

**ABSTRACTS**  
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**BREEDING AND GENETICS**

**1 Across breed EPD adjustment factors for growth traits from commonly used sire breeds.** B. R. Wiegand\*, L. A. Kriese, and J. L. Holliman, *Auburn University, Auburn, AL.*

Across-breed EPD adjustment factors were determined for Beefmaster (BM), Brahman (BR), Gelbvieh (GV), Hereford (HE) and Limousin (LM) sired calves for growth traits of birth (BW), 205 d (WW), and 365 d (YW) weight. Birth, weaning and yearling weights were taken on 540 steer and heifer progeny from Simmental x Angus dams. Traits were analyzed separately using MTDFREML and an animal model to obtain least squares means for respective sire breeds for each trait. The mixed model for BW and WW included fixed effects of birth year, sex of calf, breed of sire and age of dam. A covariate for age of calf at weaning was also included in the WW model. Random effects included in BW and WW models were direct genetic, maternal genetic, permanent environment and residual error. YW was analyzed as postweaning gain (PWG). PWG factors were added to WW factors to form YW factors. The mixed model included fixed effects of birth year, breed of sire and sex of calf. A covariate was included in the model to account for age of calf at yearling. Random effects included in the PWG analysis were direct genetic effects and random residual error. The inverse of the relationship matrix was included in the model (n=744) for all traits. Sire breed least squares means were adjusted for sire sampling, genetic trend and to a 1995 base year to form across-breed adjustment factors for BW, WW and YW. Hereford was chosen as the base breed. Pooled regressions of actual calf performance on sire EPD to adjust sire EPDs for sire sampling were  $.05 \pm 47$  kg/kg of BW EPD,  $.62 \pm .30$  kg/kg of WW EPD and  $.41 \pm .27$  kg/kg of YW EPD. Regressions were less than the expected value of 1.0. Across-breed EPD adjustment factors (kg) were:

Breed	BW	WW	YW
BM	1.90	-5.70	19.90
BR	7.40	17.90	36.80
GV	0.30	8.50	4.60
HE	0.00	0.00	0.00
LM	2.70	2.90	0.60

These across breed EPD adjustment factors are different than currently available adjustments. This may indicate a breed by region interaction.

**Key Words:** Beef Cattle, Expected Progeny Difference, Crossbreeding

**2 Sire family effects in Duroc-Chinese pigs of three stress genotypes.** K. D. Ragland\*, S. Ravungsook, T. J. Baas, and L. L. Christian, *Iowa State University, Ames.*

Ninety pigs from backcross litters and of three stress genotypes; homozygous normal (NN), heterozygous stress-carrier (Nn) and homozygous stress-positive (nn) were produced from a dam base population of 4 stress carrier Duroc boars and 11 stress negative Minzhu sows. Heterozygous stress carrier F<sub>1</sub> gilts were backcrossed to either their sire or to a heterozygous carrier boar of the same sire family to produce littermates of the three stress genotypes. Growth, carcass and meat quality traits of these genotypes were studied. Animals were tested for the effects of sire line, sex, halothane genotype and the interaction of sex and genotype and sire line and genotype. Sire family was significant (P<0.05) for tenth rib backfat (BF10), drip loss (DL), loin muscle area (LMA) and marbling score (MS). Sex effects were significant (P<0.05) for average daily gain (ADG), BF10, LMA, color score (CS), MS, firmness score (FS), Minolta reflectance (R) and ultimate pH. The effects of halothane genotype were significant (P<0.05) for BF10, DL, LMA, CS, MS, FS and R. The interaction of sex and stress genotype was significant (P<0.05) for ADG and approached significance for R. Interaction of sire and stress genotype was significant (P<0.05) for R and approached significance for DL and CS. There is little or no indication that the stress genotype effects on body composition (BF10 or LMA) were independent of their effects on muscle quality traits in any of the sire families.

**Key Words:** Halothane, Meat Quality, Chinese Breeds

**3 Genetic differences in fresh ham composition due to breed, sex, and HAL genotype.** R. N. Goodwin<sup>\*1</sup>, R. K. Miller<sup>2</sup>, E. P. Berg<sup>2</sup>, and L. L. Christian<sup>3</sup>, <sup>1</sup>*National Pork Producers Council, Des Moines, IA*, <sup>2</sup>*Texas A& M University, College Station, TX*, <sup>3</sup>*Iowa State University, Ames, IA*.

