Breeding and Genetics
Quantitative Genetics

1285 Live weights and carcass traits of steers from heifer calving ease selection and control lines. G. L. Bennett*, *USDA, ARS, US Meat Animal Research Center, Clay Center, NE.*

Intense selection since 1992 for reduced heifer calving difficulty score EPD and average yearling weight EPD in seven experimental populations of cattle has resulted in improved heifer calving ease, lighter birth weight, and similar yearling weight EPD compared to control lines. Control lines were selected for average birth weight and yearling weight EPD. This apparent genetic change in growth pattern might alter carcass composition. Females born in 1996 and 1997 were randomly retained within the two lines of each population. They were mated to sires from their own lines and produced calves as 2- and 3-yr-old cows in 1998 and 1999. Random (stratified by sire and dam) male calves from select (N = 204) and control (N = 91) lines were fed as steers and measured for live weights and carcass traits. The 295 calves were from 157 sires and 279 dams. Birth weights were 4.5 kg (11.3%) lighter in the select lines (P<0.001). Weight differences (select - control) were small and not significant at weaning (1.4 kg) and at subsequent average ages of 261 d (2.3 kg), 368 d (1.1 kg), and 436 d (-1.7 kg). Carcass weight was also similar (824 vs 825 kg). Adjusted fat thickness was greater (P<0.01) in select lines (0.91 vs 0.78 cm) and marbling score was slightly higher (P<0.10). Differences in ribeye area and KPH% were small and not significant. Results show that selection for calving ease and average yearling weight produced calves that were lighter at birth but had weights similar to control calves from weaning to 14.5 mo of age. Select animals following this genetically determined growth pattern may be slightly fatter.

Key Words: Cattle, Growth, Selection

1286 Year, season, dam age and sex effect on weaning performance of Hungarian Simmental beef calves. F. Szabo[1], Z. Lengyel[1], Zs. Wagenhoffer[1], I. Komlosi[2], J. P. Polgar[1], and L. Nagy[1], [1]*University of Veszprem, Georgikon Faculty of Agricultural Sciences,* [2]*Debrecen University, Centre for Agricultural Sciences.*

Weaning performance of 1,393 purebred Hungarian Simmental beef calves (695 male and 698 female) born from 520 cows mated with 15 sires were analyzed. Heritability of weaning weight (WW), preweaning daily gain (PDG), and 205-day weight (CWW), and the genetic, phenotypic and environmental correlations between WW and PDG were calculated. Factors that influence weaning performance (year of birth, season of birth, sex, dam age) were also analyzed. Multiplicative correction factors were computed to correct for the effects of season and dam age. The sire model of Harvey's (1990) Least Square Maximum Likelihood Computer Program and an animal model that included maternal effects in the MTDFREML program were used to compare the breedng values obtained by the two methods. The overall mean value and standard error of WW, PDG and CWW were 226.3±2.74 kg, 1200.8±16.68 g/day and 249.7±3.58 kg, respectively. The average age of the analyzed calves was 190 days. Heritabilities of the traits were between 0.10 and 0.20. The genetic, phenotypic and environmental correlations between WW and PDG were strong and positive. The factor with the largest effect was sex, and the factor with the smallest effect was sire (P<0.01). Only the first born calves had significantly lower WW than the average; therefore, the correction factor was only computed for the first calving. The spring born calves had the best results for both traits. The estimated breeding values and rank order of sires differed when using the sire model vs the animal model.

Key Words: Weaning weight, Hungarian Simmental, Environmental effects

1287 Genetic parameter estimates for yearling traits of N'Dama cattle in humid tropics of Nigeria. O.T.F. Abanikannda*[1], O. Olutogun[2], and A.O. Leigh[1], [1]*Department of Zoology, Lagos State University, Nigeria,* [2]*Department of Animal Science, University of Ibadan, Nigeria.*

