marked and sustained reduction in DMI following the reimplant event. Due to the lower DMI, the IH200 heifers had lighter final weight and lower ADG on a live basis (P<.01) than the IHFH heifers, but these differences were reduced on a carcass-adjusted basis. The IH200 heifers had significantly improved feed conversion compared to FH and R200 (P = 0.01) and tended to have better feed conversion than IHFH (P = 0.14) on a carcass-adjusted basis. The IH200 heifers had significantly higher dressing percent, less rib fat, larger ribeye area, lower average yield grade, greater percentage yield grade 1 & 2, lower EBF, and heavier predicted weight at 28% EBF than any other treatment (P < 0.01). These data indicate that Revalor-200 may improve performance and EBF-adjusted final weight compared to Finaplix-H in either single or reimplant strategies utilized in yearling heifers.

Carcass-adjusted[1] Performance and Carcass data

Item	FH	R200	IHFH	IH200
DMI, kg	7.97[a]	7.99[a]	7.92[a]	7.68[b]
ADG, kg	1.39[a]	1.42[b]	1.44[b]	1.41[ab]
F:G	5.73[a]	5.62[ab]	5.52[bc]	5.45[c]
Pr+Ch,%	55.1[a]	37.3[b]	42.1[b]	36.4[b]
YG	2.6[a]	2.4[b]	2.6[ab]	2.1[c]
EBF, %	28.4[a]	27.6[b]	28.1[a]	26.9[c]
AFBW[2], kg	505[a]	518[b]	516[b]	532[c]

[1]Adjusted for common dressing percent.
[2]Final live weight adjusted to 28% EBF; [a,b,c]differ (P<.05)

Key Words: Anabolic Implants, Feedlot, Heifer

Breeding and Genetics: Dairy Genetic Evaluation

731   International genetic evaluation of longevity traits. J. H. Jakobsen* and U. Emanuelson, *Interbull Centre, Uppsala, Sweden.*

The first test run for international genetic evaluation of longevity traits took place in March 2004 and was performed for the Holstein breed. The test run is an outcome of preliminary research studies, which showed feasibility of international genetic evaluation for longevity traits. The 14 countries participating in the research studies defined longevity either as risk of involuntary culling, length of productive life, or survived as a 0-1 trait. Traits were analyzed nationally with linear mixed models and survival analysis. International genetic evaluations were performed using Multitrait Across Country Evaluation (MACE), and correlations between countries ranged in the research study from zero to 0.92, and were on average 0.59. Two different traits have been defined within the longevity trait group. These are longevity as a direct trait and longevity as a trait combined with indicator traits. Combined longevity is a complex trait in the sense that the choice of indicator traits is very variable across countries. Also, procedures to calculate weighting factors for the deregressed national combined proofs, as input to MACE, is unresolved. The first official test run was therefore performed for direct longevity only, but research is currently going on to investigate such unresolved issues for combined longevity. Research is also ongoing to investigate feasibility of international evaluation for longevity for other breeds than Holsteins. The presentation will focus on correlations between countries and selection differentials from the March test run for direct longevity.

Key Words: MACE, longevity

732   Correlated traits used for indirect prediction of productive life in Holsteins. S. Tsuruta*[1], I. Misztal[1], and T. J. Lawlor[2], [1]*University of Georgia, Athens,* [2]*Holstein Association USA Inc., Brattleboro, VT.*

The purpose of this study was to update formulas used for indirect prediction of productive life from correlated traits. Productive life was defined as days in milk at age 84 mo within the limit of 305 DIM for each lactation. Genetic parameters for 25 traits (productive life, milk, fat, protein, somatic cell score, days open, 18 linear type, and final score) were estimated with a multiple-trait sire model via Gibbs sampling. The data contained 392,800 records for Holstein cows born from 1995 to 1997. The model included registration status, herd-year, age group, month of calving and stage of lactation as fixed effects, and random sire genetic effects and residual effects. Heritability for productive life was estimated as 0.09. Genetic correlations of productive life with milk, fat, protein, somatic cell score, days open and final score were 0.11, 0.11, 0.12, 0.32, 0.62 and 0.13, respectively. Stronger correlations with linear type traits were 0.37 for udder depth, 0.29 for body depth, 0.27 for fore attachment, and 0.25 for dairy form. Using all of the 24 traits, productive life can be predicted with the maximum reliability of 0.69. Using five traits (in order of declining importance: days open, udder depth, milk, stature and somatic cell score), the maximum reliability was 0.61. Compared to currently used correlations for indirect prediction, many correlations changed sign, indicating changes in definition of productive life and that many conformation traits have intermediate optima. Days open became the most correlated trait with productive life.

