T62 Meta-analysis to detect QTL in two connected F2 swine populations using simulation.

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All F2 inbred or outbred populations developed to detect quantitative trait loci (QTL) use parental crosses between two breeds or lines. Although many populations share one of the breeds and may have common ancestors, most studies assume independent populations and use models that do not combine the information. The benefits of combining the data from related F2 populations and using more complex models was evaluated in a simulation study. Different breed and genetic effect compositions were simulated on three grandsires mated to two groups of 18 granddams. Each population consisted of nine F1 sires, 36 F1 dams and 720 offspring. A single chromosome with 10 markers spaced 10 cM apart and one QTL fixed for different alleles in each grandparental breed was simulated. The markers have varying polymorphic information content with the frequency of the allele corresponding to the breed equal to 80% and the rest distributed among the other allele(s). Different scenarios, characterized by the total QTL effect and breed-specific allelic effects of the QTL were evaluated. A total of 1000 replicates per scenario were generated using PEDSIM (Mattis et al., 1998). The additive and dominance coefficients were computed every 1 cM using the procedure of Haley et al. (1996). Estimates of the QTL location and effect were estimated using models that contain or excluded breed differences. The statistical power to detect the QTL depended on the model considered, the magnitude of the QTL and the breed specific effects. The extended data and model permitted the accurate and precise location of QTL accounting for 5% or more of the phenotypic variance. Results from a model that excluded breed effect failed to detect QTL of any magnitude when the effect of the QTL allele of the sire breed was intermediate between those of the dam breeds. These results demonstrate the impact of the population stratification and model on the power to accurately map QTL.

Key Words: QTL, Simulation, Swine

T63 Detection of SNPs on the ovine skeletal muscle specific calpain gene using PCR-SSCP analysis.

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The ovine skeletal muscle specific gene, which is n-calpain or calpain 3, was screened with primers. The primer sequences were selected based on the bovine cDNA sequence (GenBank accession No. AF115744B). The forward and reverse primers were selected from exons 10 and 11 (CAPN31011), and exons 11 and 12 (CAPN31112). Approximately 55 purebred Polypay, 52 purebred Targhee, and 55 mixed breed sheep (Polypay, Targhee, Hampshire, Rambioullet, Dorset, and Suffolk) from the Ohio Agricultural Research and Development Center (OARDC) were used. Allele frequencies (A and B) were calculated as 0.53 and 0.47 for CAPN31011, and 0.69 and 0.31 for CAPN31112, respectively. Analysis of variance was conducted to investigate effects of the genotypes on weight traits including birth weight (BW) and weaning weight (WW). A total of 162 animals were examined. Calpain genotypes of the CAPN31011 (P=0.01) and CAPN31112 (P=0.02) segment were associated with BW. No significant influence of CAPN31011 and CAPN31112 genotypes on WW was observed.

Key Words: Calpain, Ovine, Weight

T64 Relationships between DGAT1 and Pit-1 genes polymorphism and milk yield in Holstein cattle.

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The objective of this study was to determine the relationships between diacylglycerol O-acyltransferase homolog 1 (DGAT1) gene and the growth hormone regulator gene Pit-1 with milk production. Moreover, genotypes and allele frequencies of them were determined in the population. Because our previous work showed the positive effect of genotypes of α_{s1}-casein on total milk yield (BC>BB), we put as secondary objective to examine the effect of that in joint with DGAT1 and Pit-1 genotypes on milk production in the statistical analysis. 196 Holstein first lactation cows located in Tijuana B.C. with the known genotype of a_{s1}-casein were used. The detection of the polymorphisms was by standard PCR and RFLP method. Cleavage resistance to CfrI and HinfI represent the lysine-232/alanine substitution (K232A) for DGAT1 and the A allele for Pit-1, respectively. Data was analyzed using procedures of SAS software. The frequencies of AA, AK, and KK genotypes for DGAT1 were .661, .318, and .021, respectively. Also, the frequencies of AA, AB, and BB genotypes for Pit-1 were .026, .257, and .717, respectively. Allelic frequencies for A in DGAT1and Pit-1 were .82 and .155 respectively. AA genotype of PIT1 had significant effect on the total milk yield. Statistical analysis showed that interaction between DGAT1 and Pit-1 genes had significant effect on milk yield, with a positive and conditional effect of K allele in DGAT1. Substitution of A for K allele at DGAT1 locus resulted in an increase of 263.22 kg in milk production. The substitution effect was additive significantly on milk yield in animals with AA genotype for Pit-1 gene (296.28 kg). By contrast, no important effect of substitution of K allele in DGAT1 in the AB or BB genotypes at Pit-1 locus was observed. Additionally, BC genotype at α_{s1}-casein showed the tendency of high milk yield in animals with both AA and AK genotypes at Pit-1 and at DGAT1, respectively. These results suggest in genetic improvement program of milk yield to selection animals with AA genotypes at Pit-1, which can also obtain the positive effect of DGAT1 in preference to increase in the population, animals with K allele.

