H1 with BB pigs being significantly fatter ($P < 0.01$) than LL. For LMA in H1 and H2, BB pigs had less LMA than LL ($P < 0.05$) and LB pigs ($P < 0.07$); however, LB and LL pigs did not differ. Differences ($P < 0.01$) in pH were observed across breed combinations in both H1 and H2 and BB pigs had greater

($P < 0.05$) pH when compared with all other combinations. For L within H1 and H2, loins from LL pigs were paler ($P < 0.05$) than all other combinations. In addition, loins from BB pigs had greater MARB at H1 and H2, with no differences among other combinations. Shear force followed a similar trend, with loins from BB pigs requiring less ($P < 0.05$) force than those from BL at H1 and less force than those of LL at both H1 and H2. The data suggest that F1 crosses of Berkshire and Landrace were not different in carcass composition, but were poorer in pork quality attributes than pure Berkshire contemporaries and for many quality attributes the LL pig produced inferior quality.

Key Words: Swine, Pork Quality, Carcass

817 Correlated response in fatty acid composition from five generations of selection for intramuscular fat in Duroc pigs. J. L. Burkett*, T. J. Baas, D. C. Beitz, C. R. Schwab, N. L. Berry, and S. Zhang, *Iowa State University, Ames.*

The objective of this study was to evaluate differences in fatty acid composition differences among Duroc pigs selected for increased intramuscular fat (IMF) for five generations. Selection was based on EBV for IMF estimated by fitting a two-trait animal model and the full relationship matrix in MATVEC. In the select line (SL), the top 10 boars and top 50% of gilts were used to produce the next generation. One boar from each sire family and 50 gilts representing all sire families were selected randomly to maintain the control (CL). Longissimus muscle samples ($n=175$, 136 barrows, and 39 gilts) collected from generation 5 pigs in the CL ($n=102$) and SL ($n=73$) were used to determine the fatty acid profiles of IMF. Total lipids were extracted from the trimmed longissimus samples and methylated directly with acetyl chloride and methanol. Methyl esters were quantified by using a gas chromatograph with a 100 m column and flame ionization detector. Data were analyzed using a fixed linear model containing main effects of line and gender, and covariates of carcass contemporary group and total lipid within line. Select line pigs had more ($P < 0.01$) total lipid (5.15% vs. 3.07%) than did control line pigs. There were no differences ($P > 0.05$) in SFA, MUFA, MUFA:SFA, and atherogenic index (AI) between CL and SL pigs. A significant decrease ($P < 0.01$), however, was detected in total essential fatty acid composition (18:2+18:3n3) and PUFA:SFA in the SL when compared to CL pigs. This difference could be the result of greater de novo synthesis of fatty acids in the SL resulting in a dilution effect of the essential fatty acids as based on more total lipid. These results suggest that selection for increased intramuscular fat could lead to improved meat quality without affecting nutritional value.

Key Words: Fatty Acid Composition, Intramuscular Fat, Pigs

818 Analysis of incidence of Porcine Circovirus Associated Disease (PCVAD) in a landrace/large white composite population. J. S. Bates*, A. R. Doster, and R. K. Johnson, *University of Nebraska, Lincoln.*

The objective was to determine the importance of genetic and environmental effects on the incidence of Porcine Circovirus Associated Disease (PCVAD) in pigs. 1,905 pigs from Generations 24 and 25 of two lines selected for increased reproduction and growth and two control lines were scored for symptoms of PCVAD. From 60 d of age pigs were grown in confined buildings or outside lots containing straw-bedded hoop structures. Scoring was on a scale of 0 (no symptoms),

1 (suspect), or 2 (positive) for symptoms including muscle wasting, growth retardation, rough hair coat, diarrhea, and skin lesions, and was done weekly from 70 to 180 d of age. 16.3% of the pigs received a score of 2. A sample of 37 pigs with a score of 2 were necropsied and lung, lymph node, tonsil, liver, kidney, thymus, spleen, ileum, and colon tissue was microscopically examined for lesions suggestive of PCVAD. Immunohistochemistry and RT-PCR were used to detect the presence of PCV-2 in collected tissues. All 37 pigs scored as a 2 were positive for PCV-2. PCVAD score was analyzed with ASREML using the Binomial and Probit functions to estimate genetic and environmental effects. Pigs receiving at least one score of 2 were considered positive for PCVAD; all pigs scored with a 0 or 1 were considered negative. Direct and maternal birth dam heritabilities were 0.02 ± 0.001 and 0.12 ± 0.006 , respectively. The proportion of variance due to common birth litter and common nurse litter effects were 0.13 ± 0.04 and 0.01 ± 0.001 , respectively. The proportion of variance due to pen effects was 0.05 ± 0.03 . Differences between select and control lines were not significant. Significant differences ($P < 0.05$) in weight between negative and positive pigs, estimated in MTDFREML, were 0.09 kg at birth, 0.57 kg at weaning, 4.77 kg at 70 d, and 23.74 kg at 180 d. Probability of score 2 was greatest in pigs placed outside and least for pigs in temperature-regulated buildings ($P < 0.01$). Maternal genetic, common birth litter, and environmental variation affect incidence of PCVAD.

Key Words: Genetic Variation, PCVAD, Immunity

819 Breeding for robust pigs across the year in heat stress affected areas. B. Zumbach¹, I. Misztal¹, S. Tsuruta¹, J. P. Sanchez*¹, M. J. Azain¹, W. Herring², J. Holl², and T. Long², ¹*University of Georgia, Athens,* ²*Smithfield Premium Genetics Group, Rose Hill, NC.*

The aim of this study was to describe genetic variability of pig carcass weight as a function of heat stress. Data included carcass weights of 21,653 crossbred pigs (Duroc x [Landrace x Large White]) raised on two farms in North Carolina, and harvested from May 2005 through September 2006. Weather data were obtained from a nearby weather station. Monthly heat loads were calculated as degrees of average temperature-humidity index (THI) in °C over 23. Assumed heat load (H) was a sum of heat loads 4 months prior to harvest. The H was the greatest for pigs harvested in August-October 2005 (4.3-4.5) and 2006 (3.3), respectively, intermediate in July and November, lowest in June 2005, and none for the remaining months. Variance components were estimated with 3 models: univariate - not accounting for heat stress, 2-trait and random regression using linear splines (RRMS). Effects included in all the models were contemporary group, sex, and age at slaughter, sire, and litter. The 2-trait model treated observations July/August-October ("hot") and December-June ("cold") as separate traits. RRMS added a random regression on heat load for the sire effect with 3 knots at H=0, 2.2, and 4.5, respectively. The heritability estimate \pm SE in the univariate model was 0.17 ± 0.01 . In the 2-trait model the estimates were 0.15 ± 0.01 for "cold" and 0.34 for "hot"; the genetic correlation (0.08 ± 0.15) was not significant. The heritability estimates with RRMS were 0.15 ± 0.08 , 0.27 ± 0.11 , and 0.59 ± 0.16 for H=0, 2.2, and 4.5, respectively. The genetic correlations between H=0/H=4.5, H=0/H=2.2, and H=2.2/H=4.5 were -0.45 ± 0.14 , 0.30 ± 0.16 , and 0.50 ± 0.13 , respectively. This study supports the existence of genotype by environment interaction in growth traits of pigs across commercial environments.

Key Words: Pig, Carcass Weight, Heat Stress