N'Dama cattle are a trypanotolerant breed in the West and Central part of Africa and are well adapted to the inimical environmental conditions of Southern Nigeria. Its good beef conformation, ability to withstand high ambient temperature, and the scourge of Trypanosomiasis prevalent in the sub-region has endeared this breed to animal breeders. The aim of this study was to investigate the various factors that may affect the yearling traits of this breed. A total of 419 records comprising calf birth weight (CBW), average daily gain (ADG), and adjusted yearling weight (AYW) were used in the study. Factors studied included sex of calf and season of birth as fixed factors, sire as a random factor, and age of dam as a covariate. General Linear Model for analysis of variance and variance components of Harvey's LSMLMW procedure was used to analyze the data. The mean CBW was 19.41 ± 0.13 kg, while AYW was 117.52 ± 0.79 kg; ADG was 0.359 ± 0.003 kg. With the exception of age of dam on CBW, all other factors studied exerted significant influence on all of the traits. The heritability estimates for the traits were 0.23 ± 0.12, 0.22 ± 0.11, and 0.26 ± 0.06 for AYW, ADG, and CBW, respectively. With the exception of ADG and AYW, whose genetic, phenotypic and environmental correlations were very high, correlations among the other traits were very low. The very low heritability estimates provide an indication that selecting from within the stock may not yield appreciable response within a short time interval.

Source	Degrees of Freedom	AYW Mean Square	ADG Mean Square	CBW Mean Square
Sex of Calf	1	1718.350**	0.01399*	82.482**
Season of Birth	3	1605.430**	0.02470**	25.664*
Sire	13	567.972**	0.00728**	18.441*
Age of Dam	1	857.950**	0.01499*	17.900^{ns}
Error	400	233.205	0.00300	6.951

* = P<0.05, ** = P<0.01, ns = not significant

Key Words: Genetic parameter, N'Dama, Yearling traits

1288 Effect of sire on rate and extent of postmortem increase in myofibrillar fragmentation indices of Brahman longissimus steaks. D. G. Riley*[1], C. C. Chase, Jr.[1], T. D. Pringle[2], R. L. West[3], D. D. Johnson[3], A. C. Hammond[4], T. A. Olson[3], and S. W. Coleman[1], [1]*USDA, ARS, Subtropical Agricultural Research Station, Brooksville, FL,* [2]*University of Georgia, Athens,* [3]*University of Florida, Gainesville,* [4]*USDA, ARS, SAA, Athens, GA.*

The objective of this study was to assess sire effects on postmortem tenderization associated with aging of Brahman longissimus. Brahman steers and heifers (n = 87) sired by 9 bulls were born in 1995 and 1996, and were weaned at approximately 7 mo of age. After weaning, they were sorted by weight and sex into feedlot pens and adjusted to a final diet of 72.5% corn. When each pen had a median backfat of 10 mm as measured by ultrasound, the entire pen was slaughtered. Longissimus steaks were obtained from strip loins of each carcass and myofibrillar fragmentation indices (MFI) were determined after 1, 7, 14, and 21 days of aging. Models were built using main effects (sex, year, slaughter group, and adjusted 12th rib backfat thickness as a linear covariate) and interactions ($P < 0.15$). These models were used to evaluate MFI for each aging period. Residuals from these models were fitted, using nonlinear regression, to an exponential curve: $MFI = \kappa_0 + \kappa_1 \exp\{\kappa_2 \ t\} + \epsilon$, where t represents aging in days, κ_0 is asymptotic MFI, κ_1 is the difference between initial and ultimate MFI, κ_2 is the rate of increase in MFI, and ϵ is error. When all data were fitted the κ_0, κ_1, and κ_2 estimates were 67.8 ± 1.8, 31.4 ± 1.9, and 0.15 ± 0.03, respectively. Data from individual sires were fitted separately and κ_0 estimates ranged from 56.9 ± 4.1 to 73.5 ± 9.3. Estimates for κ_1 of individual sires ranged from 37.8 ± 12.4 to 20.2 ± 4.7; κ_2 values ranged from 0.22 ± 0.1 to 0.1 ± 0.09. The progeny of sires with low κ_0 (ultimate MFI) would be expected to benefit the least from aging. Among sires with higher κ_0 values, the κ_1 (potential increase in tenderness) and κ_2 (rate of tenderization) values could be used to sort progeny carcasses into different aging periods in order to achieve maximum tenderness. Asymptotic correlations of parameter estimates (all sires) were 0.87 (κ_0 with κ_1), 0.56 (κ_0 with κ_2), and 0.24 (κ_1 with κ_2), and indicated interdependencies among the parameters estimated. Results suggest that genetic differences exist in the rate and extent of tenderization of Brahman longissimus steaks.