Key Words: DGAT1, Polymorphism, Milk yield

T65 Use of intra-ruminal monensin capsules in dairy cows under alfalfa grazing conditions. II. Reproductive performance.

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The objective of this experiment was to evaluate the effects of intra-ruminal capsules of monensin on reproductive performance and some blood parameters in dairy cows under alfalfa grazing. Fifty-six Holstein dairy cows (46 multiparous and 10 primiparous) were blocked in pairs (calving date; previous milk yield, body weight and lactation number) in a repeated measures randomized design and assigned to one of two treatments: Control and Monensin. Treated cows received the intra-ruminal capsules 30 days before the expecting calving date and 60 days after calving. All the cows were fed with the same diet, during the dry period a TMR and after calving, alfalfa pasture and supplemented with TMR. Corn silage, alfalfa hay, corn grain, cottonseed, mineral and vitamins composed the TMR. Mean quality of the diet pre and postpartum were: 57.8 and 45.6%; 12.7 and 18.8%; 1.51 and 1.65 Mcal/kgDM; 52.1 and 35.8% for DM; CP; NEl; and NDF respectively. The body condition score (BCS) evaluations were carried out a week before the treatment start and a two weeks intervals. All the cows were blood sampled at 21 days pre-calving, at calving and at 21 day post-calving to determine the concentration of glucose, non-esterified fatty acids (NEFA) and blood urea nitrogen (BUN). The reproductive performance was closely monitored during the experiment. Monensin treatment significantly ($P<0.05$) improved body condition score and reproductive performance in dairy cows grazing alfalfa. In addition, NEFA were lower and BUN was increased with no effect on blood glucose.

	Control	Monensin	Dif.	
Blood parameters				
Glucose (mg/%)	59.34	61.10	1.76	
BUN (mg/%)	18.14	20.43	2.29	*
NEFA (meq/L)	0.54	0.47	-0.07	#
Reproductive performance				
% P 1st AI	20.69	44.83	24.14	*
% P 6 weeks	41.38	55.17	13.78	
% P 12 weeks	55.17	75.86	20.69	#
BCS#	2.82	2.92	0.10	**

P = pregnancy, AI = artificial insemination, # = five point scale, # P<0.10, * P<0.05, ** P<0.01

Key Words: Monensin capsules, Dairy cows, Reproductive performance

T66 Estimation of additive and nonadditive genetic parameters in the Chilean multibreed dairy cattle population using restricted maximum likelihood procedures.

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Chile has imported Holstein semen from various countries (Canada, New Zealand, USA) for over 20 years. Most of the semen came from the USA. Chilean breeders have made a concerted effort to upgrade the original European Friesian cattle population to Holstein of US origin. This mating strategy created a complex multibreed population with more than 10 breed x country combinations. The objective here was to estimate heritabilities, interactibilities (ratios of nonadditive to phenotypic variances), and correlations (genetic, environmental, phenotypic) among 305-d ME milk yield (M), fat yield (F), and protein yield (P) from 54,035 first lactation records collected between 1990 and 2000. For simplicity, only two base breeds were defined: US Holstein (H) and Other Breeds (O). Fixed effects in the multibreed model were herd-year-season, and regression intrabreed additive and interbreed nonadditive group genetic effects. Random effects were sire and maternal grandsire additive genetic, regression intra and interbreed sire and maternal grandsire nonadditive genetic, and residual effects. Estimates of heritabilities for M, F, and P were lower for H (0.07, 0.12, and 0.26) than for O (0.17, 0.32, and 0.12), and had intermediate values for crossbred groups. Interactibility estimates were generally larger than heritabilities (0.12, 0.68, and 0.40 for H and 0.19, 0.59, and 0.12 for O). Additive correlations among the three traits were higher (0.7 to 1.0) than nonadditive correlations (0.4 to 0.8) and similar across breed groups. Environmental and phenotypic correlations tended to be lower than genetic correlations, and they were higher for H (0.84 to 0.96) than for O (0.11 to 0.92). The incompleteness of the diallel structure of the Chilean dataset produced multicollinearity not only among fixed effects, but also between random additive and nonadditive genetic effects. Thus, covariance estimates reported here should be considered as first approximations, particularly those for nonadditive genetic effects.