Purebred barrows and gilts (762) representing the purebred breeds of Berkshire, Chester White, Duroc, Hampshire, Landrace, Poland China, Spot, and Yorkshire, and two HAL genotypes (nm, mm) were evaluated. All pigs were entries in the 1996-97 National Barrow Show Sire Progeny Tests and were slaughtered at the Austin, MN Hormel Foods commercial packing plant. One ham per carcass was collected from the plant fabrication line, packaged individually, and transported to College Station, TX. Hams were separated into skin, bone, seam fat, subcutaneous fat, OUTSIDE ham (biceps femoris and semitendinosus), INSIDE ham (semimembranosus), KNUCKLE (quadriceps group), and other lean. The OUTSIDE, INSIDE, KNUCKLE, and other lean were combined for HAMLEAN. Seam fat and subcutaneous fat were combined for HAMFAT. A mixed linear model including the random effects of sire (breed) and dam (breed), and the fixed effects of sex, HAL genotype, slaughter date, breed, live animal weight (LIVEWT, kg), and carcass off-midline tenth rib backfat thickness (BF10, mm) was used to evaluate HAM, HAMLEAN, HAMFAT, BONE, OUTSIDE, INSIDE, and KNUCKLE. The 762 pigs represented 103 sire families. A REML algorithm was used to estimate sire variance. Heritabilities were calculated as four times sire variance divided by total variance. Differences in breed, sex, slaughter date, LIVEWT, and BF10 were found ( $p < 0.05$ ) for all traits. No differences in HAL were found. Barrow-gilt differences (kg) were HAM,  $-.18$ ; HAMLEAN,  $-.27$ ; HAMFAT,  $.07$ ; OUTSIDE,  $-.08$ ; INSIDE,  $-.08$ ; KNUCKLE,  $-.05$ .

**Key Words:** Pork Quality, Stress Gene, Ham Yield

**4 Genetic parameter estimates for mature weight in Angus cattle.** M. Kaps, W. O. Herring<sup>\*</sup>, and W. R. Lamberson, *University of Missouri - Columbia*.

The objective of the study was to estimate genetic parameters for mature weight in Angus cattle. The data utilized in the study consisted of repeated weight measurements of 3044 Angus cows born between 1976 and 1990. Mature weight was predicted by individually fitting Brody growth curves (asymptotic weight) and by using weights repeatedly measured after 4 y of age. (Co)variance components were estimated by REML from a single-trait animal model for asymptotic weight, a two-trait animal model for asymptotic and weaning weight, and a two-trait animal model for repeated mature weights and weaning weight. Weaning weights of 29943 calves were included in the two-trait models. Fixed effects in the model included weaning and cow contemporary groups for weaning and mature weight, respectively. Weaning contemporary group was defined as a herd at weaning, year of birth, season of birth, weaning lot date, weaning management code and sex of a calf. Cow contemporary group included definition of weaning group plus yearling lot date, yearling and cow herds. Random effects for weaning weight included direct genetic, maternal genetic and permanent environmental effects; and for mature weight, direct genetic and repeated measurements (if in the model). Estimates of heritability for weaning weight were similar for both two-trait models (.52 and .53). Estimates of heritability for mature weight were .44, .51 and .57 for the single-trait model with asymptotic weight, two-trait model with asymptotic weight and two-trait model with repeated weights, respectively. The estimate of genetic correlation between mature and weaning weight was much higher for the repeated measures model (.69 vs. .43). Use of a multiple trait animal model accounts for the effects of culling and allows prediction of breeding values for animals which have not had mature weights recorded.

**Key Words:** Mature Weight, Cattle, Heritability

**5 Proportion of variance of cytoplasmic effects due to REML bias for milk yield using animal and sire models.** P. R. N. Rorato<sup>1</sup>, L. D. Van Vleck<sup>\*2</sup>, and J. F. Keown<sup>1</sup>, <sup>1</sup>*University of Nebraska, Lincoln*, <sup>2</sup>*USDA, ARS, USMARC, Lincoln*.