Key Words: Brahman, Postmortem changes, Tenderness

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1289   Sire differences for growth, carcass, and tenderness traits of Brahman steers. J. D. Domingue*[1], T. Smith[1], T. D. Bidner[1], J. C. Paschal[2], G. Whipple[3], and D. E. Franke[1], [1]*Louisiana State University Agricultural Center, Baton Rouge,* [2]*Texas A&M University, Corpus Christi,* [3]*University of Nebraska, Lincoln.*

Brahman bull calves (n=440) were purchased at weaning from private breeders in Louisiana (1996 through 2000) to evaluate sire variation (n=68) for growth, carcass and tenderness traits. Bull calves were castrated, dehorned, dewormed, vaccinated and backgrounded. Steers were grazed on ryegrass an average of 120 d and shipped to South Texas for feeding. Each year steers were harvested in two groups when about half the pen reached an average of 500 to 575 kg body weight and 7 to 10 mm fat thickness. Carcasses were electrically stimulated and chilled for 24 hr. A 15-g 24-hr longissimus muscle sample was taken for calpastatin assay. A primal rib was purchased and two 2.54-cm-thick steaks cut for 7- and 14-d aging. Steaks were cooked to an internal temperature of $70°$C. Tenderness was measured by averaging the force required to cut each of six 1.27-cm cores taken parallel to the muscle fibers and sheared once each on an Instrom Universal Testing Machine with a Warner-Bratzler shear attachment. Sire differences were evaluated with PROC GLM. REML estimates of sire variances and sire solutions were obtained with PROC MIXED. Overall means $\pm$ sd were 1.5 $\pm$ .2 kg/d for ADG, 337 $\pm$ 37 kg for carcass weight, 86 $\pm$ 9 cm^2 for longissimus area, 8.8 $\pm$ .4 mm for fat thickness, 391 $\pm$ 62 for marbling score (Slight plus), 4.6 $\pm$ 1.2 kg for 7-d shear force, 3.8 $\pm$ .9 kg for 14-d shear force, and 4.5 $\pm$ 1.2 for calpastatin. Sire differences were significant for all traits. The ranges from low to high sire EPDs were .26 kg for ADG, 57 kg for carcass weight, 12.4 cm^2 for longissimus area, 3.3 mm for fat thickness, 50 units for marbling score, .64 kg for 7-d shear force, .59 kg for 14-d shear force, and 1.69 for calpastatin. Genetic variances were within mid to high ranges of reported estimates.

Key Words: Brahman, Carcass composition, Tenderness

1290   Use of computer image analysis to evaluate heart-shaped ribeyes in Wagyu cattle. K Kuchida*[1], A Kikuchi[1], K Kato[2], M Suzuki[1], and S Miyoshi[1], [1]*Obihiro Univ. of AVM, Obihiro-shi Japan,* [2]*Livestock Improv. Assoc. Makubetsu-cho Japan.*

A depression formed by intermuscular fat ingrowing into the upper side of the M. longissimus dorsis (i.e., heart-shaped ribeye) causes decreased carcass value in Japan. The purpose of this research was to propose a new method to evaluate the level of the heart-shaped ribeye by computer image analysis and to investigate the influence of sire on the appearance of the heart-shaped ribeye in Wagyu cattle. Digital images of the M. longissimus dorsi (ribeye) between the 6th and 7th ribs were taken by equipment developed by the authors. The resolution of the image was 1800 $\times$ 1200 pixels with a file size of 800 to 900 KB in JPEG format. A five times dilation and thinning process was performed to smooth the contour line of the ribeye, which was semi-automatically detected from the binary image using computer software developed by the authors. The area, maximum length, and pattern width were measured in an area structured with a convex polygon and the contour line of the upper side over the major axis of the ribeye. The level of the heart-shaped ribeye was assigned to one of four levels (None, Small, Middle, Large). Multiple regression equations with an average heart-shaped ribeye level as assigned by researchers as the dependent variable used the stepwise method with 18 covariates associated with image analysis traits. The number of depression pixels, depth of depression and interaction between the depth and length of depression were selected for the multiple regression equation ($R^2 = 0.84$). These results indicated that the level of heart-shaped ribeye could be automatically and subjectively estimated by the image analysis method. The percentage difference between the level assigned by the researchers and by multiple regression within $\pm$ 0 was 89.5%. The level of heart-shaped ribeye was progeny tested with 237 (32 sires) Japanese Black steers using image analysis. Heart-shaped ribeyes were confirmed in 37 cattle. The effect of the sire on level of heart-shaped ribeye was highly significant (P < 0.01). A trend towards high frequency of heart-shaped ribeyes in progeny from several sires was found. Heart-shaped ribeyes were recognized in all six steers from one sire.