Key Words: Cattle, Milk, Heritability

T67 Estimation of genetic trend for milk yield in two dairy herds involving inheritance of holstein cows in baja california, mexico.

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The most accurate method of estimating genetic trend would be to predict the genetic value of all animals in the population and obtain the average for each year. Earlier evaluation procedures with varying bases and unspecified properties were no suitable. 1351 records of first, second and third complete lactations for milk yield of Holstein cows, daughters of 44 Holstein sires were analyzed by using a sire model. The objective was to estimate genetic trend for milk yield in two dairy herds involving inheritance of Hostein in Baja California, Mxico. The average milk yield values 305 2X in the two herds were 8862 and 8312 kg, respectively. The average values for milk yield were 81461310.90, 82461324.16 and 88961125.37, and 86901275.27, 92391173.33 and 95221142.91kg to first, second and third complete lactations in herds 1 and 2 respectively. The average values of age at parturition were 24.9, 40 and 64.50, and 25.20, 39.60 and 73.70 month for cows of first, second and third complete lactations, in herds 1 and 2, respectively. The generational interval was 4.3 years. The average phenotypic mean values for milk yield and the projected milk yield to mature equivalent ME were 8587 and 10,838.64 kg, respectively. The estimates correlation of milk yield of first lactations cows to mature equivalent was (r_{xy}=0.87).The estimates for annual genetic progress was 80.85 kg for milk yield, the estimated breeding value for milk yield was 421 kg. To increase actual progress to levels closer to optimum will require strict adherence to basic rules of selection, the most accurate methods of genetic evaluation and intense selection.

Key Words: Generic trend, Progeny test, Selection

T68 Genetic evaluation of male and female fertility using longitudinal binary data.

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Long time selection for production responses has deteriorated some secondary traits such as fertility or health conditions. It is important to estimate male and female fertility simultaneously, such that both components are inferred correctly. With the current methodology such objective is not fulfill. Not accounting properly for male fertility will bias the genetic evaluation of female fertility and compromises the improvement of reproduction performances. Furthermore, existing methodologies do not make use of all available information leading to less precise prediction. Often, cows need more than one insemination per conception and at best, it is possible to account for only one of service bulls. Another issue of interest is the sequence of mate bulls used for cows having more than one insemination. For two cows having the same number of inseminations and sired by the same bulls but in different order is not accounted for with actual models, which may bias fertility estimation. A simulation study was carried out. The data set consisted of 6918 binary responses from 2780 cows. The pedigree file included 3100 animals. The simulation model at the liability scale included one systematic effect of 50 classes, one covariate on days between calving and insemination, service bull effect (30 bulls), cow effect and permanent effect. The correlation between true and predicted breeding values was 0.98 and greater than 0.99 between true and estimated service bull effects. No significant differences were noted between the true and estimated genetic parameters. To compare the proposed model with the actual methodology used for male and female fertility estimation, only first insemination records from the simulated data set were used. The correlation between the true and predicted breeding values from the second analysis was 0.82 and 0.84 between true and estimated service sire effects. These results indicate the incapacity of the actual methodology in estimating correctly both male and female fertility. The proposed methodology is being evaluated using real data.

Key Words: Male fertility, Longitudinal, Binary responses

T69 Genetic relationships between ewe mature size and measures of lamb feed efficiency and postweaning growth in Targhee sheep.