Key Words: Genetic correlation, Productive life, Holstein

733   Analysis of the relationship between type traits and functional survival in Canadian Jersey cows. A. Sewalem*[1,2], G. Kistemaker[2], and B. Van Doormaal[2], [1]*Agriculture and Agri-Food Canada,* [2]*Canadian Dairy Network.*

The aim of this study was to explore the impact of type traits on the functional survival of Canadian Jersey cows using a Weibull proportional hazard model using the Survival Kit. The data set consisted of 49,791 cows from 900 herds calving from 1985 to 2003. Functional survival was defined as the number of days from the first calving to culling or death or censoring. Type information consisted of phenotypic type scores of 8 composite traits and 20 linear descriptive traits. The statistical model included the effects of stage of lactation, season of production, the annual change in herd size, type of milk recording supervision, age at first calving, effects of milk, fat and protein yields calculated within herd-year-parity deviations, herd-year-season of calving, one type trait and the sire. Analysis was done one at a time for each of 30 type traits. The relative culling rate was calculated for animals in each class after accounting for the above-mentioned effects. Among the composite type traits with the greatest contribution to the likelihood function were final score, mammary system, fore udder, rear udder and dairy character, all having a strong relationship with functional survival. Cows with low scores (i.e., classified as Poor) for these traits had higher risk of culling ranging 2 to 5 times compared to higher scores (i.e., classified as Excellent). Linear type traits with the greatest contribution to the likelihood function were style, fore attachment, udder texture and udder depth. Rump angle and set of rear legs had no strong relationship with functional survival compared to other linear type traits.

Key Words: Functional Survival, Jersey, Type Trait

734   Potential of three-stage selection strategies for enhancing the efficiency of progeny testing programs in US dairy cattle. K. Weigel* and N. Zwald, *Department of Dairy Science, University of Wisconsin, Madison.*

The focus of dairy cattle improvement programs has evolved from single-trait selection for milk yield to multiple-trait selection for production, type, and various measures of health, fertility, longevity, and calving performance. In the US, national genetic evaluations for productive life (PL), somatic cell score (SCS), daughter calving ease (DCE), and daughter pregnancy rate (DPR) have all been implemented in the past decade. However, the reliabilities (REL) of predicted transmitting abilities (PTA) for these "functional" traits are low for many important bulls, because heritability parameters for these traits are =10% and because progeny groups for first-crop artificial insemination (AI) sires in the US typically contain only 60-80 daughters. This can lead to errors in selection of sires of sons. For example, 18 of the top 50 Holstein bulls for Lifetime Net Merit (LNM) $in February 2002 ranked below the 80th percentile for LNM$ in February 2004, long before their sons had completed progeny testing. Our objective was to evaluate the potential for a "third stage" of selection among elite AI sires at 84-90 mo of age (in addition to pedigree selection at 0-6 mo of age and first-crop progeny selection at 48-54 mo of age) resulting from the distribution of additional semen for the top 50% of "sires in waiting" (based on updated parent averages) at 30-36 mo of age. Because service sire calving ease data are typically available

by 30 mo of age, this semen could be used safely on both milking cows and virgin heifers. Based on our analysis, it appears that additional semen collected from sires in waiting could replace sales of semen from the bottom 50% of actively marketed proven sires with no adverse effects on genetic progress. More importantly, distribution of additional semen from potential future sires of sons at 30-33 mo of age would provide REL = 80% for traits such as PL, SCS, DCE, and DPR and REL = 90% by the time AI stud managers make final semen collection decisions on their yearling sons.

Key Words: Progeny Testing, Functional Traits

735   Genetic base and trait definition update. P. M. VanRaden*, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Base changes provide an opportunity to revise trait definitions and to review genetic progress. Genetic bases were updated previously in the United States in 1965, 1974, 1984, 1989, 1995, and 2000, and the next is scheduled for February 2005. Interbull survey forms indicate that 18 of 25 countries plan to update their genetic bases for yield traits on this recommended 5-yr schedule; the other 7 countries update every year or at each evaluation. Countries may each define their own scales of expression and bases, but international marketing would be simpler with some uniformity and harmonization. For Interbull evaluations of udder health (UH), 9 of 19 countries currently reverse their scales so that lower somatic cell scores (SCS) result in higher evaluations. Six countries in northern Europe report relative breeding values with a mean of 100 but different multipliers (4, 5, 7, 10, or 12) of genetic standard deviation (SD). The four countries that report clinical mastitis evaluations all reverse their scales. The United States could report predicted transmitting abilities (PTA) for UH using the formula PTA UH = -5(PTA SCS breed mean). This formula converts to the reversed, standardized PTA scale used by France and Spain with mean of 0 (instead of breed mean) and SD of 1. One unit of PTA UH would decrease somatic cell count by 13%. The range for PTA UH is similar to those for conformation, productive life, and daughter pregnancy rate PTA. If many traits are evaluated, sub-indexes may provide the public with fewer numbers that are easier to use. For most traits, genetic progress during the last 5 yr was similar to progress during the previous 5 yr. The genetic variance base was last updated in 1995. The SD of PTA for yield traits will increase by about 10% as a result. At the last base change, net merit units were revised from a per-lactation to lifetime-profit basis. Breed-association, USDA, and foreign selection indexes and genetic evaluations might be easier to use if further revised to obtain similar units, directions, and bases.