Key Words: Wagyu, Image analysis, Heart-shaped ribeye

1291   Pedigree analysis using the Python programming language. J. B. Cole* and D. E. Franke, *Louisiana State University, Baton Rouge, LA.*

The utility of the programming language Python as a tool for rapid application development is demonstrated with PyPedal, a package for pedigree analysis. Python is an interpreted, object-oriented programming language. It is a full-featured language which supports modern design paradigms, is available free of charge, and is ideally suited to rapid application development. Animal breeding applications are typically complex and computationally demanding. For the sake of efficiency such applications are usually written in a compiled language such as Fortran 90. The gain in efficiency from such languages is accompanied by complex syntax and primitive libraries for tasks such as I/O. This often makes the implementation of new algorithms non-trivial and results in long development cycles. While Python is not well-suited for applications such as the quarterly USDA dairy cattle genetic evaluations, it is ideal for exploring new methodologies or writing tools to perform common tasks. PyPedal is capable of many operations on pedigrees, including error-checking, construction of A and A^{-1}, calculation of average coefficients of inbreeding and relationship, and calculation of effective founder number using direct and approximate methods. Diagnostic and error messages are written to the standard output device. Output is stored in text files. A pedigree containing records for 304 Brahman cattle was used to demonstrate PyPedal. A and its inverse were calculated and stored using one direct and two indirect methods. A was very sparse and contained 92,416 elements. Population average coefficients of inbreeding and relationship were 0.001 and 0.004, respectively. There were 152 actual founders in the pedigree. The effective number of founders was 95.86 by the direct and 132.57 by the indirect methods, respectively. The difference in effective founder numbers is accounted for by the lack of precise generation information needed for accurate results from the approximate algorithm. The lack of useful generation information prevented the estimation of effective ancestor number. Total processing time was 68s on a 450 MHz Pentium II computer with 128 MB of RAM. PyPedal is available upon request from jcole@lsu.edu.

Key Words: Pedigree analysis, Programming languages

1292   A population study of milk urea nitrogen. J. E. Vallimont[1], J. Hyman[1], G. W. Rogers*[2], L. A. Holden[1], M. L. O'Connor[1], C. D. Dechow[2], and J. B. Cooper[2], [1]*Penn State University, University Park, PA,* [2]*University of Tennessee, Knoxville, TN.*

Successful population studies require a large database of valid and accurate data that has been carefully edited. Test day and lactation data for over 625,000 cow lactations with milk urea nitrogen (MUN) values were obtained from Dairy Records Management Systems, Raleigh, NC, to study the heritability of MUN and the impact of MUN on reproduction and metabolic disease in Holstein cattle. Data were included from October 1998 through February 2001, after national changes in MUN calibration standards occurred. Herds were excluded if their milk testing lab could not be identified. Cows purchased in the middle of a lactation were excluded; however, subsequent lactations were included. Edits were imposed to ensure accurate family relationships and randomness of data: herds must have at least 20 cows with sire identification and 75% or more of cows must have been tested for MUN on a test day to include that test day. Test day records were edited for 6-305 DIM, and milk fat and protein percentages must be >0. Although the standard deviation of the MUN mean increased as milk fat percentage increased, the standard deviation of the MUN mean of the entire dataset did not change whether the maximum fat percentage was set to 6.0% or 9.9%. Values for MUN >39 were excluded. Reproductive analyses were limited to outcomes of first services within 30 d of a MUN measurement. The final dataset contained almost 150,000 cow lactation records. Significant predictors of MUN resulting from preliminary analyses of the final dataset included lactation number (1 or 2+), season of calving (winter: October through March and summer: April through September), method of MUN measurement (infrared or wet chemistry), and stage of lactation. Judicious data editing is crucial to obtaining results that are useful.

