282 Differential response from feeding high levels of vitamin E on quality of stored pork from two genotypes.

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This study examined the effects of feeding high levels of vitamin E on the quality of stored pork from different genotypes. Pigs (n=240; initial BW=87 kg) were allotted by weight to one of ten treatments (8 pens/trt, 3 pigs/pen) in a 2 x 5 factorial arrangement. Factors included: 1) genotype (Berkshire sired and Hampshire sired) and 2) supplemental levels of vitamin E (0, 75, 150, 300 and 600 mg/kg). Corn-SBM basal diets containing 2.5% added fat, 0.83% lysine and 15 mg/kg vitamin E were fed for 6 weeks. Drip loss, color, and TBARS were measured in loin chops displayed for 0, 2, 4, 6, and 8 d at 4C. Drip loss from Hampshire crosses was greater (3.16 vs. 1.77%; $P < 0.001$) compared to Berkshire crosses, but was not affected by vitamin E level ($P > 0.10$). Chops from Berkshire crosses were darker (L*: 52.4 vs. 54.3; $P < 0.05$), less red (a*: 7.87 vs. 8.94; $P < 0.001$), and less yellow (b*: 7.87 vs. 8.71; $P < 0.05$) compared to Hampshire crosses, but were not affected by vitamin E level ($P > 0.10$). Greater oxidation (TBARS) occurred in Hampshire cross display chops (day x genotype; $P < 0.01$) on d 0 (0.77 vs. 0.65; $P < 0.02$), d 4 (1.09 vs. 0.83; $P < 0.001$), d 6 (0.62 vs. 0.47; $P < 0.002$) and d 8 (1.31 vs. 1.17 mg MDA/kg sample; $P < 0.01$). TBARS (day x vitamin E; $P < 0.06$) decreased linearly on d 4 (1.13 to 0.79; $P < 0.001$), d 6 (0.76 to 0.48; $P < 0.02$) and d 8 (1.40 to 1.04 mg MDA/kg sample; $P < 0.001$) with increasing levels of vitamin E. TBARS in display chops from Hampshire cross (genotype x vitamin E; $P < 0.02$) decreased linearly (from 1.02 to 0.66 mg MDA/kg sample; $P < 0.001$) with increasing vitamin E level. These data reinforce that Hampshire crosses produce paler, more exudative pork that is more susceptible to oxidation than Berkshire crosses. However, increasing supplemental vitamin E levels will improve storage as indicated by reduced oxidation of lower quality pork, but will not impact oxidation in higher quality pork.

Key Words: Vitamin E, Pork, Quality

283 The effects of niacin on growth performance and meat quality in grow-finish pigs.

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Two experiments were conducted to determine the effects of additional dietary niacin on growth performance and meat quality in finishing pigs. All pigs were blocked on weight and assigned to one of six dietary treatments. Pigs were housed with 2 pigs per pen (6 pens/treatment/sex) in Exp. 1 and approximately 26 pigs per pen (4 pens/treatment/sex) in a commercial research barn in Exp. 2. In both trials, dietary treatments consisted of a corn-soybean meal-based control diet or the control diet with 27, 55, 83, 110, or 550 mg/kg additional niacin. In Exp. 1, 144 pigs (initially 51.2 kg) were fed diets in two phases from d 0 to 25 and d 25 to 62 that were formulated to 1.00 and 0.75% lysine, respectively. In Exp. 2, 1243 pigs (initially 35.9 kg) were fed diets in four phases (d 0 to 28, d 29 to 56, d 57 to 84, and d 85 to 117). Diets were formulated to 1.25, 1.10, 0.90, and 0.65% lysine in the respective phases and contained 6.0% added fat in the first three phases. In both trials, gilts grew slower ($P<0.001$), were leaner at the tenth rib ($P<0.03$), and had higher fat-free lean percentages ($P<0.01$) than barrows. Overall, in Exp. 1, feeding additional niacin had minimal effects on growth performance. However, niacin tended to increase ($P<0.06$) 24 hr pH (5.44, 5.49, 5.49, 5.46, 5.49, and 5.48). In the commercial environment in Exp. 2, increasing niacin increased (quadratic, $P<0.05$) ADG (760, 775, 762, 775, 754, and 753 g/d) and improved (quadratic, $P<0.01$) G/F (.352, .362, .357, .375, .367, and .366). Niacin supplementation also decreased (linear, $P<0.04$) carcass shrink and drip loss percent (2.00, 1.90, 1.93, 1.90, 1.23, and 0.80) and increased (linear, $P<0.01$) subjective color scores, L* values, and ultimate pH (5.67, 5.73, 5.77, 5.76, 5.85, and 5.94). Results from these two studies show that additional dietary niacin can be fed to pigs to improve pork quality as measured by drip loss, pH, and color.