Milk yields (2x, 305 d, ME) from the first three lactations of 139,869 Holstein cows produced from 1980 through 1991 were used. Cytoplasmic line was assigned by tracing female paths to last female ancestor using DHI records from 1950 through 1991. The data were divided randomly by herd code into 10 samples with averages of 13,987 lactation yields of 6,806 cows with 2,026 cytoplasmic lines. Two single trait models for milk yield were used with fixed effects of herd-year-seasons of freshening to estimate relative variance due to random effects of direct genetic value of cow ( $g^2$ ) (or sire,  $.25 g^2$ ), sire by herd interaction ( $s^2$ ), cytoplasmic line ( $c^2$ ), cow permanent environmental ( $p^2$ ), and residual ( $e^2$ ) for both an animal and unrelated sire model. For the data of each sample, 10 additional analyses were performed with levels for cytoplasmic and sire by herd effects assigned randomly to records within a herd. The estimates were obtained with a derivative-free REML algorithm using numerator relationship matrices computed from the samples (animal model). Standard errors (SE) were computed from the average information matrix. Mean estimates were compared for the 10 original samples (DAT) and for the 100 simulated analyses (SIM). For the animal model,  $g^2$  averaged .300 and .321 with sample SE of .025 to .029;  $p^2$  averaged .242 and .235 with SE, .024;  $s^2$  averaged .015 and .003 with SE, .008; and  $c^2$  averaged .011 and .003 with SE, .007 for DAT and SIM, respectively. For the sire model,  $g^2$  averaged .232 and .258;  $s^2$  averaged .018 and .004, and  $c^2$  averaged .038 and .003 for DAT and SIM, respectively, with similar SE as for animal model. Results show that REML bias did not account for all of estimates of  $c^2$  and  $s^2$ . In the analyses with randomly assigned levels of cytoplasmic lines and sire by herd interactions the mean estimates of  $c^2$  and  $s^2$  were about .003 compared to estimates of .011 to .038 for actual data. Failure to account properly for  $s^2$  and  $c^2$  seemed to inflate slightly estimates of  $g^2$  with both animal and sire models.

**Key Words:** Holstein, Lactation

**6 Effect of PTAs for type and production traits in determining semen price of Holstein and Jersey AI bulls.** M. A. Chrystal<sup>\*1</sup>, A. J. Seykora<sup>1</sup>, and B. G. Cassell<sup>2</sup>, <sup>1</sup>*University of Minnesota, St. Paul*, <sup>2</sup>*Virginia Polytechnic Institute and State University, Blacksburg*.

The data consisted of active AI Holstein and Jersey available in the US for the years 1986, 1989, 1992, 1995, and 1997. The correlations between semen price and PTAs of production and type traits for Holstein AI sires in August 1997 were: Milk .36, fat .26, protein .46, calving ease .04, productive life .09, somatic cell score .00, and type score .37. A multiple regression model was performed on this data set using price as the dependent variable. Included in the model as independent variables were stud, reliability for milk and fat, and PTA's for protein, type, productive life, somatic cell score and calving ease. Stud, reliability, PTA protein and PTA type significantly affected semen price ( $p < .01$ ). Productive life, somatic cell score and calving ease were not associated with semen price ( $p < .05$ ). A model including stud, reliability, PTA protein and PTA type was performed on both the Holstein and Jersey data sets. An increase in reliability increased the semen price for Holsteins ( $p < .01$ ) but not for Jerseys. PTA protein and type affected semen price for all years ( $p < .01$ ).

*Trends in Emphasis:* Dollar increase in semen cost per standard deviation increase in PTA protein and type.

Holsteins	1986	1989	1992	1995	1997
PTA protein	\$5.70	\$7.03	\$5.89	\$4.94	\$5.51
PTA type	\$3.68	\$4.04	\$4.19	\$3.86	\$4.20
Ratio protein:type	1.55:1	1.74:1	1.41:1	1.30:1	1.31:1
Jerseys					
PTA protein	2.94	2.38	3.36	2.94	3.08
PTA type	1.81	2.32	1.98	1.53	1.95
Ratio protein:type	1.54:1	1.03:1	1.70:1	1.92:1	1.56:1

These results illustrate that PTA protein had a slightly greater effect on semen price than type for both Jerseys and Holsteins.