Key Words: Genetic Base, Udder Health, Scales

736   International evaluation of Milking Shorthorn-type dairy cattle for production traits. R. A. Barrett*[1], F. Miglior[2], J. Jamrozik[1], and G. Jansen[1], [1]*CGIL, Department of Animal & Poultry Science, University of Guelph, ON, Canada,* [2]*Agriculture & Agri-Food Canada, Guelph, ON, Canada.*

Pedigree information and test-day records for the first three parities from Canada, Australia, New Zealand, the United Kingdom, and the United States were received and edited. Number of milk yield test-day records used for each country was 607,655 for Australia, 17,802 for Canada, 155,134 for the United Kingdom, 61,439 for New Zealand, and 176,498 for the United States. Single-country, single trait parameter estimation was done for each data set using a random regression test-day model using Gibbs sampling and Legendre polynomials of order four. Fixed effects in the model included herd-test day class and age at calving-parity-season of calving class. Average daily heritabilities in first lactation ranged between 0.332 and 0.474 for milk and between 0.370 and 0.445 for protein across the five countries. Correlations between lactations were higher for the United States and Canada for both milk and protein, with the more grazing-dependant countries having lower between lactation correlations. Common sires and daughters of common sires were identified, and these daughters were used to select a subset of herds for multiple-country, single trait parameter estimation. Variance component estimation of the multiple country data is underway using a random regression test day animal model using Gibbs sampling and Legendre polynomials of order 4.

Key Words: Dairy cattle, International evaluation, Milking Shorthorn

737   Accounting for differences in rate of maturity in yield evaluations. G. R. Wiggans* and P. M. VanRaden, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Genetic evaluations that include repeated records usually assume genetic merit is the same across all lactations. Repeatability models are simpler to set up and solve than models with separate genetic effects for each lactation, but may be less precise if animals differ in rate of maturity. Several countries now model the first three lactations as separate traits in published evaluations for yield traits. An alternative is to include a regression on maturity in traditional repeatability models. This allows data from five or even all lactations to be modeled by two genetic effects using single-trait rather than multi-trait programming. Maturity effects were scaled to measure the difference between first and second lactation yield, with smaller differences among later parities. The model was tested on US Jersey data of over 3 million lactation records. Maturity regression coefficients for lactations 1 to 5 were set to [-0.7 0.3 0.4 0.4 0.4] based on preliminary analysis. Parent averages calculated from calvings before 1999 were compared to February 2004 breeding values (BV) calculated from all records or from only first parity records. For bulls born since 1990 with reliabilities above 60% for the current evaluation, within birth year correlations were 0.01 to 0.02 higher for predicting first parity BV from a model with 8% of variance assigned to maturity effects than from a model without this effect. For most birth years after 1989, correlations were not higher for predicting the all parity BV from models with maturity effects as compared to the current repeatability model. A range of maturity variances from 2 to 16% was tested. If 8% of phenotypic variance was assigned to maturity effects, genetic correlations of first with second through fifth parity were assumed to be 0.89, 0.87, 0.87, and 0.87. Correlations among third through fifth were 1 and second with later were >0.99. This random regression approach accounts for genetic differences in rate of maturity with little computational expense, but most genetic parameters tested did not result in improved evaluations

Key Words: Parity, Random Regression, Maturity

738   Prediction of service sire fertility. M. T. Kuhn*[1], J. L. Hutchison[1], and J. S. Clay[2], [1]*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD,* [2]*Dairy Records Management Systems, Raleigh, NC.*