Key Words: milk urea nitrogen, data editing

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1293   Analysis of calving interval, age at first calving, and herd life in Japanese Holstein cows. C Fujita*[1], M Suzuki[1], and S Matsumoto[2], [1]*Obihiro University of A&VM*, [2]*Livestock Improvement Association of Japan.*

The objective of this study was to investigate the relationships among calving interval, age at first calving, herd life, and production traits by year of birth in Holstein cows. Data used in this study were provided by the Livestock Improvement Association of Japan and consisted of calving interval records for 1,671,476, 1,321,611, and 951,411 cows in first, second, and third lactation, respectively. Production traits were milk, fat, protein, and SNF yields from test-day records. All cows were milked twice per day. Pedigree information consisted of three generations. The average herd life decreased from 2,363 d in 1975 to 2,012 d in 1995. Calving interval for the first three lactations decreased until 1990 and lengthened in recent years. The phenotypic correlations between herd life and age at first calving by birth year were low, ranging from 0.064 to 0.185. The phenotypic correlations by birth year between calving interval and protein, calving interval and fat, and calving interval and SNF were low and negative. Also, the phenotypic correlations between calving interval and herd life by birth year were low, ranging from 0.02 to 0.12. The average calving intervals by birth year were 403 to 424 d, 402 to 421 d, and 404 to 421 d on first, second, and third lactation, respectively. The modes were about 360 d and 25 mo for calving interval and age at first calving, respectively. The average ages at first calving by birth year were between 27.5 and 27.6 mo.

Key Words: Holstein, Calving interval, Herd life

1294   Factors affecting fertility traits of Holsteins and Jerseys. R. H. Miller*[1], H. D. Norman[1], and J. S. Clay[2], [1]*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*, [2]*North Carolina State University, Raleigh, NC.*

Dairy Herd Improvement data from 3,604,990 Holstein and 264,775 Jersey lactations were used to assess variation in 70-d nonreturn to first service, days from calving to first service, days from calving to last reported service, calving interval, and number of services. Data were restricted to artificial inseminations from 1995 through 2000. Mean nonreturn rate was calculated by herd-year, and herd-years with nonreturn rates of <10% or >90% were excluded. Nonreturn rate was not examined for cows that left the herd within 70 d or if first service was after September 15, 2000. Mean nonreturn rate was 55.0% for Holsteins and 57.3% for Jerseys; mean calving interval was 410 d and 397 d, respectively. Factors evaluated were lactation stage at first service, parity, and partial regressions on peak yields for milk, fat, and protein and on age within parity. Lactation stage was evaluated only for nonreturn rate and number of services. The least-squares model absorbed herd-year-month of first service. Nonreturn rate was lowest for services before 50 d for both breeds and highest for services after 139 d for Holsteins and between 120 and 129 d for Jerseys. For both breeds, fertility for all five traits was highest for third parity. Fertility was lowest for both breeds for parities after fifth as measured by nonreturn rate and number of services and for first parity as measured by days to first service and calving interval. Days to last breeding were greatest for first parity for Holsteins and for parities after fifth for Jerseys. Partial regressions of fertility on peak yield were generally significant (P < 0.01) for all breed-trait combinations. Fertility generally declined as peak milk and fat yields increased but increased with peak protein yield when peak milk and fat yields were held constant. Fertility was markedly lower for breedings <50 d after calving for Jerseys and <90 d after calving for Holsteins. For Jerseys, first service occurred significantly later in first parity than in subsequent parities. All the examined effects influenced fertility and should be considered in genetic evaluation of reproductive traits.