Key Words: Niacin, Meat quality, Finishing pigs

284 Role of pantothenic acid as a modifier of body composition in pigs.

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Fifteen sets (7 barrows, 8 gilts) of four individually penned, littermate pigs were utilized to determine the effect of pantothenic acid (PA) additions on growth, body composition and meat quality in pigs fed from 10 to 118 kg BW. Pigs from a high lean strain were reared via a SEW scheme and self-fed a diet containing 19 ppm PA from weaning to 10 kg BW. Pigs were then fed a basal diet (analyzed 6 ppm PA) and allotted within litter to one of four dietary additions of PA (0, 30, 60, 120 ppm) from d-calcium pantothenate. The basal diet consisted of a corn-SBM-3% choice white grease mixture and contained 1.5, 1.2, and .95% lysine for pigs fed from BW of 10 to 46, 46 to 80 and 80 to 118 kg, respectively. All vitamins except PA were fortified to 600% of NRC (1998) for each stage of growth. As dietary PA concentration increased, longissimus muscle area increased quadratically (43.9, 48.0, 45.4, 47.5 cm^2, $P<.06$) and tenth rib backfat decreased quadratically (2.25, 2.04, 2.07, 1.95 cm, $P<.05$) resulting in a quadratic increase in fat-free lean (51.4, 53.4, 52.5, 53.6%, $P<.04$). The magnitude of these responses were larger ($P<.09$) for barrows than gilts. Daily body weight gain (933, 916, 940, 914 g) and gain:feed (429, 433, 428, 431 g/kg) were not altered by dietary PA. In addition, measures of meat (longissimus) quality including intramuscular fat content (4.4, 4.2, 4.6, 4.0%), Hunter L (54.5, 54.2, 54.3, 54.3) and Hunter a (8.7, 9.1, 8.9, 8.5) color values and water loss under retail storage (4.7, 4.9, 5.1, 4.7%) at 96 hours post-kill were not ($P>.10$) altered by dietary PA. Based on these data, dietary pantothenic acid at concentrations greater than that required to maximize body weight gain elicits reductions in subcutaneous fat thickness while increasing carcass lean content of market weight pigs without altering meat quality.

Key Words: Pigs, Pantothenic acid, Body composition

285 Impact of a targeted B-Vitamin regimen on rate and efficiency of growth on lean growth genotype pigs from 6 to 110 kilograms of body weight.

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Four hundred, four week old pigs (5.5 kg initial BW) were utilized in a 5x2 factorial design (10 reps/treatment) to determine the effects of five B-vitamin (riboflavin, pantothenic acid, niacin, B_{12} and folic acid) fortification levels (NRC, 2X, 4X, 8X, 16X NRC) and two levels of stress (low and moderate) on the performance of 5.5 kg to 110 kg pigs (128 trial days). Diets were formulated to be isocaloric and isonitrogenous. The diets were fed in pellet form. Pigs raised under moderate stress conditions during performance period 1(19 days, 12 kg bw) gained 506^{d}, 533^{cd}, 544^{bcd}, 559^{abc} and 569^{ab} g/day and had corrected feed efficiency of 1.929^{d}, 1.899^{cd}, 1.889^{bcd}, 1.871^{abc} and 1.828^{a} when supplemented with NRC, 2X, 4X, 8X and 16X NRC B-vitamins, respectively. For the overall performance at 128 days pigs raised under moderate stress, had an ADG of 814^{c}, 829^{bc}, 844^{abc}, 850^{ab} and 865^{a} g/day had corrected feed efficiency of 2.583^{c}, 2.499^{b}, 2.466^{ab}, 2.444^{ab} and 2.419^{a} when supplemented with NRC, 2X, 4X, 8X and 16X NRC B-vitamins, respectively. Across stress levels, increasing vitamin supplementation increased loin eye area (39.72^{c}, 40.25^{c}, 42.96^{b}, 44.06^{ab} and 44.96^{a} cm^2) and decreased backfat(16.65^{d}, 16.61^{c}, 16.41^{bc}, 16.06^{a} and 16.02^{a} mm)when supplemented with NRC, 2X, 4X, 8X and 16X, respectively. Pigs fed 16X NRC levels had a $5.91/pig advantage and 500% return over 2X NRC and $3.69/pig advantage and 400% return over 4X NRC.

