

There were no interactions among the VTM and RAC treatments for last rib backfat thickness, broken vertebrae, or scores for stomach ulcers ( $P > 0.21$ ). Also, deletions of VTM premixes did not affect these same measurements ( $P > 0.22$ ). However, RAC decreased ( $P < 0.01$ ) backfat thickness by 8% and tended to decrease scores for stomach ulcers ( $P < 0.06$ ). In conclusion, there were no interactions to suggest that the effects of RAC on growth performance and carcass leanness were altered by deletion of VTM.

Item	With	VTM	Without	VTM	SE
	Without RAC	With RAC	Without RAC	With RAC	
ADG, kg	1.09	1.09	1.02	1.06	0.02
ADFI, kg	2.95	2.65	2.82	2.60	0.08
Gain/feed	0.371	0.413	0.361	0.408	0.008
Backfat thickness, mm	18	17	20	17	1
Broken vertebrae	0.27	0.28	0.09	0.35	0.10
Stomach ulcers	0.01	0.00	0.04	0.00	0.01

**Key Words:** Pigs, Vitamin and mineral premix, Ractopamine

## ASAS/ADSA Breeding and Genetics: Breeding Strategies for Dairy Cattle

**99 Evaluation of corrective mating programs for dairy cattle in the U.S.** E.N. Sonnek\*, L.B. Hansen, and A.J. Seykora, *University of Minnesota, St. Paul, MN.*

Corrective mating programs have been popular with dairy producers for many years, and recently they have been promoted as tools to avoid inbreeding. Six AI companies, two breed associations, and one commercial vendor answered a 42-question survey on the details of their corrective mating programs. The total number of cows mated annually in the US is about 2.7 million with individual programs ranging from about 90,000 to about 600,000. Corrective mating programs use phenotypes and PTAs for multiple traits (including production and type) to optimize mate selection. All of the programs mate heifers by PTAs from pedigrees, by phenotype on linear type traits, or a combination of the two. Most of the programs are run on a laptop on the farm or on a PC in the evaluator's office. Two programs are run strictly from the organization's headquarters. All programs are flexible regarding which traits of animals are used as well as methods for sire selection. When gathering pedigrees on females, six of the programs use only sire and maternal grandsire (MGS). Of these six, five programs use three-generation pedigrees of the selected mate, the female's sire, and MGS to check for common ancestors. Of these five, three check for common ancestors only among the males of these three-generation pedigrees. The sixth program (that gathers only the female's sire and MGS) utilizes complete pedigrees back to the 1960's. Two programs gather the maternal great-grandsire of the female in addition to the sire and MGS. One of these programs uses a three-generation pedigree including males and females while the other uses a five-generation male only pedigree when checking for common ancestors. Finally, only one program uses full pedigrees of selected mates and females back to the 1960's when calculating inbreeding coefficients. Obviously, great differences exist on the depth of pedigrees utilized to accurately prevent inbreeding depression. A significant portion of potential inbreeding is not detected if only a few generations are used, especially considering that the two bulls with highest relationship to the breed would appear several generations back in pedigrees.

**Key Words:** Corrective mating, Negative assortive mating, Inbreeding

**100 Analysis of the relationship between linear type traits, inbreeding, and survival in US Jersey cows.** Daniel Z. Caraviello\*, Kent A. Weigel, and Daniel Gianola, *University of Wisconsin, Madison WI/USA.*