Key Words: Fertility, Nonreturn rate, Reproduction

1295   Heritabilities and correlation among body condition scores, dairy form, stature, strength and final score. C. D. Dechow*[1], G. W. Rogers[1], L. Klei[2], and T. J. Lawlor[2], [1]*The University of Tennessee, Knoxville, TN*, [2]*Holstein Association USA, Inc., Brattleboro, VT.*

The objectives of this study were to estimate the heritability of body condition score (BCS) and the genetic relationships among BCS, dairy form (DF), stature (STAT), strength (STR) and final score (FS).

Records were obtained from the Holstein Association USA Inc. Body condition scores are assigned on a scale of 1 (thin) to 50 (obese). Because BCS is a new trait for Holstein classifiers, distribution patterns and scoring accuracy for some classifiers were not normal. Therefore, edits were made to retain BCS that would represent data likely to be used to estimate genetic evaluations for BCS in the future. Additional edits included: a minimum of 20 daughters per sire, a minimum of 10 cows per herd-classification date (HD-CL), 0 to 305 days in milk (DIM), 20 to 60 months of age at calving and a single observation per cow. After edits, 207,149 records were used in the analyses. Heritabilities and correlations were estimated with ASREML and using multiple trait sire models that included: age at calving nested within lactation, 5th order polynomials for DIM, fixed HD-CL, and random sire and error. Genetic correlation estimates between data edited for classifiers and unedited data were generated to determine the effect of classifier edits on BCS variation. The genetic correlation estimate between BCS in edited and unedited data sets was 0.9954, but genetic variation was 28% higher and heritability 4% higher for the edited data. Heritability estimates were 0.22 for BCS, 0.24 for DF, 0.37 for STAT, 0.27 for STR and 0.25 for FS. Genetic correlation estimates of BCS with DF, STAT, STR, and FS were -0.72, 0.27, 0.69 and 0.08, respectively. Genetic correlation estimates of FS with DF, STAT, and STR were 0.34, 0.56 and 0.42, respectively. Sires with daughters that have high BCS have daughters that are less dairy and stronger. Body condition scores were not genetically correlated with final score as strongly as DF, STAT, or STR.

Key Words: Body condition score, Holstein, Type traits

1296   Estimation of genetic and phenotypic correlations between type traits and milk yield in Holstein dairy cows in Iran. Ali Toosi*, *Ferdowsi University,College of Agriculture.*

Type scores and milk yield records of 302 grade Holstein cows from two herds were used to estimate genetic and phenotypic correlations between type traits and milk production. The type information included first classification scores for 12 traits on a 50 point linear scale, 4 score card traits (including General appearance, Dairy character, Body capacity, and Mammary system) and final score. Milk yield was 2x, 305-day mature equivalent yield. Data were analysed by method of least squares analysis of variance with unequal subclass numbers. Sire and residual variance components were estimated by method 3 of Henderson. Most of the phenotypic correlations were low and nonsignificant (P>0.05). Udder depth and rear udder width had the highest significant phenotypic correlations with milk yield (-0.18 and 0.20, respectively; P < 0.05). These correlations indicate that cows with higher milk production also tend to have deeper udders with wider rear attachments. Genetic correlations between type traits and milk yield were higher than their corresponding phenotypic correlations in absolute values. The highest estimated desirable genetic correlations were found between rear udder height (0.59), rear udder width (0.56), dairy character (0.41), and angularity (0.34) in one side, and milk yield on the other side. Udder depth (-0.86) and fore udder attachment (-0.77) had the highest undesirable estimated genetic correlations with milk yield. These results suggest that continued selection for milk yield would result in serious weaknesses of udder attachments. Results also showed that the relative genetic progress in milk production, if selection is on final score, is expected to be 17 percent of that which can be obtained by selecting on the basis of milk production alone.