Key Words: Swine, Vitamins, Performance

ASAS/ADSA Breeding and Genetics: Genetic Parameters of Swine and Sheep

286 Relationship between post-weaning performance and reproductive performance in first parity Landrace females.

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Data from the National Swine Registry STAGES program were used to examine the relationship between the post-weaning performance (growth, backfat, and loin muscle area) of Landrace females and their subsequent first parity reproductive performance. Genetic parameters were estimated from first parity Landrace females (n=5247) for which post-weaning performance had also been recorded. These records rep-

resented 710 sires and 2346 dams. Additive genetic (animal/gilt), common environmental (litter, c^2), mate (service sire for reproduction traits only), and residual variances and covariances were estimated for days to 113.5 kg (DAYS), tenth rib backfat (BF), loin muscle area (LMA), number born alive (NBA), and litter weaning weight (LWT) using the multiple-trait animal model REMLF90 program of Misztal. NBA was pre-adjusted for age and parity of sow and LWT for age of pigs at weaning while post-weaning performance traits were pre-adjusted to 113.5 kg. The model included fixed effects of contemporary group (both post-weaning and reproductive) and random effects of animal, litter, mate, and residual error. Heritabilities were similar to literature estimates. Common litter effects were high (.28) for DAYS. Genetic correlations between post-weaning performance and reproduction traits for first parity were generally low. Post-weaning performance traits have little effect upon subsequent first parity maternal performance.

	DAYS	BF	LMA	NBA	LWT
DAYS	0.33	0.13	0.06	-0.17	-0.15
BF		0.44	-0.57	-0.08	-0.07
LMA			0.34	-0.02	-0.13
NBA				0.13	0.30
LWT					0.12
c^2	0.28	0.18	0.13	0.03	0.14
Mate	—	—	—	0.03	0.04

Heritabilities on diagonal, genetic correlations above diagonal.

Key Words: Genetic parameters, swine

287 Effects of inbreeding of sow on reproduction and litter performance in a closed population of Landrace pigs.

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Declines in growth and reproductive performance in livestock often sound the alarm that inbreeding depression may be a causal effect. However, many studies have reported inconclusive results. Five generations of single trait selection conducted in a line of Landrace pigs based on BLUP EBVs for increased ultrasound loineye area at the Swine Breeding Research Unit in Auburn University resulted in an increase in average inbreeding of sows from zero in base generation to 19.4% and 6.4% in the select and control lines, respectively. The objective of this study was to examine the effects of sow's inbreeding levels on reproduction and performance of her litter. Data from 192 first parity sows that were progenies by 68 sires and out of 135 dams were available for this study. Traits analyzed were litter size at birth (LSB), number born alive (LSBA), number weaned at 21 d (LS21), number weaned at 35 d (LS35), litter weight at birth (LWTB), litter weight at 21d (LWT21) and litter weight at 35d (LWT35). Analyses were carried out using the mixed model procedure in SAS, fitting generation, line and generation by line interaction as fixed effects, inbreeding coefficient of the sow within line as covariate, and sire of the sow, dam of the sow and residual error as random effects. To adjust litter weights to common litter size, LSB, LSBA and LS21 were included as covariate in models for analyzing LWTB, LWT21 and LWT35, respectively. Inbreeding of sow did not significantly affect LSB, LSBA, LS21 or LS35 (P values ranged from .11 to .17) though the slopes of the regression lines for sow's inbreeding effect were negative for litter sizes. Regression slope for LSB in the select line differed from zero ($P<0.05$). Inbreeding levels of sow had no effect on LWTB and LWT35, but affected the LWT21 ($P<0.05$). The regression slopes were negative for LWT21 and LWT35 in both select and control lines. The LSB, LSBA and LS21 had significant influence on LWTB, LWT21 and LWT35 ($P<0.001$). Inbreeding of sow did not seriously affect reproduction or litter performance.