The ability of a dairy cow to resist involuntary culling is of high economic importance to the dairy farmer. Genetic improvement of survival can lead to lower replacement costs, decreased veterinary costs, more opportunities for voluntary culling, and a higher proportion of cows producing at a mature level. The objective of this study was to evaluate the relationship between linear type traits and survival in Jersey cattle. Because some traits may have an intermediate optimum or a threshold above which there is little impact on culling, we were interested in both linear and nonlinear relationships. Data for this study were obtained from USDA Animal Improvement Programs Laboratory, and these included 124,953 Jersey cows in 2258 herds with first calving between January 1, 1981 and December 31, 1993. Average age at termination was 1978 days. Our model included the effects of herd, year of calving, season of calving, age at first calving, and within-herd quartiles for mature equivalent milk, fat, and protein yield in the terminal lactation. Linear and quadratic regression coefficients corresponding to inbreeding coefficients and thirteen linear type traits were added to the

model one at a time. Linear regressions on strength, dairy form, foot angle, rear legs side view, rump angle, thurl width, fore udder, rear udder height, rear udder width, udder depth, suspensory ligament, and front teat placement were all positive and significantly different from zero. Quadratic effects of strength, foot angle, rear legs side view, rump angle, thurl width, fore udder, rear udder height, rear udder width, udder depth, suspensory ligament, and front teat placement were all significant and negative, indicating the likelihood of nonlinear relationships between type traits and survival. Inbreeding had a highly significant negative relationship with survival; a one percent increase in inbreeding resulted in a decrease in survival of approximately 40 days. Results of the linear model analysis will be verified using survival analysis methodology.

**Key Words:** Survival, Type Traits, Inbreeding

**101 Effects of information in pedigrees on estimates of inbreeding depression for days to first service and summit milk yield.** B. G. Cassell\* and V. Adamec, *Virginia Polytechnic Institute and State University.*

Data from Holstein cows processed by DRMS Raleigh were used to estimate inbreeding depression in number of days to first service and summit milk yield. Pedigree information on all cows in this study was retrieved from AIPL, Beltsville, MD and combined with cow records. A procedure based on contribution of each ancestor in a five-generation pedigree to inbreeding coefficient was used to evaluate percentage of information present in cow pedigrees. Four groups of herds with about 50,000 cows each were randomly selected from the data. Group one included herds of grade cows where at least 85% of cows had 0-30% of available pedigree. Groups two (grade, 31-70%), three (grade, 71-100%) and four for herds with registered cows above 70% pedigree were formed similarly with 7% of herds contributing data to both group 3 and group 4. Inbreeding was calculated using standard methods and averaged 0.03%, 1.8%, 2.0%, and 3.7% for groups 1 to 4, respectively. Standard deviations were 0.7%, 2.0%, 2.2%, and 2.4% for the same groups. Mixed models for the two traits included herd-year-season (random), lactation number, inbreeding covariate, animal and permanent environmental effects associated with a cow. Three generations of pedigree were used in the numerator relationship matrix. Estimates of inbreeding depression from MTDFREML analysis of days to first service were -0.23 ( $p=0.10$ ), 0.07 ( $p=0.13$ ), 0.15 ( $p=0.003$ ) and 0.03 ( $p=0.27$ ) days for groups 1 to 4. Summit milk yield averaged between 36-38 kg in all groups, with estimated inbreeding depression of -0.12, -0.06, -0.06, and -0.07 kg. Effects of inbreeding were significantly different from zero ( $p<0.001$ ) with significance increasing from group 1 to group 4. Estimates of inbreeding depression for days to first service were greater from grade herds with more pedigree data, a trend not confirmed in registered cows.

**Key Words:** Days to first service, Summit milk, Inbreeding depression, Pedigree

**102 Minimization of rate of inbreeding for populations with overlapping generations combining live and frozen genetics.** A.K. Sonesson\* and T.H.E. Meuwissen, *Institute of Animal Science and Health, Lelystad, The Netherlands.*