Key Words: Genetic correlations, Type traits, Milk yield

1297   Genetic and environmental factors affecting some linear type traits in Holstein dairy cows in Iran. Ali Toosi* and Fereidoon Eftekhari, *Ferdowsi University.*

Records on 550 Holstein cows classified for 28 linear type traits were analysed by method of least squares to determine the effects of herd, month, age, and stage of lactation at classification on variability of these traits. Heritabilities of and genetic and phenotypic correlations among type traits were estimated from paternal half sisters analyses. (Co)variance components were estimated by Henderson's method 3. Herd, month, and age at classification were important sources of variation for most of the traits. Phenotypic correlations among type traits were in the range of -0.23 (between udder depth and rear udder width) to 0.89 (between strength and body capacity). Genetic correlations were in the range of 0.75 (between fore udder attachment and udder support) to 0.98 (between dairy character and final score). High genetic

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correlations among most of the type traits and final score suggest that continued selection on the latter is an effective means for improving the former. Heritabilities of the linear type traits were in most cases lower than those reported by others, ranging from zero for back and fore udder length to 0.31 for stature. Results of this study suggest that phenotypic selection on most of the type traits will yield low to moderate genetic improvement in the next generation.

Key Words: Type traits, Genetic correlations, Heritabilities

1298   Comparison of occurrence and yields of daughters of progeny-test and proven bulls in artificial insemination and natural-service bulls. H. D. Norman*, R. L. Powell, and J. R. Wright, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Extent of artificial-insemination (**AI**) use was determined for Ayrshire, Brown Swiss, Guernsey, Holstein, and Jersey breedings since 1959. Yield deviations for milk, fat, and protein of daughters of progeny-test (**PT**) bulls were compared with those of daughters of AI-proven bulls and natural-service (**NS**) bulls available contemporaneously. Bulls were categorized as 1) PT through a major AI organization, 2) PT through a minor AI organization, 3) proven through a major AI organization, 4) proven through a minor AI organization, 5) marketed through AI based on an NS evaluation, or 6) used through NS. Only Holstein results are reported. Percentages of daughters that first calved in 1998 with lactation records used in USDA genetic evaluations were 15, 2, 63, 12, 2 and 6% for bulls in categories 1 through 6, respectively. Percentage of daughters sired by PT bulls increased from 8% in 1984 to 17% in 1998, while percentage sired by bulls brought into AI based on NS daughters decreased from 19 to 2% and percentage of NS daughters dropped from 12 to 6%. Percentage of daughters of AI-proven bulls from major AI organizations changed little (from 61 to 63%), but percentage from minor AI organizations increased from 0 to 12%. Those changes were caused by a large reduction in the number of bulls entering AI based on an NS evaluation, plus a moderate increase in percentage of AI use and herds participating in PT programs. From 1984 to 1998, Holstein daughters of AI-proven bulls annually produced 107 to 199 kg more milk and 2 to 5 kg more fat and protein than PT daughters and 366 to 443 kg more milk, 10 to 14 kg more fat, and 9 to 11 kg more protein than NS daughters based on mean yield deviations. Those mean yield differences supported PTA differences (not shown). Use of AI in place of NS would increase annual income of producers by approximately $96 per cow.

Key Words: Artificial insemination, Natural service, Progeny test

1299   Genetic correlations between semen production and economic traits of swine. S. H. Oh*[1], M. T. See[1], T. E. Long[2], and J. M. Galvin[2], [1]*North Carolina State University, Raleigh, NC,* [2]*NPD USA, Roanoke Rapids.*

Currently boars selected for commercial use as AI sires are usually evaluated on grow-finish performance and carcass characteristics. If AI sires were also evaluated and selected on semen production, it might be possible to reduce the number of boars required to service sows, thereby improving the productivity and profitability of the boar stud. The objective of this study was to estimate genetic correlations of semen production with average daily gain (ADG), backfat thickness (BF) and muscle depth (MD). The semen collection records and performance data for 599 boars and two generations of pedigree data were provided by NPD USA. Semen production was defined as the mean of repeated measurements of number of doses per ejaculate (1 dose = 3.05 billion sperm cells per 500 ml). Backfat thickness and MD were estimated by real-time ultrasound. Genetic parameters were estimated from a four-trait animal model using MTDFREML. Breed and contemporary group were included as fixed effects, and were highly significant($P<.0001$) for all four traits. Heritability estimates were .46 for semen production, .46 for ADG, .47 for BF and .33 for MD. The genetic correlations between semen production and ADG, semen production and BF, and semen production and MD were .21, -.01 and -.01, respectively. Genetic correlations between ADG and BF, ADG and MD, and BF and MD were .55, .54 and .39, respectively. Semen production showed a positive genetic correlation with ADG, but was not genetically correlated with BF and MD. Therefore, current AI boar selection practices should not have a detrimental effect on semen production.