Key Words: Sow's Inbreeding, Reproduction, Litter Performance

288 Correlated responses in sow productivity in a line of Landrace pigs selected for increased ultrasound loineye area.

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Positive genetic changes in lean muscle content in pigs might impose some negative effects on sow's productivity. Five generations of single trait selection conducted in a line of Landrace pigs for increased ultrasound loineye area (ULEA) at the Swine Breeding Research Unit in AU showed a difference of 10.6 cm^2 in average EBVs between select (SL) and control (CL) lines for ULEA. The objective of this study was to examine the impact of increased ULEA on sow productivity. Real-time ULEA data at the 10th rib of 1406 pigs at 168 d of age, and litter performance records for number born (NBORN), litter weight at birth (LITBWT), number weaned at 35 d (NWN35) and litter weight at 35 d of age (LITWT35) from 192 sows that had ULEA were used for this study. Heritabilities and genetic correlations were estimated by the multivariate REML procedure using MTDFREML. For ULEA, the model considered the fixed effects of generation, sex, covariate of 168 d weight, and random effects of animal, litter and error. For sow productivity traits, fixed effect of generation and random effects of animal and error were considered. Estimates of heritabilities for ULEA, NBORN, LITBWT, NWN35 and LITWT35 were .47, .07, .25, .25 and .53, respectively. Genetic correlations of ULEA with sow productivity and litter performance traits ranged from -.01 to -.38. The most undesirable genetic correlation was between ULEA and NBORN (-.38). Genetic correlations of ULEA with NWN35 and LITWT35 were -.20 and -.17, respectively. Genetic correlations among litter sizes and litter weights were all positive and ranged from .20 to .98. Average EBVs of SL sows that produced the fifth generation pigs were 1.31 and 1.04 less pigs/litter than CL sows for NBORN and NWN35, respectively. Compared to CL sows, the average EBVs of SL sows showed differences of -.63 and -12.0 kg/litter for LITBWT and LITWT35, respectively. Selection for increased ULEA appears to have some negative effects on sow productivity.

Key Words: Selection, Loineye Area, Sow Productivity

289 Models for predicting the market weight of finishing pigs based on current age and weight.

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Data from the National Pork Producers Council's Maternal Line National Genetic Evaluation Program were used to develop prediction equations for weight of finishing pigs. The pigs represented barrows and gilts from six maternal genetic lines mated to a common terminal genetic type to produce four parities. Three replicates were performance tested for finishing growth and feed intake using the Feed Intake Recording Equipment (FIRE) system. Target market weight was 113.4 kg. In each replicate performance tested pigs had an initial and ending weight. In replicates 2 and 3 serial weights were recorded at approximately 21-day intervals.Three regression models were evaluated. In model 1 ending weight was fit to the linear and quadratic terms for initial weight and age and ending age. In Models 2 and 3 growth curve equations were developed by fitting initial, serial and ending weights to their corresponding linear and quadratic terms for age and to a logarithmic fuction of age, respectively. Model 1 error term was 25.29 kg ($R^2=0.26$). The error terms for models 2 and 3 were 62.90 kg ($R^2=0.905$) and 65.81 kg ($R^2=0.901$), respectively. The computed equations were tested for equality of coefficients across barrows, gilts and each genetic type. For model 1 the hypothesis that the coefficients were the same for each sex and for each genetic type was accepted. For Models 2 and 3 the coefficients for barrows and gilts were significantly different ($P<0.05$), as were the coefficients for two of the six genetic types. These results suggest that a prediction equation for market weight based on current age and weight and projected market age is reasonably robust in that it is applicable across barrows and gilts and a range of genetic types. Predictions of market weight based on growth curves account for more of the variation and have greater standard errors. However, finishing growth curves tend to be specific for each sex and certain genetic types. This suggests that their application may dictate individual equations for barrows, for gilts and certain genetic types.