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The purpose of this study was to estimate the genetic relationships between ewe mature size and measures of lamb feed efficiency and postweaning growth in Targhee sheep. Mature size (weight) was the average fall weight after weaning for ewes with records from age 3 to 6 yr born between 1977 and 1983 (n = 373). Overall average mature weight was 69.3 ± 0.39 kg. Ram and ewe lamb data collected from 1978 to 1984 were used to estimate residual and total feed intake, gain to feed ratio (952 records), and postweaning ADG (1,047 records). Approximately 21 d after weaning, lambs were group fed for 4 wk, and then individually fed for 6 wk before returning to group feeding for another 4 wk. Overall average total feed intake, gain to feed ratio, and ADG were 89.5 ± 0.5 kg, 0.116 ± 0.001, and 0.250 ± 0.002 kg/d, respectively. Estimates of heritabilities and correlations were obtained by running two-trait animal models using REML. The single-trait model heritability estimate for mature weight was 0.66, which was similar to two-trait model estimates (0.60 to 0.66). Genetic correlations of mature weight with residual feed

intake, total feed intake, gain to feed ratio, and ADG were 0.22, 0.53, 0.50, and 0.63, respectively. Heritability estimates for these same traits from the two-trait models were 0.28, 0.32, 0.11, and 0.38, respectively. Environmental correlations were low (-0.23 to 0.14). Estimated genetic parameters suggest selection could improve feed efficiency and postweaning growth, with associated changes in mature size. Selection against residual or total feed intake would be accompanied by a corresponding decrease in mature size. Conversely, selection for increased gain to feed ratio and ADG would indirectly increase mature size. Appropriate use of selection pressure through a selection index, for example, could result in increased feed efficiency and postweaning growth, while maintaining mature size and(or) moderating the amount of change in mature size.

Key Words: Mature size, Feed efficiency, Genetic parameters

T70 Estimates of genetic parameters for reproduction and weight in the progeny of Nubian, French Alpine, Saanen, Toggenburgh, and Spanish goats mated to Boer sires.

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Data came from a commercial goat stud at Imperial Valley California. The objectives were to compare the performance of the progeny of dams involving inheritance of Nubian(N), French Alpine (A), Saanen (S) Toggenburgh (T), and Spanish (P) genotypes (n=160) and to estimate genetic parameters of growth traits. Traits analyzed were prolificacy (P), weight at birth (BWT) and weaning (WWT), and average daily gain (ADG) from birth to weaning. Separate analysis for each trait used least squares mixed model SAS (1992). The analytical model included: breed of dam, age of dam, sex of the kid, season of parturition as fixed effects; sire, sire x breed of dam interaction and the residual as random components. The overall mean for prolificacy was 1.310.72). The average values for prolificacy of dams were (1.270.71, 1.280.72, 1.330.74, 1.360.69, and 1.290.73) for N, A, S, T and P, respectively. The overall mean values for weight at birth and weaning were: 1.99 and 12.89 kg, respectively. The average values for weight at birth were (2.12.0.07, 2.11 .06, 2.04.05, 1.95.06, 2.10.05 and 1.98.07, 1.97.06, 1.93.05, 1.83.05, 1.96.06) for males and females kids respectively. The average values for weaning weights were (13.990.37, 13.29 .0.33, 13.250.34, 12.670.31 and 13.510.43, and 12.500.29, 12.48 0.30, 11.98 0.29, 12.68 0.41 and 12.600.32 kg) for male and female kids, respectively. The estimated average daily gain from birth to weaning was 2200.32 g. The average values for daily gain were: 1360.36 and 127 0.43 g for male and female kids, respectively. The unadjusted survival rate at birth and weaning was (87.37 and 64.97%) respectively. Estimates of heritability direct values were (h^2= 0.070.04, h^2= 0.200.03, h^2= 0.15 0.03 and h^2=0.250.05) to prolificacy, weight at birth, weaning and average daily gain, respectively.

Key Words: Genetic parameters, Reproduction, Boer goat

T71 Relationships among measures of body weight, thoracic diameter and age to scrotal circumferences of boer goat.