Estimated relative conception rates (ERCRs) are phenotypic predictions of service sire (SSR) fertility computed by Dairy Records Management Systems. ERCRs are based on first service 70-d non-return rate using a linear model that includes the fixed effects of herd-year-month of service, parity, days in milk at breeding, birth year of SSR, and energy-corrected milk yield and the random effects of animal (cow), permanent environment (PE) of the cow and SSR by herd interaction. The ERCR, then, is simply the SSR solution. This research investigated an alternative linear model using all services. The model included the fixed effects of herd-year-season of service, state-month of breeding, parity, and stud; the linear and quadratic effects of milk yield, days-in-milk at breeding, age of cow at breeding, age of SSR at breeding and the linear effects of expected future inbreeding of the daughters (EFI) and inbreeding coefficient of the SSR and also the random effects of animal (SSR), cow and PE of the SSR. A sire's predicted conception rate (CR) was calculated as the sum of his animal, PE, and stud solutions plus the regression on his age, his EFI, and his own inbreeding coefficient. Data for prediction was the result of breeding (0,1) for 530,380 Holstein cows calving between 1995 and 1997. For unconfirmed records, the last service was considered successful unless the cow was coded as sold for reproductive reasons. To assess accuracy of the predictor, mean CR in 1998 was calculated for each SSR and correlated with predicted CR. For bulls with at least 100, 500, and 1000 matings in the predictor, the correlation between predicted and actual CR in a future year was 0.16, 0.26, and 0.36, respectively. For bulls with breedings to at least 1000 cows, in contrast to just 1000 services, the correlation between predicted and future CR was 0.52. Further research will focus on other alternative models, appropriate data edits, and methods to handle the last service where pregnancy status is not known with certainty.

Key Words: Male Fertility

739   Estimation of the economic impact of a unit change in PTA for daughter pregnancy rate. E. Yook*[1], R. E. Pearson[1], and P. M. VanRaden[2], [1]*Virginia Tech, Blacksburg,* [2]*Animal Improvement Programs Laboratory, Animal Research Service, USDA, Beltsville, MD.*

The economic impact of a unit change in PTA of daughter pregnancy rate (DPR) on lifetime profit estimates of a bulls daughters was estimated from DHI records for 71,094 cows to determine an economic weight for the PTAdpr in economic indexes. A cows relative net income (RNI) was calculated using all production initiated prior to her tenth birthday with milk-fat-protein pricing. The basic RNI function consisted of [total milk, fat, and protein income − feed cost for production] (YI) + [net value of calves + net salvage value] (NYI) − rearing cost (RC) − [(daily cost for labor, maintenance feed, supplies, and fixed expenses)×days in herd] (DC). The basic RNI was augmented (ARNI) by adding the products of sire PTA for various traits and the net income for those traits proposed in the Net Merit calculation but not included in the basic RNI function; specifically, SCS(M), type composites (T), and DPR and daughter calving ease (PRCE). Regression analyses including herd and birth year in the model were used to estimate the simple and partial regressions of ARNI or partitioned ARNI on PTAdpr. Partial regression included all PTAs in Net Merit, except sire calving ease. Each 1% change in PTAdpr increased ARNI $23.64 through increasing YI by $90.44, NYI by $9.15, M by $5.26, T by $2.34, PRCE by $4.51, and DC by $89.04 and decreasing RC $0.98. Thus, ignoring other PTA left a substantial positive impact of PTAdpr. Correspondingly, changing PTAdpr by 1% barely broke even when other PTA were held constant because the loss in YI was greater than the savings in daily cost.

Regression coefficients (β) for y on PTAdpr

| | | | | Response (y) | | | | |
	ARNI	YI	NYI	RC	DC	M	T	PRCE
Simple	23.64	90.44	9.15	0.98	-89.04	5.26	2.34	4.51
Partial	1.81	-51.11	2.00	1.59	46.46	0.00	0.00	2.88

Key Words: Daughter Pregnancy Rate, Relative Net Income, Economic Weight

740   Genetic parameters for days open and pregnancy rate in US Holsteins. S. Oseni, I. Misztal*, S. Tsuruta, and R. Rekaya, *The University of Georgia, Athens.*

