

**154 Evaluation of a risk assessment tool in characterizing environmental Salmonella and Mycobacterium paratuberculosis status in dairy herds.** D. Collette\*, L. Minicucci, and S. J. Wells, *University of Minnesota, St. Paul.*

The objective of this study was to evaluate the validity of an on-farm risk assessment tool in characterizing the status of manure-cycle pathogens on dairy farms from environmental samples. A risk assessment tool developed by study investigators was used to evaluate management practices on Minnesota dairy farms targeting Salmonella and *M. paratuberculosis*, the causative agent for Johne's disease (JD). Two visits were conducted by two evaluators to Minnesota dairy herds randomly selected from a list of state JD control program herds. Data was collected using the risk assessment tool from 36 herds from January to June 2004 and again from 38 herds from June to August 2004. Environmental samples were collected from high risk areas on the farms, including cow alleyways, fresh cow pens, and manure storage, and bacterial culture was performed to characterize Salmonella and *M. paratuberculosis* environmental status. The highest mean

Salmonella risk scores were from the cow herd, biosecurity, and growing heifer areas and the highest mean Johne's disease risk scores were from the cow herd, biosecurity, and site management areas. At the first visit, 33% of herds had positive environmental samples for Salmonella and 37% of farms were positive at the second visit. Forty-two percent of herds were categorized as high *M. paratuberculosis* bacterial load herds at each herd visit. The criteria for a high bacterial load herd was defined as having an environmental sample with a shedding score of three or four. At the first herd visit, herds with high environmental *M. paratuberculosis* bacterial loads were more likely to be Salmonella-positive farms than herds with low *M. paratuberculosis* bacterial load ( $P < 0.05$ ). Preliminary analysis demonstrated lack of association between mean risk scores overall or within individual management areas and Salmonella or *M. paratuberculosis* environmental status. This is an indication that an evaluation of herd management on-farm using a risk assessment tool does not predict manure-cycle pathogen environmental status on the day of the herd visit.

## Breeding and Genetics: Dairy Breeding

**155 Genetic impact of utilizing female-sorted semen in commercial and nucleus herds.** G. Abdel-Azim\* and S. Schnell, *Genex Cooperative Inc., Shawano, WI.*

This study was designed to investigate genetic effects of using sorted semen in a dairy cattle population. Progress was monitored in elite and commercial animals over 20 years of selection. To study the genetic impact of utilizing sorted semen in commercial herds, a scenario in which female-sorted semen was available to commercial herds was evaluated. Second, to study the genetic impact of utilizing sorted semen in nucleus herds, scenarios in which female-sorted semen was used only in a nucleus herd, where multiple ovulation and embryo transfer (MOET) took place, were simulated. Finally, because of the additional advantage of marker-assisted selection when sorted semen is used in nucleus herds, utilization of sorted semen in scenarios that employed marker-assisted selection was simulated. In the scenario where female-sorted semen was used in commercial herds, a large genetic advantage was observed early in commercial cows. Average superiority in first-lactation cows exceeded 30% in year 11 but continued to decrease until it reached 9% in year 20. The increased selection intensity in commercial cows contributed to the genetic merit of future cows (cow→cow contribution) but the contribution of the nucleus grew over time, and gradually marginalized the cow→cow contribution. The genetic advantage of gender control in the MOET scheme was minimal except when marker-assisted selection was also available. Two factors that affected the contribution of marker-assisted selection were studied: within versus across family selection of donors and the number of loci in the QTL component. Schemes that selected donors regardless of their family structure were superior, and more loci in the QTL component increased the effectiveness of sorted semen. Finally a reduced MOET scheme where harvested females were reduced from 42 to 25 per year was studied. It was found that the reduced scheme in combination with female-sorted semen was not genetically inferior to the large scheme in combination with regular semen.