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The lack of effective means for selecting males with superior fertility is due primarily to two factors: i) the lack of information on basic measurable traits of male reproduction that are related to fertility, and ii) the cost and difficulty of obtained accurate fertility on individual sires. If testicular size is to be considered in selection programs for breed differences, heritabilities and relationships of testicular measurements to age and body weight must be established for young beef bucks. Data came from a goat stud in Imperial Valley California, under an irrigated grazing system during May to October, and total confinement from November to April. The objectives of this study were to estimate the average scrotal circumferences of (n= 31) Boer bucks, and to estimate correlations among measures of body weight, thoracic diameter and age to scrotal circumferences of Boer bucks. Data was analyzed by SAS, 1992, by using PROC MEANS. The estimated average values 25.595.40 and 90.7118.38 cm corresponded to scrotal circumferences, and thoracic diameter, respectively. The unadjusted average values were: 64.5916.90 kg and 45.8014.51 month for weight and age of bucks at time to take the measurements, and age of bucks, respectively. The estimates of correlations among thoracic diameter and weight to scrotal circumference were highly significant (P<0.01) and positive (r_{xy}=0.56 and r_{xy}=0.52) respectively. The estimates of correlation between age and scrotal circumference diameter was positive (r_{xy}=0.14) but non significant (P>0.05). A large range in testis size was observed within bucks.

Key Words: Escrotal circumferences, Correlations, Boer goat

T72 Calving ease of heifers bred to Angus and Simmental sires selected for decreased dystocia.

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The objective of this study was to compare birth weight, gestation length, and percent assisted births of calving ease Simmental and low birth weight Angus sires. Angus yearling heifers were bred in two consecutive years (1999 and 2000) at four locations by AI using semen collected from Simmental (n = 20) and Angus (n = 27) sires. Birth weights, gestation lengths, and calving ease scores (1 = unassisted, 2 to 4 = various levels of assistance) of 1,039 births in 2000 and 2001were analyzed to determine sire breed effect. Calving ease scores were recorded so that the percentage of assisted births could be calculated. The statistical model included the fixed effects of year of birth, sire breed, calf sex, ranch, two-way, and three-way interaction. Sire breed affected (P < 0.01) birth weight, gestation length, and percent assisted. Simmental sired calves were 2.13 ± 0.37 kg heavier at birth, 2.90 ± 0.48 days longer in gestation length, and assisted 1.44 more times than Angus sired calves. Calf sex affected (P < 0.01) birth weight and gestation length. Bull calves were 2.77 ± 0.25 kg heavier at birth and 1.30 ± 0.27 days longer in gestation length than heifer calves. Furthermore, bull calves were assisted 2.51 and 1.36 times more than heifer calves, 2000 and 2001, respectively. In this study calf sex was the leading cause of dystocia, followed by sire breed.

Key Words: Dystocia, Angus, Simmental

T73 Odds ratios for failure to calve and wean for Senepol- and Tuli-Angus cows compared to Brahman-Angus cows.

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The objective of this study was to compare reproductive performance of F_1 Senepol- and Tuli-Angus cows to that of F_1 Brahman-Angus cows (bred to Charolais bulls) using calving (n = 640) and weaning (n = 633) records from 1996 to 2001. Traits evaluated were 1) failure to calve, and 2) failure to wean a calf. Cows failing to calve or to wean a calf in a given year were coded 1; otherwise they were coded 0. Traits were modeled as binomially-distributed using repeated measures, generalized estimating equations, and a logit link function to an assumed underlying normal distribution. Effects investigated included breed, year, cow age, cow birth year, and sire of cow. Clustering associated with cow age was modeled using repeated measures analysis with an unstructured covariance matrix. Odds ratios (OR) and 95% confidence intervals (CI) were generated to compare breeds. Cow breed, year, cow birth year, and breed × year interaction were highly significant in all analyses. Sire of cow ($P > 0.25$) was excluded from final models. Senepol F_1s had significantly greater odds of failure to calve than Brahman F_1s in 1997, 1998, 2000, and 2001, as indicated by OR (CI) of 1.87 (1.09, 3.2), 3.81 (1.01, 14.32), 2.88 (2.47, 3.36), and 11.69 (9.49, 14.4), respectively. Senepol F_1s had greater odds of failure to wean a calf than Brahman F_1s in 1997, 1998, 2000, and 2001, as indicated by OR (CI) of 2.29 (1.66, 3.16), 4.88 (1.2, 19.82), 2.81 (2.3, 3.42), and 9.18 (3.41, 24.71), respectively. In contrast, Tuli F_1s were similar to Brahman F_1s, but had lower odds of failure to calve (OR = 0.09; CI = 0.04, 0.2) or wean (OR = 0.19; CI = 0.06, 0.58) than Brahman F_1s in 1999 and greater odds of failure to wean a calf than Brahman F_1s in 2000 (OR = 2.64; CI = 2.22, 3.13). Results indicate that the Tuli breed may be a viable source of non-Zebu adaptation to the subtropics.