**Key Words:** PTA, Production Traits, Semen Price

**7 Reproduction and maternal performance of F<sub>1</sub> cows by diverse sire breeds.** L. V. Cundiff\*, K. E. Gregory, and H. C. Freetly, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

F<sub>1</sub> cross cows from Hereford, Angus, and composite MARC III (25% each Angus, Hereford, Red Poll and Pinzgauer) dams and by Hereford and Angus (H&A), Brahman (Bm), Boran (Bo), Tuli (Tu), Piedmontese (Pm) and Belgian Blue (Bb) sires were evaluated for reproduction and maternal performance when mated to produce progeny by Red Poll sires at 2 yr of age and Charolais and Belgian Blue F<sub>1</sub> sires at 3 or 4 yr of age. Male calves were castrated shortly after birth. Calves were born in the spring of 1994 to 1996 and weaned at about 7 months of age. Significant differences were found among F<sub>1</sub> cow breed groups for calf crop weaned (CALFWN, %), unassisted calvings (UNAST, %), birth weight (BWT, kg), calf survival to weaning (CSURV, %), and 200 d weaning weight (WNWT, kg), but not for calf crop percentage born or 200 d weaning wt per cow exposed (WNWT/EXP, kg). Number of cows exposed (NEXP), breed group means, and mean least significant differences (LSD.05) were:

F <sub>1</sub> COW	NEXP	CALFWN	UNAST	BWT	CSURV	WNWT	WNWT/EXP
HA	469	80.2	87.3	38.2	92.4	204.5	161.0
Bm	368	72.0	92.9	35.1	85.1	220.0	155.5
Bo	373	84.4	85.9	34.5	93.7	206.5	170.5
Tu	417	78.6	86.6	35.5	91.0	197.5	152.0
Pm	130	78.0	74.9	37.8	91.6	204.5	154.5
Bb	424	74.6	82.2	39.1	90.2	209.0	153.0
LSD.05		9.8	7.9	1.5	8.2	8.0	21.0

**Key Words:** Beef Cattle, Sire Breeds

**8 Comparison of generalized linear mixed models for the analysis of reproductive rates.** V. E. Vega-Murillo\*<sup>1</sup>, A. Rios-Utrera<sup>2</sup>, and M. Montano-Bermudez<sup>3</sup>, <sup>1</sup>*University of Nebraska, Lincoln*, <sup>2</sup>*CIPEP-INIFAP*, <sup>3</sup>*CENIFMA/ INIFAP (Mexico)*.

Reproductive data on 979 cow exposures and subsequent calvings from 1983 to 1989 were used to evaluate the reproductive performance of *Bos indicus* cows mated to *Bos taurus* and *Bos indicus* bulls, and to compare three methods of analysis. Brahman and Indu-Brazil bulls were mated to cows of their own breed, and Angus, Charolais Hereford and Brown Swiss bulls to Zebu cows in two breeding season each year. Traits studied were pregnancy, calving, and weaning rates. Cows diagnosed pregnant, calving and weaning a calf were given a score of 1 or otherwise a 0. Each trait was analyzed with a generalized linear mixed model assuming three different link functions or distributions: 1) identity link and normal distribution, 2) logit link and binomial distribution, and 3) probit link and binomial distribution. The analysis was made with the GLIMMIX macro (SAS, 1994). The model for each trait included the fixed effects of breed of sire, year, season of breeding and interactions found significant in preliminary analysis and the random effect of sire within breed of sire. The condition of the cow at the beginning of the breeding season was used as a covariate. Effects of breed of sire were significant for calving rate and weaning rate ( $p < 0.05$ ) with all the models. Interaction of breed of sire x season of breeding was significant ( $p < 0.03$ ) for all traits with all models. The model with identity link function and normal distribution tended to have standard errors slightly larger than the logit or probit links and binomial distribution. In almost all the cases the logit and probit analysis resulted in exactly the same estimated probabilities of success. The model with identity link function and normal distribution, did not fit the data adequately, there was strong evidence for under dispersion compared to the logit and probit models.

**Key Words:** Breeds, Cross-breeding, Beef Cattle

**9 Genetic parameters for growth, reproduction and wool traits in Columbia, Polypay, Rambouillet and Targee breeds.** C. M. van Zyl\*<sup>1</sup>, L. D. Van Vleck<sup>2</sup>, and G. D. Snowder<sup>3</sup>, <sup>1</sup>*University of Nebraska, Lincoln*; <sup>2</sup>*USDA, ARS, USMARC, Lincoln*, <sup>3</sup>*USDA, ARS, USSES, Dubois, ID.*