The influence of different editing of days open (DO) records on genetic parameters of DO and pregnancy rates (PR) in US Holsteins was investigated. Data included first parity 305-d milk yields and DO records in eight states: GA, FL, NC, TX, AZ, CA, NY, and WI. Pregnancy rates was computed as $1/[((DOX))/HI+1)]$, where X was the approximate voluntary waiting period, and HI was the heat interval set to 21 d. Upper limit for PR was set to 1.0. A bivariate animal model with DO (or PR) and 305-d milk yield as dependent variables was fit separately for each state. The model included fixed effects of herd-year, month of calving and age of cow, and random animal and residual effects. In separate analyses, large DO records were limited to 150, 250 and 365 d. Additionally, analyses for PR used values of 50, 80 and 120 d for X. PR assigns more weight to small DO records, and larger heritability for PR indicates larger contributions of such records. Large changes in heritability when an interval was limited indicated genetic variability within that interval. Genetic and residual variances for DO were strongly dependent on the upper limit, with residual variances changing up to 10 times. Estimates of heritability for DO varied between 3 and 6 %. Increase of heritability with the upper limit changing from 150 to 250 d was over 30% for FL and NC, and smaller to flat for the other states. The increase from 250 to 365 caused small changes. The genetic correlation between milk and DO was the highest for FL (0.6) and the smallest for GA (0.1 - 0.2). For PR with X=50, the heritability was higher than for DO for GA, equal for AZ, and smaller for the remaining states. For most states, highest heritabilities for PR were obtained at X = 80 (NY, TX, WI) or X=120 (CA, FL, NC). Records of DO > 250 d carry little genetic information whereas records < 120 d carry more or less information depending on management. Days open and PR are strongly influenced by differences in management between states.

Key Words: Days Open, Pregnancy Rate, Genetic Parameters

741   Genetic relationships of milk yield for different parities between bulls and their sons. H. D. Norman*, R. L. Powell, J. R. Wright, and P. M. VanRaden, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

This research examined how bulls differ in rate of maturity of their daughters. The 305-d milk records for Holsteins with first parity calving dates between 1960 and 1998 were used to calculate three predicted transmitting abilities (PTA) for each bull. The first genetic evaluations included only first lactations on daughters and contemporaries (PTA_1). The second and third sets included the first two and three lactations available, PTA_{1-2} and PTA_{1-3}, respectively. The contribution from individual parities, two (PTA_2) and three (PTA_3), were approximated using a weighted average of the (single trait) evaluations, PTA_1, PTA_{1-2}, and PTA_{1-3}. Weights were based on number of daughters with a second (or third) lactation. Bulls (2864) with $\geq$500 daughters ranged from +295 to -290 kg in difference between PTA_{1-3} and PTA_1, with a SD of 85 kg. In contrast, when the same bulls were ranked on the differences between their contribution to separate parities, they ranged from +555 to -610 kg, for PTA_3 - PTA_1 with a SD of 179 kg. To determine if these difference were transmitted, comparisons were made across a generation. For 16,643 sons with $\geq$40 daughters, expected regressions of son PTA on sire PTA calculated within sire and son birth years (YOB) was 0.44. Actual regressions for PTA_1, PTA_{1-2}, PTA_{1-3}, PTA_{1-2} - PTA_1, PTA_{1-3} - PTA_1, and PTA_{1-3} - PTA_{1-2} were 0.44, 0.43, 0.43, 0.43, 0.43, and 0.42, most with standard errors (SE) = 0.01. Regressions were also derived on the bulls' specific contribution to second and third parities. Actual regression calculated within YOB for PTA_2, PTA_3, PTA_2 - PTA_1, PTA_3 - PTA_1, and PTA_3 - PTA_2 were 0.42, 0.44, 0.44, 0.45, and 0.43, most with SE = 0.01. These results suggest that differences observed in high reliability bulls as their daughters mature is transmitted to their sons daughters. Modeling separate PTAs for each parity should increase accuracy of, and reduce unnecessary oscillation in, genetic evaluations when number of records per daughter changes.

Key Words: Milk Yield, Parity, Lactation Number

742   Effects of udder traits on milk flow and their associations with temperament of first lactation dairy cows during milking time. B. rekik*, A. Ben gara, R. Bouraoui, and K. kouki, *ESA Mateur, Tunisia.*

The effects of the main udder traits of 120 first lactating Holstein-Friesian cows on milk flow were studied around the lactation peak using linear regression. Associations of these traits with temperament of cows during milking time were detected using logistic regression. Most of cows had an overall satisfactory mammary system. The main conformation traits of the udder were interrelated. Pearson correlation coefficients ranged from -0.59 (udder cleft with teat placement) to 0.30 (height with width of rear attachment). Mean milk flow was 22.50gr/s with a minimum of 9.14gr/s and a maximum of 36.81gr/s. This rate of yield production was found to vary with udder balance (P<0.05), rear udder width (P<0.01), side teat distance (P<0.05), and udder cleft (P<0.05). Milk was better extracted when udder traits tended towards optimal scores. The odds of an easy milking were four and five times greater than those of a difficult milking when teats are neither too long nor too short (P<0.05) and udder is balanced (P<0.01), respectively. Cows are more likely to get anxious at milking when their udders are not balanced and their teats are shorter or longer than an optimal length.

Key Words: Udder Traits, Milk Flow, Cow Temperament