Key Words: Brahman, Senepol, Tuli

T74 Divergent selection for blood serum insulin-like growth factor I concentration does not change age of Angus heifers at puberty.

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The objective of this study was to determine effects of divergent selection for blood serum insulin-like growth factor I **(IGF-I)** concentration on age of heifers at puberty. Data were obtained from an ongoing divergent selection experiment involving Angus beef cattle at the Eastern Ohio Resource Development Center. Selection was based on the mean IGF-I concentration of three blood samples taken at d 28, 42, and 56 of the 140-d postweaning test, which were abbreviated as **IGF28**, **IGF42**, and **IGF56**, respectively. Data were analyzed using SAS. All models used in the analysis included line-season and the random effect of sire nested within line-season. Age of dam and on-test age of calf were added to the models as a fixed effect and a covariate, respectively. Blood samples were collected weekly for 17 wk from 61 heifers in each of the fall- and spring-calving groups during the postweaning test period. Mean on-test age of heifers in the spring- and fall-calving groups were 260 and 265 d, respectively. Progesterone concentration was determined using RIA. Puberty was assumed attained if the progesterone concentration exceeded 2 ng/mL in a single or 1 ng/mL in two consecutive blood samples. Age at puberty was obtained by subtracting 7 d from the first date progesterone exceeded 1 or 2 ng/mL. Ten heifers (five high and five low line) did not attain puberty during the period in which blood samples were collected. Higher mean IGF-I concentration in the high line heifers (50.0 10.2 ng/mL; $P < 0.004$) did not result in a change in age at puberty (2.5 6.2 d younger in high line; $P = 0.71$). Mean age at puberty was 356 d. Residual correlations of age at puberty with IGF28, IGF42, IGF56, and mean IGF-I were -0.27 ($P = 0.10$), -0.20 ($P = 0.24$), -0.31 ($P = 0.06$), and -0.27 ($P = 0.10$), respectively. Cubic relationships were observed between age of heifers at puberty and IGF-I concentrations ($P = 0.0009$, 0.06, 0.08, and 0.003 for the cubic regression of age of heifers at puberty on IGF28, IGF42, IGF56, and mean IGF-I, respectively). These results suggest that changes in IGF-I concentration are not associated with changes in age of heifers at puberty, but some phenotypic relationships exist between these two variables.

Key Words: Insulin-like Growth Factor I, Age at puberty, Selection

T75 Effectiveness of performance testing for beef carcass traits to use embryonic cloning technique in Wagyu.

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Embryonic cloning can be a technique for producing multiple offspring from one embryo and can be used for a diverse range of comparative trials and performance tests. Embryonic clone testing could shorten the generation interval of traditional progeny testing and lead to efficiency of genetic improvement. The objective of this study were to investigate similarities for shape of muscle, fat area ratio to the muscle area (FATPER), and coarseness of marbling particle with computer image analysis on the quadruplets and quintuplets derived from each embryo, and on two sets of traditional progeny testing. Blastomeres obtained from Japanese Black donors were collected, and male clones were produced by cell fusion with electro-stimulation using enucleated oocytes from ovaries of Holsteins. Four and five clones were fattened with the method of Wagyu progeny testing until 21 months. Eight and nine half-sib steers from two sets of progeny testing were treated as control. The areas of *M. longissimus dorsi, M. trapezius, M. rhomboideus, M. semispinalis capitis, M. semispinalis dorsi, M. anterior serratus* and *M. iliocostalis* at the 6th and 7th rib, and FATPER of those muscles were measured by image analysis. Coarseness of marbling particles of *M. longissimus dorsi* was calculated by image analysis method. The ranges of carcass weight (CWT) and area of *M. longissimus dorsi* (RIBEYE) for two sets of embryonic clones were 369 to 435 kg and 336 to 393 kg, and 48.2 to 63.6 cm^2 and 38.5 to 50.4 cm^2, respectively. The ranges of CWT and RIBEYE for two sets of traditional progeny testing were 312 to 406 kg and 277 to 392 kg, and 38.0 to 54.8 cm^2 and 35.0 to 47.2 cm^2, respectively. This indicates that the degree of similarities for CWT and RIBEYE between embryonic clone steers were not high. The ranges of FATPER of *M. longissimus dorsi* were 35.0 to 37.6 % and 27.2 to 28.4 % for two sets of embryonic clones, and those for two sets of traditional progeny testing were 22.6 to 45.3 % and 25.4 to 40.9 %. This shows that the similarity of FATPER of *M. longissimus dorsi* on embryonic clones was high compared with that on half-sib progeny. The same trend was recognized for other muscles. Low similarity was recognized for the coarseness of marbling particles on embryonic clones as well as on half-sib steers.