Genetic parameters for Columbia, Polypay, Rambouillet and Targee sheep were estimated using REML with animal models for fertility, growth and wool traits. As a measure of ewe productivity, total litter weight weaned at 120 d per ewe lambing was included as a composite trait. Total number of observations ranged from 5,140 to 7,095 for fertility traits, from 7,750 to 9,530 for growth traits, from 4,063 to 34,746 for wool traits, and from 4,609 to 6,469 for the composite trait. Model 1 for fertility traits included additive genetic effect and permanent environmental effect of the ewe and residual effect. Model 2 for growth traits included additive genetic effect of the animal and additive maternal effect and permanent environmental effect of the dam, with correlation between direct and maternal genetic effects. Model 3 for wool traits included both additive and permanent environmental effects of the animal. Model 4 for the composite trait was same as Model 1 but with additional random effect of mating sire. Heritability estimates ranged from .07 to .11 for litter size at birth and number of live births and from .03 to .07 for litter survival to weaning. Heritability estimates ranged from 0.16 to 0.22 for birth weight, from 0.09 to 0.20 for weaning weight and from 0.07 to 0.19 for average daily gain. Heritability estimates ranged from .47 to .53 for fleece weight, from .25 to .49 for fleece grade and from .36 to .53 for staple length. Heritability estimates ranged from .03 to .12 for litter weight weaned. Relative variances of permanent environmental and/or random effects of mating sire were small for fertility traits and moderate for growth-, wool- and composite traits. Variance of additive maternal effects were smaller than for additive direct effects for growth traits. Heritability estimates for fleece traits were high and genetic progress could be expected from selection. Results also indicate that litter weight weaned can be used in selection.

**Key Words:** Sheep, Heritability, Breeding

**10 Influence of breed of dam on across-breed adjustment factors.** L. D. Van Vleck\* and L. V. Cundiff, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Records of progeny of sires of 12 breeds mated to Angus (2413 progeny), Hereford (1875), and MARC-III (603) composite (3 breeds of sire) dams at the US Meat Animal Research Center provide estimates of breed of sire differences that are adjusted for genetic level of bulls used at MARC to calculate across-breed adjustment factors to add to within-breed EPD. For birth weight, estimable differences among sire breeds were essentially the same for the breeds of dams. Regression on calendar day of birth for MARC-III was significantly different from that for Angus or Hereford dams. Difference between bull and heifer calves was significantly larger for MARC-III than for Angus or Hereford dams. For weaning weight, differences among sire breeds were not significantly different for the dam breeds. The male-female difference at weaning was significantly different for MARC-III from that for Hereford or Angus dams. For yearling weight, breed of sire differences were generally larger for Hereford than for Angus dams. Hereford-Brahman sire breed difference was significantly larger for MARC-III than for Angus dams. Regression on day of birth was positive for MARC-III but negative for Hereford and Angus dams. Male-female difference was larger for Hereford (significant) and for MARC-III than for Angus dams. Genetic correlations between expression of a sire's genotype were from .86 to 1.00 in Angus and Hereford dams, from .66 to .88 in Hereford and MARC-III dams and from .65 to .83 in Angus and MARC-III dams with smallest correlations for weaning weight. Phenotypic variances, although not coefficients of variation, were greatest for progeny of MARC-III dams. Conclusions are that 1) estimates of differences for sire breeds for birth and weaning weight do not depend on breed of dam, 2) regression on day of birth should be within dam breed, 3) breed of dam by sex of calf combination should be considered in the analysis model, and 4) expression of sire superiority may be somewhat different in progeny of MARC-III and Hereford or Angus dams.

**Key Words:** Growth, Beef Cattle, Genetic Parameters

**11 Probability of genetic identity for a panel of nine microsatellite markers in commercial pig lines.** S. T. Finn, P. A. Dyas, A. A. Paszek\*, S. W. Buttram, and B. A. Didion, *DEKALB Swine Breeders, Inc. DeKalb, IL.*

Genetic progress depends on accurate identification of animals selected into nucleus herds. The utility of hypervariable DNA loci in paternity testing was reported for humans and animals. The objective of this study was to estimate probabilities of genetic identity using a panel of nine microsatellites (MS) for commercial nucleus herd pigs. MS were selected based on marker heterozygosity, ease of genotyping, multiplexing capacity and genomic location. MS located on different chromosomes were preferred. The MS panel included CGA, S0059, TNFB, SW830, SW398, SW936, SW1111, SW840 and SW787. The company pedigree database for banked DNA samples was scanned and 84 unrelated animals (no common grandparents) representing five nucleus lines were identified. Lines originated from Large White (LW), Landrace (L) and Pietrain (P) breeds. DNA samples were genotyped on an ABI373. The lowest MS heterozygosities were observed in Pietrain line and the largest in Large White line. The estimates for probability of identity were found acceptable for paternity analysis in each genetic nucleus line.