We present a method that minimizes the rate of inbreeding ( $\Delta F$ ) for small unselected populations with overlapping generations. It minimizes the increase of coancestry of parents and optimizes the contribution of

each selection candidate. The carrying capacity of the population is limited to a fixed number of animals per year. For survival rates <100 % the algorithm has to optimize the use of few old and less related animals with many young and higher related animals. For a scheme where the oldest animals were selected,  $\Delta F$  increased with 18-52 % compared with the proposed method. When freezing semen of all sires in a gene bank and assuming that each sire can be used infinitely, the relationships are set in the first 2-3 years, and thereafter the average coancestry of the population stays about the same, such that  $\Delta F$  is approximately zero. Thus, the relationships among the live animals converges to that of the cryo-conserved sires. The level of inbreeding in the optimal schemes with 6 new-born animals per year (3 sires + 3 dams) is 0.060, which is lower than the expected level of inbreeding when simply the 3 founder sires were cryo-conserved, i.e. this would result in an inbreeding coefficient of 0.083 ( $=1/(4*3)$ ). The latter implies that the optimal method also conserves genes of the founder dams by using frozen semen of their male offspring.

**Key Words:** Minimization of Rate of Inbreeding, Overlapping Generations, Genebank

**103 Non-random mating schemes for selection with restricted rates of inbreeding.** A.K. Sonesson\* and T.H.E. Meuwissen, *Institute of Animal Science and Health, Lelystad, The Netherlands.*

Non-random mating has been shown to decrease rate of inbreeding ( $\Delta F$ ), but have no effect on genetic gain for BLUP and phenotypic selection. However, with optimum contribution selection,  $\Delta F$  is restricted and the improved family structure due to non-random mating is instead used to increase selection differential, i.e. increase genetic response. For schemes with discrete generations,  $\Delta F$  restricted to 1.0% and 100 selection candidates per generation, minimum coancestry mating with only one offspring per mating pair (MC1), increased genetic gain with 22% compared with random (RAND) mating. The increased genetic gain is mainly because MC1 mating results in more independent selection within and over generations. Compensatory mating on either the average relationship or the genetic contributions, which reduces the  $Q^2$  effect of Robertson by connecting successful with unsuccessful families, resulted in just somewhat higher genetic gain than RAND mating. For schemes with a less stringent constraint on  $\Delta F$  (2.5%) or more candidates (200), the genetic superiority of MC1 mating was reduced to 5-6%. Schemes with overlapping generations are mostly larger than schemes with discrete generations, because there are several reproductive age classes, which would decrease the effect of non-random mating for schemes with overlapping generations. There are however also more different family structures over the age classes, which would increase the effect of non-random mating. We compared the effect of non-random mating for discrete and overlapping generations at the same  $\Delta F$  (0.25%) and genetic gain per generation. This comparison resulted in 17 and 3 % higher genetic gain for MC1 for schemes with overlapping and discrete generations, respectively.

**Key Words:** Selection, Inbreeding, Non-random Mating

**104 Implementation of an approximate multitrait BLUP evaluation to combine production traits and functional traits into a total merit index.** V. Ducrocq\*, D. Boichard, A. Barbat, and H. Larroque, *Station de Génétique Quantitative et Appliquée, INRA, Jouy-en-Josas, France.*

The new total merit objective function for French dairy breeders combines information on production traits (50% of the total weight in Holstein) and functional traits (with weights of 12.5% for somatic cell count, female fertility, functional longevity and overall type). Traditionally, total merit indexes are constructed based on index selection theory, for bulls and cows separately, and often neglecting correlations between records from one same cow or differences in reliability between traits. In order to approximate an optimal evaluation procedure in a general, yet simple framework, a multiple trait BLUP evaluation applied to an animal model was implemented: pre-adjusted records for production traits, somatic cell scores, female fertility, length of productive life and some (4-6) type traits considered as good predictors of functional longevity and somatic cell scores were derived from each trait evaluation, eliminating the influence of environmental factors. It was checked that in the case of functional longevity, the newly defined pre-adjusted record and its associated weight led to univariate BLUP EBVs for bulls very close to those obtained with the survival analysis mixed model currently used.

Then for each trait, the pre-adjusted record for each cow could just be described as an overall mean plus an additive genetic effect. The combination of this simple model and of a canonical transformation of the data applicable to situations with missing records and variable weights made the multiple trait BLUP evaluation computationally feasible. The total merit index for males and females was obtained as a linear combination of the resulting EBVs, based on the true economic weights of the traits. An interesting by-product of this strategy was the production of improved EBVs for functional longevity combining direct information with information from early predictors.