Key Words: Finishing, Prediction, Weight

290 Genetic correlations among piglet survival, birth weight and performance traits.

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Genetic relations between piglet survival and birth weight on one side and performance traits on the other were studied. Measurements were taken on animals in a commercial sire line. For birth weight and survival traits (farrowing, pre-weaning and total) 29,200 observations were available. Performance traits were measured in two test periods, one beginning at 294 kg and lasting 56 days (Phase1, 2019 observations) and one beginning at the end of Phase1 and lasting another 56 days (Phase2).

Daily gain and backfat thickness were available for both phases and feed intake only was available for Phase2 (1622 observations). Protein and lipid depositions were estimated for both phases and residual feed intake was estimated for Phase2. For birth weight a model with a direct and a maternal animal factor was used; this resulted in heritabilities of 0.05 and 0.20, respectively. The maternal component of birth weight had positive genetic correlations with lifetime daily gain (0.240.12), and estimated protein deposition during Phase2 (0.460.18) and a negative correlation with Phase2 backfat (-0.250.11). For pre-weaning survival a model with a direct (piglet) and a nurse sow animal effect was fitted. Estimated heritabilities were 0.02 and 0.03, respectively. The direct effect of pre-weaning survival had a positive genetic correlation with average daily feed intake (0.440.22), Phase1 backfat (0.410.19), Phase2 backfat (0.510.18), and lipid deposition during Phase2 (0.440.19) and a negative correlation with estimated residual feed intake (-0.640.28). The nurse sow effect of pre-weaning survival had a negative genetic correlation with Phase2 gain (-0.410.21) and especially with estimated protein deposition during Phase2 (-0.630.24). The study indicated that selection against backfat will increase birth weight and decrease piglet survival, while selection for increased pre-weaning survival will increase gain, feed intake and backfat.

Key Words: Piglet Survival, Genetic Parameters, Performance Traits

291 The Association Between the Estrogen Receptor Locus and Growth, Carcass, and Developmental Traits in Pigs.

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The association between the estrogen receptor (ESR) locus and growth, carcass, and developmental traits in swine was investigated in a population of purebred and crossbred Large White and Yorkshire animals. A total of 724 animals were genotyped at the ESR locus (AA, AB, or BB) via a PCR-RFLP procedure or by pedigree analysis and were measured for traits including teat number (TN), individual birth weight (IBW), weaning weight (WW), age at 109 kg (AGE), average daily gain (ADG), ultrasonic backfat thickness (BF), and loin-muscle area (LMA). WW, AGE, BF, and LMA measurements were adjusted to a standardized weight or age prior to the statistical analysis using guidelines provided by the National Swine Improvement Federation. Data were analyzed using a linear model including the fixed effects of ESR genotype, breed composite, sex, season, and parity and interactions including ESR genotype # breed and ESR genotype # sex. ESR genotype was found to be a significant ($P < 0.05$) contributor to the phenotypic variance for BF and nominally significant ($P < 0.10$) for IBW. Animals possessing at least one copy of the B allele had 0.156 0.059 cm more BF than homozygous A animals ($P < 0.01$). Heterozygous animals were 0.054 0.024 kg heavier at birth than the average of the homozygous animals ($P < 0.05$). There were no detectable ESR genotype effects for TN, WW, AGE, ADG, or LMA ($P > 0.10$). Results of this study give evidence of a QTL in the vicinity of the ESR locus affecting BF and IBW. Utilization of the ESR B allele in a marker-assisted selection program for increased litter size, as suggested in previous studies, may have a detrimental effect on BF.