Marker	Heterozygosity					Probability of Identity				
	Nucleus Lines					Nucleus Lines				
	LW1	LW2	L1	L2	P	LW1	LW2	L1	L2	P
CGA	0.79	0.85	0.80	0.83	0.69	0.07	0.04	0.07	0.05	0.15
S0059	0.74	0.62	0.60	0.78	0.54	0.11	0.19	0.19	0.09	0.24
TNFB	0.71	0.85	0.79	0.73	0.51	0.13	0.04	0.06	0.11	0.28
SW830	0.60	0.63	0.73	0.77	0.66	0.23	0.17	0.12	0.09	0.16
SW398	0.68	0.78	0.57	0.74	0.68	0.14	0.19	0.22	0.18	0.15
SW936	0.52	0.75	0.47	0.49	0.68	0.26	0.12	0.39	0.33	0.16
SW1111	0.24	0.60	0.60	0.67	0.67	0.60	0.23	0.24	0.17	0.15
SW840	0.46	0.50	0.00	0.08	0.00	0.39	0.37	1.00	0.90	1.00
SW787	0.70	0.77	0.79	0.68	0.39	0.14	0.09	0.08	0.14	0.40
All MS	0.60	0.71	0.59	0.64	0.54	1/4	1/26	1/6	1/20	1/0.4
						mln	mln	mln	mln	mln

**Key Words:** Pig Lines, Microsatellite Panel, Paternity

**12 Growth hormone genotypic effects on calf growth traits, carcass traits, and cow production traits.** J. H. Kim\* and D. M. Marshall, *South Dakota State University, Brookings.*

Effects of a growth hormone (bST: bovine somatotropin) marker on cow production traits, calf growth traits, and carcass traits were estimated. The bST genotypes of 380 cows and 359 calves were determined by Alu-I digestion of PCR product (A allele: 264bp, 96bp, 51bp, and 16bp; B allele: 264bp, 147bp, and 16bp). The bST genotypic frequencies of AA, AB, and BB, respectively, were 58.2 (209), 36.5 (131), and 5.3% (19) within the calves and 51.1 (194), 41.3 (157), and 7.6% (29) within the cows. Data were analyzed by mixed model, accounting for cow breed-type, sire-type, sex, cow age, and bST genotype (either cow or calf) as fixed effects and cow's sire within cow breed-type and calf's sire within sire-type as random effects. Final age of calf was included as a covariate to evaluate effects of calf genotype on carcass traits. Cow bST genotype was not significantly associated with cow production traits (milk yield, average weight, hip height, and condition score) or calf weight at birth or weaning. Calf birth weight, weaning weight, carcass weight, marbling score, and percentage choice grade were not affected by calf bST genotype. Calf bST genotype affected external fat thickness ( $P = .07$ ), estimated KPH fat percentage ( $P = .05$ ), and cutability ( $P = .04$ ). Carcasses of AA calves had the most external fat and lowest cutability, whereas AB calves had the largest percentage of estimated KPH fat. In conclusion, bST genotype effects were significant for some traits related to carcass cutability but not to calf growth, marbling, or cow productivity.

**Key Words:** Beef Cattle, Growth Hormone, Genetic Marker

**13 Association of a genetic marker with blood serum IGF-I concentration and growth traits in Angus cattle.** W. Ge\*, M. E. Davis, H. C. Hines, and K. M. Irvin, *The Ohio State University, Columbus.*