**Key Words:** Total merit index, Dairy cattle, Multiple trait evaluation

**105 Is Crossbreeding the Answer to Questions of Dairy Breed Utilization?** A J McAllister\*<sup>1</sup>, <sup>1</sup>University of Kentucky.

The current interest in crossbreeding in the commercial dairy industry, even though it is quite limited, raises questions of breed utilization. Less than 5 percent of U.S. dairy cattle are other than purebred or grade Holsteins. The large advantage of Holsteins for additive genetic merit for lactation milk yield is apparently responsible. Why then is there this interest in crossbreeding? The economic importance of traits such as reproduction, health and survival in dairy production systems is likely the basis for the interest in crossbreeding, even though these traits are secondary to milk yield. Several U.S. studies and a Canadian study confirmed that while several crossbred groups were equivalent to Holsteins for lactation milk yield none was superior. Two crossbred groups in the Canadian study had equivalent lifetime yields, milk value and net returns to Holsteins. In the New Zealand study, Friesian-Jersey reciprocal crossbreds were predicted to exceed Friesians in first lactation fat yield. Crossbred performance is dictated by a combination of additive and non-additive genetic effects. Evidence exists for direct, maternal, heterosis and cytoplasmic maternal effects. Heterosis of 15-20% for lifetime traits was found in two studies. Results from previous crossbreeding studies have something to recommend for inclusion of Holstein, Ayrshire, Brown Swiss and Jersey breeds in a crossbreeding scheme. However, multiple generation lifeline performance on an array of purebreds and crossbreds under U.S. condition does not exist. Full unique identification of individual animals, including breed, permits the use of DHIA data to examine field data for the traits recorded therein. Survival data from birth and health data would need to be fully recorded to provide complete data on lifetime performance. Self-propagation of crossbred replacements is mandatory if any crossbreeding system is to be successful. At present a two breed rotational crossing systems appears to be the most viable system to maximize economic merit. Full-scale long term breeding experiments or analysis of field data paired with a comprehensive modeling of use of alternative breed utilization strategies for U.S. conditions are recommended.

**Key Words:** crossbreeding, breed utilization

**106 Heterosis and breed differences for yield and somatic cell scores of US dairy cattle in the 1990s.** P.M. VanRaden\*, *Agricultural Research Service, USDA, Beltsville, MD.*

Yields and somatic cell scores (SCS) of 8806 F1 crossbreds and 81,409 purebreds were examined using test-day data from 320 US herds that each had  $\geq 10$  crossbred cows born since 1990. Comparisons were made within herd, year, and 3-mo calving season, although some groups contained only purebreds or only crossbreds. The model included effects of age and lactation stage, parent breeds, regression on sire predicted transmitting ability, and general heterosis. Estimates of heterosis for first parity were 4.6% for milk yield, 5.3% for fat yield, 4.9% for protein yield, and 0.6% (unfavorable) for SCS. Corresponding estimates for all parities were 4.7, 5.0, 4.9, and 0.3%. A model without an adjustment for sire merit produced slightly lower estimates. For Brown Swiss X Holstein crossbreds, daily fat yield (1.08 kg) and protein yield (0.88 kg) equaled yields for Holsteins, but milk yield was slightly lower (27.6 versus 28.9 kg). For Jersey X Holstein crossbreds, fat yield was equal to Holsteins, but protein yield (0.85 kg) and milk yield (25.7 kg) were lower. With cheese yield pricing, crosses of Brown Swiss or Jerseys with Holsteins may be more profitable than purebred Holsteins if heterosis for health, fertility, and mortality traits are considered. Yields for all other breeds and breed crosses were lower than yields for purebred Holsteins, but feed costs are lower for breeds with smaller body size. Because inbreeding coefficients are increasing by 2 to 3% per decade, heterosis for yield should increase by .6 to .9%. Although genetic progress is slower

within the less numerous breeds, increasing breed differences, current heterosis for yield traits is sufficient to make some dairy breed crosses worth considering. Animals should receive credit for heterosis when considered as mates for another breed. A combined national evaluation of data for all breeds and crossbreds may be desirable but would require an extensive programming effort.