Key Words: Estrogen Receptors, Backfat, Pigs

292 Estimation of genetic parameters for lactation yields of milk, fat and protein of New Zealand dairy goats.

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The New Zealand dairy goat industry is orientated to the production of dairy products for niche markets. Routine genetic evaluation for the identification of superior animals requires knowledge of the genetic parameters for traits of financial importance. Repeatabilities, heritabilities and genetic and phenotypic correlations for lactation yields of milk, fat and protein were obtained in this study. The data set comprised 22,358 lactation records from 9,443 Saanen, Nubian, Alpine, Toggenburg and crossbred does kidding between 1986 and 1999 in 30 co-operative herds. A total of 296 sires were represented. The raw average yields of milk, fat, and protein were 603.9304.0 L, 20.710.6 kg, and 17.88.8 kg, respectively from an average of 201.864.1 days in milk. Estimates of (co) variances were obtained using the ASREML program (Gilmour et al., 2000) with a multiple-trait repeatability animal model. The model included contemporary group (does kidding in the same herd, year and month), age of the doe, day of the month starting the lactation, proportion of genes from Saanen, Nubian, British, Toggenburg, and "unknown" breeds, and individual heterosis as fixed effects, and random additive genetic and permanent animal effects. Repeatabilities for milk, fat, and protein yields were 0.420.008, 0.410.008, and 0.420.008, respectively. Corresponding heritabilities were 0.250.019, 0.240.019, and 0.250.019. Genetic correlations were 0.900.002 between milk and fat yields, 0.960.001 between milk and protein yields, and 0.920.001 between fat and protein yields. Phenotypic correlations were 0.810.017 between milk and fat yields, 0.930.007 between milk and protein yields, and 0.880.012 between fat and protein yields. Estimates of (co)variances from this study are currently used for the genetic evaluation of animals from the Dairy Goat Co-Operative (NZ) Ltd. Results from the genetic evaluation allows the selection of animals to be used as parents based on their estimated genetic merit and culling of lactating does based on producing ability.

Key Words: Dairy goats, Milk traits, Genetic parameters

293 Models for birth, weaning and fleece weights, and litter size for a population of Targhee sheep.

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Many models (17) were compared for birth weight of 33,994 lambs recorded at USSES (1950-1998). Initial intent was to estimate fractions of variance due to cytoplasmic line (c^2; 892) and sire by cytoplasmic line interaction (sc^2; 17,557). The basic model included direct genetic (fractional variance, a^2; 35,684), maternal genetic (m^2, with correlation r-am), and maternal permanent environmental (p^2; 8,418) effects. The model with sc^2 was significantly better than the basic model with and without c^2. When other random effects were added, sc^2 became zero. Significant effects were associated with dam by year (dy^2; 24,801), sire by dam (sd^2; 23,924) and dam by number born (dn^2; 12,944) random interaction effects. Estimates with all effects in the model were: (a^2, .24; m^2, .19; r-am, .11; p^2, .05; c^2, .00; dn^2, .04; dy^2, .06; sd^2, .05; sc^2, .00). Estimates for a^2, m^2, and r-am were the same for all models. Estimate of p^2 changed when other effects were added to model. Largest estimates for non-genetic effects were: p^2, .08; c^2, .00; dy^2, .13; sd^2, .11; and sc^2, .04. With or without Westell groups (91) in the model, estimates were similar. For weaning weight (120-d, n = 32,715) estimates of variances of effects added to the basic model were all near zero (a^2, .18; m^2, .12; r-am, -.01; p^2, .06). For number born (NB, n = 37,020) and fleece weight (FW, n = 36,197), animal permanent environmental effects were added to the model (ap^2, 9,871 and 9,760) and r-am was dropped. For neither trait did any effects beyond the basic model have large variances. For NB, non-zero estimates with the full model were: (a^2, .10; ap^2, .01; dy^2, .0; sc^2, .01) and for FW were: (a^2, .54; m^2, .02; ap^2, .02; dy^2, .04 and sc^2, .02). For these traits, cytoplasmic effects were not important. Addition of unusual random effects to the model did not change estimates for the basic model. Although some of these effects were significant, especially for BW, the effects on genetic evaluations are likely to be small.