Key Words: Genetic correlation, Semen, Pigs

1300   Relationship of body length to number of teats and litter size for four breeds of swine. Z.B. Johnson*[1] and R.A. Nugent, III[2], [1]*University of Arkansas, Fayetteville,* [2]*The Pork Group, Rogers, AR.*

The objective of this study was to estimate relationship of body length to number of teats and number of pigs born alive in first parity pigs from Landrace, Yorkshire, Duroc, and Hampshire breeds of swine. Data consisted of performance test records collected in a commercial swine operation from 1992 to 1999. Boars from 60% of the litters were culled at weaning based on a combination of maternal and performance indexes which differed by breed. Remaining boars and all females were weighed at 100 d of age (WT100) and selected for performance testing based on recalculated indexes. For three years (1992 to 1995), the number of teats (NT) was counted on both sexes at 100 d of age (n = 4,162 for Landrace, 18,986 for Yorkshire, 3,814 for Duroc, and 2,932 for Hampshire). For all years body length (LEN) was measured at the end of the 77-d performance test, and number born alive (NBA) at the first parity was recorded. Number of records for WT100 was 8,611, 38,979, 7,046, and 4,878 for Landrace, Yorkshire, Duroc, and Hampshire, respectively. Of these 825 Landrace, 3,140 Yorkshire, 4,237 Duroc, and 441 Hampshire had records for NBA. For each breed, genetic parameters were estimated using an animal model with litter effects and multiple-trait DFREML procedures. Three-trait models including WT100, LEN, and either NT or NBA were examined. Fixed effects included contemporary group and the appropriate age as a covariate for WT100 and LEN. Heritability estimates for NBA were 0.02 for Landrace, 0.15 for Yorkshire, 0.05 for Duroc, and 0.14 for Hampshire. Estimates of heritability for NT were 0.06, 0.29, 0.04, and 0.08 for Landrace, Yorkshire, Duroc and Hampshire, respectively. Genetic correlations between body length and NBA were 0.22, -0.02, -0.07, and 0.72 and between LEN and NT were -0.17, 0.04, 0.41, and -0.27 for Landrace, Yorkshire, Duroc, and Hampshire, respectively. Estimates of heritability of NBA and NT were low, and no consistent relationship with body length was observed in these data.

Key Words: Body length, Litter size, Number of teats

Dairy Foods
Micro

1301   Efficacy of spices alone or in combined with bifidobacteria to control *Escherichia coli* O157:H7. S.A. Ibrahim*, S.R.K. Dharmavaram, G. Shahbazi, and C.W. Seo, *North Carolina Agricultural and Technical State University, Greensboro, NC.*

Escherichia coli O157:H7 is one of the leading causes of bacterial food-borne disease outbreaks in the United States. An estimated 73,000 cases of infection and 61 deaths occur each year. Many of these outbreaks are associated with the consumption of meat and meat products such as ground beef and ground beef patties. Spices are usually added to meat products to improve the quality and shelf life. Our research hypothesis is that manganese (Mn^2), a common element in many spices, could stimulate the production of organic acids and antimicrobial compound by lactic acid bacteria. Therefore, combinations of starter cultures and spices would enhance the biosafety of these consumable products. The objective of this research was to determine the effectiveness of combinations of bifidobacteria and spices on inactivation of *E. coli* O157:H7 in ground beef. Ground Beef (93% lean meat) was inoculated with *E. coli* O157:H7 (380-94) to make the initial inoculum level of 2.0 log cfu/ml. Inoculated ground beef was mixed with different spices (garlic, ginger, jalapeno pepper and commercial spice, served as antioxidant) at the level of 2% (W/V). Bifidobacteria was then added to a final level of 5.00 log cfu/ml. Beef samples were held at 37 C for 48hr. Changes in the populations of *E. coli* in meat samples were followed on EMB agar plates. The results showed that ground beef treated with commercial spice had the highest inhibitory effect against *E. coli* ($P< 0.05$), followed by jalapeno pepper and garlic. Ginger had little effect on the