**Key Words:** Crossbreeding, Heterosis, Dairy cattle

**107 Strategies for continual application of MAS in an open nucleus population.** A. Stella\*<sup>1</sup>, G. Jansen<sup>2</sup>, G. Pagnacco<sup>3</sup>, and P. Boettcher<sup>4</sup>, <sup>1</sup>CERSA-FPTP, Italy, <sup>2</sup>CGIL, University of Guelph, Canada, <sup>3</sup>University of Milan, Italy, <sup>4</sup>ANAFI, Italy.

The objectives of this study were to develop and simulate the implementation of several strategies for repeated application of quantitative trait loci (QTL) detection and marker assisted selection (MAS) and to compare the short-term and continual genetic responses. A finite locus model was simulated with 20 QTL randomly distributed across 30 chromosome. Three hundred markers with 6 alleles were evenly spaced across the genome. Allelic effects were sampled from a double exponential distribution. A daughter design was used, every generation, to determine the marker alleles associated with QTL effects. Within family MAS was applied to young bulls, prior to progeny testing, as part of an open nucleus. Young bulls were selected using strategies based on a) the single marker with greatest contrast (BEST1), b) the sum of n greatest contrasts (BESTn), c) the best n contrasts, limited to one per chromosome (LIMn), d) the sum of all contrasts exceeding a given threshold (THRES), and e) the sum of contrasts exceeding a threshold, but limited to one per chromosome (LIMT). Maximum progress was achieved by strategies that selected upon several markers flanking multiple QTL in each generation. When THRES was applied, the mean TBV of selected bulls was increased by 11.98% over conventional selection versus 6.73% for BEST1 in the first generation. On average, 19 marker locations exceeded the 1.96 critical value for THRES. For all approaches, the advantages of MAS decreased to roughly a half by generation five. These decreases occurred because selection decreased the amount of genetic variability in the population and the expected difference between sire alleles at the QTL. The QTL accounting for the greatest proportion of genetic variance in the commercial population was often not selected for in the nucleus, because many nucleus sires were homozygous at that locus. Applying a full genome scan in each generation allowed selection for different QTL across time. By selecting for multiple QTL over time, MAS maintained superiority over conventional selection for many generations.

**Key Words:** QTL detection, Marker Assisted Selection

**108 Superiority of QTL-assisted selection in different dairy cattle breeding schemes.** Gamal Abdel-Azim\* and A. E. Freeman, Iowa State University.

The effect of varying the system of dairy cattle breeding on the superiority of QTL-assisted selection (QAS) over QTL-free selection is investigated. Stochastic computer simulation was used with realistic structure and proportional parameters to the US Holstein population. QTL-assisted selection was based on breeding values that were estimated by an animal model that accounted for the identified QTL as fixed factors and QTL-free selection was based on a conventional animal model. Three aspects of the superiority of QTL-assisted selection were evaluated: genetic response, accuracy of evaluation, and selection pressure on the favorable QTL allele. Aspects of superiority were examined for active sires, young bulls, bull dams, and commercial cow population. The breeding systems compared were: first a conventional progeny testing plan against a progeny testing plan that employed a nucleus herd. The nucleus herd simulated was a hybrid closed nucleus herd with a hierarchical mating design. Second, early selection of young bulls at the age of 3 and 4 years was compared against conventional waiting plans of 5 years. QAS performed potentially better in nucleus herds than in conventional two-stage selection, and in early selection plans than conventional plans. It was found that QAS performed the poorest for the 4-year plan. In addition, QAS superiority for the favorable allele frequency was very similar to its superiority in terms of genetic response. On the contrary, accuracy superiority trends did not parallel response superiority trends across the systems or across the paths of selection. QAS accuracy superiority consistently decreased with time because of the accumulation

of pedigree and phenotypic information. The study shows that the superiority expected from QAS is highly dependent on the breeding system implemented. The low superiority of QAS observed in conventional progeny testing schemes suggests that limited benefit is to be expected from using QTL information in genetic evaluation without modifying such schemes to maximize the superiority of QAS.