Key Words: Extranuclear Effects, Genetic by Environment , Genetic Evaluations

294 Estimation of genetic parameters of lamb mortality using survival analysis.

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Mortality records from 8,642 lambs from a composite population at the US Meat Animal Research Center were studied using time-to-event Weibull and Cox sire models. To account for the different genetic and environmental sources of variation from birth to 365 d of age (BY), survival from birth to weaning (BW) and from weaning to 365 d of age (WY) were also studied. Records from lambs culled during the study were treated as censored on the day of culling. Male lambs had a significantly ($P<0.01$) greater hazard of mortality (23 to 40%) than female lambs in all periods. Type of birth was significant ($P<0.01$) in the BW and BY periods with multiple born lambs having a greater hazard of mortality than single- or twin-born lambs. Age of dam was significant ($P<0.01$) in the BW and BY periods with lambs from 1-year-old dams having a greater hazard of mortality than those from older dams. Lambs raised by their dams had a significantly ($P<0.01$) lower hazard than lambs raised in the nursery in all periods. Estimates of sire variance and heritability from the Weibull model weregreater than those from the Cox model in all periods. Modal estimates (and standard errors) of heritability from the Weibull and Cox models in the BW, WY and BY periods were 0.21(0.07) and 0.19(0.12), 0.15(0.05) and 0.16(0.06), 0.18(0.12) and 0.12(0.05), respectively. These estimates indicate potential for effective selection for increased lamb survival, enhancing sheep production and welfare.

Key Words: Sheep, Frailty, Cox and Weibull

295 Effect of duration of feeding on variance component estimation for ADG of lambs.

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Variance components were estimated from Targhee data collected from 1978 to 1984 on a total of 1,047 ewe and ram lambs at the U.S. Sheep Experiment Station, Dubois, ID. Lambs were fed for 14 wk with ADG recorded every 2 wk. Lambs were provided ad libitum access to a commercial pelleted feed of barley grain and ground alfalfa. ADG for the entire 14-wk period across all years was 249.3 ± 56.5 g. Variance components for ADG were estimated from a single trait animal model using REML for sequential combinations of duration of time on feed (n = 9) with a range of 4 to 14 wk. The model included fixed effects for year (1978 to 1984), sex of lamb (ewe or ram), and genetic line (selected or control), and two covariates (age on test and initial weight at beginning of feeding). Phenotypic variances for ADG decreased with extended time on feed: 0.54 and 0.14 g^2 at 4 and 14 wk on test, respectively. Estimates of direct heritability increased with extended time on feed; 0.20 ± 0.06 and 0.35 ± 0.07 at 4 and 14 wk on test, respectively. There was little increase of direct heritability estimates after 8 wk on feed (0.33, 0.33, 0.38, and 0.35 for 8, 10, 12, and 14 wk, respectively.) Genetic and environmental correlations among duration of feeding combinations (n = 16) were estimated from a two-trait model. All genetic correlations among duration of feed groups were greater than 0.82 and infer that all measures of ADG were genetically similar. However, environmental correlations among duration of feeding groups ranged from 0.41 to 1.00 with the smaller environmental correlations occurring between 4 or 6 wk and 12 to 14 wk on feed. These results indicate that a period of 8 wk or greater is sufficient to observe differences among animals for ADG due to direct genetic effects under this environment.