This study was conducted to evaluate a two-allelic genetic marker identified in the first promoter region of the bovine IGF-I gene. Four hundred forty six Angus calves born in spring and fall of 1994 and 1995 were scored for the marker genotype. Direct EPD and maternal EPD were estimated for IGF-I concentrations, and for weights and weight gains using MTDFREML with an animal model that included fixed effects of birth year, birth season, sex, age of dam and age of calf, and random maternal and permanent environmental effects. Regression of direct and maternal EPDs on genotype was performed by coding the genotype as 0 for AA, 1 for AB and 2 for BB. Average effect of allele substitution and dominance deviation were estimated by regression and by the difference between predicted and observed EPDs of the heterozygotes, respectively. Regression coefficients of direct EPD on genotype were significantly different from zero for IGF-I concentrations at d 28, 42 and 56 of the postweaning period, and for weaning weight, on-test weight, weights at d 28, 42 and 56 of the postweaning period, off-test weight, preweaning gain, and weight gain during the first 20 d after weaning, but not for birth weight ( $P = .95$ ; age of calf not included in the model) or postweaning gain ( $P = .24$ ). Allele substitution accounted for 8% of the variability in direct EPD for weight gain during the 20 d period immediately after weaning. Coefficients for regression of maternal EPD on genotype were significantly different from zero for all traits evaluated. Allele substitution explained 7.5% of the variability in maternal EPD for weight gain during the 20 d period immediately after weaning. Dominance effects of the marker were not significant ( $P > .10$ ). The genetic marker in the first promoter region of the bovine IGF-I gene has a significant effect on growth of Angus cattle during the first 20 d after weaning.

**Key Words:** Genetic Marker, Growth, Beef Cattle

**14 A method of detecting toxigenic *Pasteurella multocida* in swine using the polymerase chain reaction.** M. Chen\*, G. V. Amargo, P. A. Dyas, E. A. Amargo, and B. A. Didion, *DEKALB Swine Breeders, Inc., DeKalb, Illinois.*

Progressive atrophic rhinitis is a bacterial based disease which destroys the turbinate bones leading to an increased susceptibility to other infections. The increased susceptibility to infections can lead to retarded growth. Toxigenic *Pasteurella multocida* (PM+) has been identified as the causative organism of progressive atrophic rhinitis. The toxin gene has been cloned and sequenced. The objective of this project was to adopt a PCR method for the identification of animals harboring PM+. Isolation of bacteria was conducted via nasal swabs streaked onto selective blood agar plates and grown at 37C for 24 hours. Colonies resembling *Pasteurella multocida* were sampled using sterile pipet tips and the bacteria were released into 300ul of TRIS-EDTA buffer in a 1.5ml microcentrifuge tube. The sample was boiled for 15 minutes and used immediately for PCR or stored overnight at 4C. A 0.5ul sample volume was used in PCR for amplification of two DNA fragments (350 and 290 base pairs) within the 4000 base pair toxin gene. A 96-well format was used for sample throughput. PCR products were electrophoresed on a 1.5% agarose gel and visualized using a UV transilluminator following ethidium bromide staining. Gels were photo-documented using a Sony video printer and the print was scored for PM+ incidence. The PCR based test is a rapid and low cost method for identification of animals harboring PM+ bacteria.

**Key Words:** *Pasteurella multocida*, Pigs, PCR

**15 Evaluation of Genetic Markers linked to Quantitative Trait Loci for Ovulation rate in Commercial pig lines.** P. A. Dyas\*, S. T. Finn, M. Chen, A. A. Paszek, and B. A. Didion, *DEKALB Swine Breeders, Inc., DeKalb, Illinois.*

The number of pigs produced per sow per year is a valuable measurement for economic productivity in swine production. The use of marker assisted selection to make genetic gains in litter size has economic merit. Previous data (Rathje et al., *J. Anim. Sci.*, 1997, 75:1486; Paszek et al., *J. Anim. Sci.*, 1996, 74:(suppl. 1:24); Wilkie et al., *PAGV*, 1997, No.P315) has indicated that swine chromosome 8 may contain quantitative trait loci (QTL) for ovulation rate in swine. The objective of this study was to evaluate the effect of genetic markers located in chromosome 8 QTL regions on sow fertility. Reproductive data was used from two commercial sow lines. Two genetic nucleus lines composed of Large White and Landrace were evaluated. Only those females having litter size records for the first three parities were evaluated. Means and standard deviations (S.D.) were calculated for total number born for the first three parities. The Large White line had 281 females evaluated for litter size with a mean equal to 32 offspring and a S.D. of 6.3 piglets. The Landrace line had 254 females evaluated with a mean equal to 31.5 offspring and a S.D. of 7.5 piglets. Fifteen microsatellites were selected to surround the SW444 and SW790 regions of chromosome 8: Sw1037, Sw933, Sw211, Sw205, Sw444, Sw7, Sw1070, Sw29, S0017, S0225, Sw763, S0144, Sw1085, Sw61, and S0178. Microsatellite heterozygosities were determined based on 20 randomly selected animals from each of the two nucleus lines. Females with the performance of one S.D. greater and one S.D. less than the mean from each nucleus line were genotyped with informative markers using a Perkin-Elmer ABI373. Information will be reported on: marker heterozygosities; allele frequencies; comparisons of marker variability estimates between sows with high and low reproductive rates in both genetic nucleus lines; and marker effects on litter size.