Key Words: Embryonic clone, Wagyu, Image analysis

T76 Effect of calving difficulty on cow survival.

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Cow loss following different degrees of dystocia, and its associated cost was estimated for Australian Holstein-Friesian cows, for use in the calculation of the economic weights for bull breeding values for dystocia. Cow termination (i.e. non-survival through culling or death) due to the effects of dystocia was considered over two periods: before or after 21 days post partum. Two cost outcomes, death or sale, were considered. Separate estimates were made for primiparous and multiparous cows. Any degree of dystocia increased both the short and long-term likelihood of cow termination for all cows. Increasing severity of dystocia increased the likelihood of termination. Termination rates increased from early to late lactation for cows requiring surgery. Average cow loss cost was estimated to be A$1,071 for periparturient termination and A$713 for termination after 21 days. Termination patterns for cows with and without dystocia were not the same. Cows that had dystocia were more likely to be terminated early in the lactation or before a lactation record was initiated.

Key Words: Dystocia, Cost, Holstein-Friesian

Nonruminant Nutrition

T77 Effects of supplemental pantothenic acid during all or part of the grow-finish period on growth performance and carcass composition.

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Ninety barrows and 90 gilts were used in a 15-wk experiment to study the effects of supplementing pantothenic acid (PA) to the diet during all or part of the grow-finish period. Pigs were blocked by sex and weight (initial BW=29 kg), randomly assigned to pens (30 pens, 6 pigs/pen), and fed four phases of split-sex diets during the grow-finish period. Treatments included: 1) Control (13.2 ppm PA), 2) Control + 30 ppm PA added in the grower and finisher phases, and 3) Control + 30 ppm PA added in the finisher phases only. Pig BW and pen feed intake were recorded biweekly. Ultrasonic scans of tenth rib loin eye area (LEA) and backfat thickness were performed at 4-wk intervals on 3 pigs/pen. At the end of the experiment, pigs were harvested at a commercial slaughter facility and individual hot carcass weights, Animal Ultrasound System (AUS) backfat, and loin muscle depths (LMD) were recorded. There were no treatment x sex interactions ($P>.10$), and therefore, only the main effects of treatment are presented. Supplementation of PA did not affect ($P>.10$) ADG or feed efficiency. Overall ADFI was higher ($P<.05$) for pigs fed PA during the finisher phase only compared to pigs fed PA during the grower and finisher phases. However, overall ADFI was not different between the PA treatments and control fed pigs. Ultrasound LEA were larger ($P<.003$) at the end of the grower phase for pigs fed diets supplemented with PA. However, there were no differences ($P>.10$) in LEA at the end of the experiment. Tenth rib and last rib ultrasound backfat depths were not different ($P>.10$) between control fed pigs and PA supplemented pigs. Tenth rib carcass fat depths were numerically lower for pigs fed diets with supplemental PA, but differences were not significant ($P>.10$). Likewise, there was no effect of PA supplementation on carcass tenth rib LMD ($P>.10$). Carcass lean percent tended to be higher for pigs fed PA during the growing and finishing periods compared to control fed pigs. However, carcass weights were approximately