**Key Words:** QTL-Assisted Selection, Mixed Models, Dairy Cattle Breeding Systems

**109 Optimal selection on two quantitative trait loci with linkage.** J. C. M. Dekkers\*<sup>1</sup>, R. Chakraborty<sup>1</sup>, and L. Moreau<sup>2</sup>, <sup>1</sup>Iowa State University, Ames, IA, <sup>2</sup>INRA, Gif-sur-Yvette, France.

Methods have been developed to optimize selection on a single identified quantitative trait locus (QTL) over multiple generations but in practice multiple QTL must be selected on simultaneously. Our objectives were to develop a method to optimize selection on multiple QTL and to apply it to selection on two linked or unlinked additive QTL. Effects of the QTL were .25 and .375 phenotypic standard deviations for a trait with heritability .25. Initial frequencies of the favorable QTL alleles were .1. Strategies to maximize total or cumulative discounted response (CDR, 10% discount rate) over ten generations were compared to standard QTL selection on the sum of breeding values for the QTL and an EBV for polygenes, and to phenotypic selection. For unlinked QTL, optimal selection resulted in 6.9% greater total and 2.6% greater CDR than standard QTL selection and 2.4% greater total and 5.6% greater CDR than phenotypic selection. Linkage (recombination rate 0.05) between the QTL slightly reduced response for standard QTL and phenotypic selection but increased response for optimal selection, which capitalized on linkage by emphasizing selection on favorable haplotypes. When the objective was to maximize total response after ten generations and QTL were unlinked, optimal selection increased QTL frequencies to fixation in a near linear manner and equal emphasis was given to each QTL, regardless of a difference in effects of the QTL and regardless of linkage. The average emphasis given to individual QTL was, however, not additive. These results demonstrate the ability of optimal selection to capitalize on information on the complex genetic basis of quantitative traits that is forthcoming as a result of advances in molecular genetics.

**Key Words:** Marker-assisted selection, Quantitative loci

**110 Real options analysis applied to dairy cow breeding and replacement decisions.** H Groenendaal\* and D.T. Galligan, University of Pennsylvania, School of Veterinary Medicine, Kennett Square, PA, USA.

Many investments allow for active management decisions that can improve their value. However, traditional discounted cash flow (DCF) analysis assumes a passive management (as in the marginal net revenue approach) or attempts to value real investment opportunities that have discretionary asymmetrical cash flows by using an inappropriately constant risk-adjusted discount rate (as in dynamic programming). Therefore DCF neglects the value of active management and under-estimates the true value of investment opportunities. However, the real option approach, developed in the financial markets, captures the value of managerial flexibility.

The goal of this presentation is to describe the real options approach. In addition, this analysis will be applied to the evaluation of a simplified hypothetical breeding and replacement decision of a dairy cow. The conclusion from the traditional DCF method was not to invest in breeding the dairy cow and cull her at the end of the current lactation because the value of the next lactation, if the cow got pregnant, was negative (- US dollar 5). In contrast, the real option approach showed insemination was economically attractive, the value of the pregnant cow's next lactation value was positive (US dollar 34). The difference between the value calculated with both methods, (US dollar 39) was attributable to the extra value of active management.

It was concluded that the real options analysis provided an analytical infrastructure that is more appropriate to be used in situations where managerial flexibility exists. Due to the active role of management as well as the volatility in many livestock investments, real option analysis will allow for better valuation than DCF.

**Key Words:** Real options, Discounted cash flow, Replacement