**Key Words:** Swine, Litter Size, Quantitative Trait Loci

**16 Physical mapping of beta-2 integrin subunit (ITGB2) and myxovirus resistance 1 (MX1) to pig chromosome 13 confirms conserved synteny with human chromosome 21.** G. T. Cravens\*, H. S. Sun, and C. K. Tuggle, *Iowa State University, Ames, Iowa.*

Chromosome painting results indicate human chromosome 21 (HSA 21) genes are entirely located on the distal part of pig chromosome 13 (SSC13). To test this result, and to determine specific gene order on distal SSC13q, we are mapping HSA21 genes in the pig. The HSA21 gene integrin beta-2 (ITGB2) encodes CD18, a cell surface antigen that functions in cell adhesion (Weitzman et al., 1991). ITGB2 was recently linkage mapped to SSC13 (Hu et al., 1997). The protein encoded by the myxovirus resistance gene 1 (MX1) has been shown to provide resistance to influenza in mice. MX1 has been genetically linked to SSC13, but only physically assigned to SSC13 using synteny mapping. Physical mapping in the pig was accomplished by PCR reactions using primers designed from published porcine ITGB2 sequence. These primers were designed to amplify intron sequence between exons six and seven. PCR yielded an approximately 800 base pair fragment; sequencing of this fragment confirmed that it was the correct product (Genbank accession number G36355). To map ITGB2, the same PCR reaction was run using DNA from a rodent-pig somatic cell hybrid panel. The same panel was used to map MX1 by using published MX1 primers to amplify a 216 base pair PCR product. The cell hybrid panel mapped both ITGB2 and MX1 to SSC13q 41/46-49 with 100% and 87% concordance, respectively. Therefore, regional mapping of CD18 and MX1 confirms conserved synteny between human chromosome 21 and pig chromosome 13. To continue testing this synteny, we are currently in the process of mapping another HSA21 gene, interferon alpha/beta receptor (IFNAR), in the pig. Physical and linkage mapping of these three genes will reveal their order and location on SSC13 and provide information for future comparative mapping in this region.

**Key Words:** Pig, Physical Mapping, Comparative Mapping

**17 Identification of Putative QTL for Reproduction in Swine.** L. J. Alexander<sup>1</sup>, P. J. Wilkie<sup>1</sup>, A. A. Paszek<sup>2</sup>, R. J. Hawken\*<sup>1</sup>, G. W. Flickinger<sup>1</sup>, M. B. Wheeler<sup>3</sup>, and L. B. Schook<sup>1</sup>, <sup>1</sup>University of Minnesota, St. Paul, <sup>2</sup>DeKalb Swine Breeders, Inc., Liberal, KS, <sup>3</sup>University of Illinois, Urbana.

As a part of our program for increasing swine production efficiency a genomic scan for eight reproductive and farrowing traits was performed. The descendants of 3 Meishan boars and 7 Yorkshire sows from 25 full and half-sib families (312 individuals) were genotyped with 119 microsatellite markers. The average marker interval was 24 cM. F-ratios supporting QTL locations were calculated using the least squares regression method program developed by Knott and Haley, of the Roslin Institute. Reproductive traits examined were gestation length, number of corpora lutea, total fetuses and uterine length. Farrowing traits included total piglets born, number of piglets born live, number of stillborn piglets and number of piglets weaned. Putative QTLs for number of stillborn piglets, corpora lutea and gestation length were identified on chromosomes 4, 8 and 9, respectively, based on a genome-wide suggestive F-ratio threshold (F-ratio > 6.29). In order to further investigate these region associated with the putative QTL we are generating additional microsatellites from yeast artificial chromosomes. These new microsatellites will allow us to further refine the map position of the QTL and to extend these studies into other population and families.

**Key Words:** Reproductive Traits, Genomic QTL Scan, Pig