Key Words: Gain, Heritabilities, Selection

296 Genetic parameter estimates for prolificacy, growth and wool characteristics of Rambouillet sheep.

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Heritabilities and genetic correlations for prolificacy, growth and wool traits were estimated from Rambouillet data collected from 1950 to 1998 at the US Sheep Experiment Station, Dubois, ID. Number of records ranged from 39,816 to 44,211, 34,114 to 35,604, and 3,574 to 39,821 for prolificacy, growth and wool traits, respectively. Direct heritability estimates from single trait animal model analyses using REML were .09 for litter size at birth (LB), .06 for litter size at weaning (LW), .09 for litter weight weaned (LWW), .27 for birth weight (BW), .20 for weaning weight (WW), .16 for fleece grade (FG, visual spinning count), .51 for fleece weight (FW) and .58 for staple length (SL). Maternal heritability estimates were .19 for BW and .10 for WW. Estimates of genetic correlations among prolificacy traits were positive (.76 for LB-LW, .72 for LB-LWW, .95 for LW-LWW). Between BW and WW both the direct and maternal genetic correlations were positive (.60 for direct and .36 for maternal). FG was negatively correlated genetically with both FW (-.47) and SL (-.52); FW was positively correlated with SL (.46). Estimates of genetic correlations were low to moderate between BW and the prolificacy traits (.24, .00, .37 for LB, LW, and LWW) and moderate between WW and the prolificacy traits (.49, .56, .64 for LB, LW, and LWW). Estimated genetic correlations were small between fleece characteristics and prolificacy traits: for FW (-.08, -.04, .09), for FG (-.11, -.10, -.11) and for SL (-.16, -.04, -.07) with LB, LW and LWW, respectively. Growth traits were positively correlated genetically with FW (.21, .27 for BW and WW); negatively correlated with FG (-.15, -.14 for BW and WW) and positively correlated with SL (.14, .09 for BW and WW). These estimates can be used for multiple-trait, multi-flock genetic evaluations and for deriving selection indexes to optimize profitability of genetic selection.

Key Words: Heritabilities, Genetic Correlations, Selection

ASAS/ADSA Extension Education and PSA Extension and Instruction: Dairy, Swine, and Poultry

297 BASECOW: An Excel add-in specific for the dairy production consultant.

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Basecow is an Excel add-in containing over 100 functions that are useful in animal production medicine consulting and modeling. Basic function categories currently include: epidemiology, nutrition, statistical, reproduction, production, and management. Once installed in Excel as an add-in, the functions can be used in any opened work book. Like any Excel function, Basecow functions require the user to enter a call name and a list of arguments appropriate to a given function: Function Name (argument1, argument n). Example (1) If 30 cows all test negative to a test with a sensitivity of 45% and specificity of 98%, what is the probability that at least 1 or more of the 30 are infected if the underlying prevalence of the disease is estimated at 5%? = **Grouppos(sensitivity, specificity, prevalence, number tested negative)** = Grouppos*(.45, .98, .05, 30)* = 58%. Example (2) What is the optimal economic order quantity (EOQ) for a feed additive costing $800/ton, used at 40 tons/year, with an ordering cost of $20/order and holding cost at 5%/year? = **EOQ(demand, order cost, holding cost/unit/year)** =EOQ*(40,20,.05*800)* = 6.3 tons/order. Example (3) What is the water intake of a cow weighing 1400 lbs, milking 80 lbs of milk at 3.6% fat? =**Waterlb(weight, milk, fat %, status)** =Waterlb*(1400,80,3.6,L)*= 289 lbs. The add-in is available for downloading at http://CAHPWWW.NBC.UPENN.EDU web site. The program is continually updated with new functions. An on line help system is available for many of the commands. The help menu describes command use through an example application and includes reference sources.

Key Words: Spreadsheet, Functions, Excel Add-in

298 Helping the dairy producer make decisions 1: evaluating dairy herd production records.

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A web-based program, Dairy MAP(Dairy Management Analysis Program), has been developed to assist the dairy producer in the analysis of dairy herd production records and to help set priorities for areas of improvement. The system utilizes DHIA benchmark production parameter values which are specific for region and herd size. General herd information entered by the user includes herd size, state, SCC and component sampling options and percent AI sire usage. The DHI-202 herd summary report is the source of management data including rolling herd average production, summit milk, stage of lactation milk production, standardized milk and management information related to SCC, feed costs, reproduction and genetics. The first output table shows herd input values and percentile rankings of similar size herds in the same region. The percentile rank of the herd value is highlighted. The second output table compares herd inputs for summit milk, stage of lactation milk production and standardized milk to expected mean values by rolling herd average. Herd input values are highlighted by production level. More extensive analysis of SCC, production, genetics and reproduction are accessed in succeeding stages if the dairy producer wishes to proceed. Management input values are compared to expected mean levels by rolling herd average with deviations expressed as percentages. Output tables showing deviations from expected values as a series of asterisks ranging from 1 = poor to 6 = excellent assist in identifying areas for improvement.

Key Words: dairy management, decision making, web