**Key Words:** Dairy cattle breeding, Marker-assisted selection, Sorted semen

**156 Net present value of an artificial insemination: non-sexed versus sexed semen.** N. J. Olynk\* and C. A. Wolf, *Michigan State University, East Lansing.*

Sexed semen has been a long anticipated tool by dairy farmers to obtain more heifer calves. Using flow cytometry to separate male- and female-bearing sperm decreases sperm numbers per straw and negatively affects sperm viability and longevity leading to decreased conception rates (CR). This decreased CR makes virgin heifers better suited for insemination with sexed semen than lactating dairy cows. Budgets were developed to calculate the net present value (NPV) of an artificial insemination of a virgin heifer using non-sexed and sexed semen. With heat detection rates (HDR) varying widely between farms, and CR varying based on both animal and management factors, multiple scenarios were required to assess differences in NPV with non-sexed versus sexed semen. Bull and heifer calf values were held constant in all scenarios, with heifer calves valued at \$500 and bull calves valued at \$110. Costs per straw were held constant at \$15.00/straw for non-sexed semen and \$45.00/straw for sexed semen of approximately the same genetic value. With sex ratios of 49.2% female with non-sexed semen and 90% female for sexed semen, a sample scenario was performed holding heat detection constant at 51%. Base values for CR with non-sexed of 58% and sexed semen of 31% were obtained from K.A. Weigel (2004). With these HDR and CR we observed an approximately \$50 decrease in the net present value of an insemination with sexed semen. Holding all other factors constant in this scenario, the CR with sexed semen would need to decrease by no more than 6 percentage points to achieve the NPV obtained with non-sexed semen. In this scenario the value of an average calf increased approximately \$150 with sexed semen, although this difference is overwhelmed by the nearly 50% decrease in pregnancy rate. To achieve a positive NPV assuming a 51% HDR, the CR with sexed semen must be at least 20%; assuming a 70% HDR, the CR with sexed semen must be at least 15%. Other considerations include the effect on dystocia, biosecurity, and internal herd growth implications.

**Key Words:** Sexed semen, Heifer reproduction, Artificial insemination

**157 Domestic versus imported artificial-insemination semen for Holstein graziers in the United States.** H. D. Norman, J. R. Wright, and R. L. Powell\*, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

In recent years, interest has increased in the United States regarding grazing of dairy cows to reduce machinery, feed, and labor costs. Success with grazing requires that cows begin lactations when pasture is ready, which places a premium on fertility, a trait that has been declining. Grazing has been the general practice in New Zealand (NZ) for many years. Use of semen from NZ bulls in the United States assumes that bulls selected for superior daughter performance in NZ will be good choices for US graziers. The study compared US performance of daughters of NZ artificial-insemination (AI) bulls with that of US-sired contemporaries. Data were milk, fat, and protein yields, somatic cell scores (SCS), and days open (DO) from 161 US herds with daughters of 26 NZ Holstein-Friesian bulls. For each of those 565 daughters, difference in standardized phenotype from 6,506 US-sired herd contemporaries was computed for parities 1, 2, and 3. Daughters of the 1,168 US bulls were higher for milk (473 to 545 kg) and protein (5 to 6 kg) yields for each parity and lower for SCS (0.2 units) for parities 1 and 2. Daughters of NZ bulls were slightly higher (1 to 2 kg) for fat yield. First-parity DO were lower (7 d) for NZ daughters, with a possible DO superiority indicated for NZ daughters for parity 2 (1 d) and for US daughters for parity 3 (8 d). Differences favored US bulls for milk and protein yields and SCS; NZ bulls were favored for DO for parity 1. Daughters of US bulls had higher linear composite indexes for body size, feet and legs, and udders, but data were limited. Bulls were compared to all AI bulls in their own country that were born from 1994 to 1996 and found to be generally in percentile 50 or higher (percentiles 47 to 76) for most traits; NZ bulls were in higher percentiles as expected because imported semen is selected based on foreign progeny tests. Importation of semen from bulls selected under NZ conditions has not been advantageous for yield, SCS, and DO to date for US grazing operations.

**Key Words:** Genetic evaluation, Grazing, Imported semen

**158 Assessment of the economically optimal voluntary waiting period for first breeding in dairy cattle.** A. Bell\*, A. de Vries, and P. J. Hansen, *University of Florida, Gainesville.*

Objective of this study was to assess the economically optimal voluntary waiting period (VWP) for first breeding for individual dairy cows. Recently, greater VWP have been recommended because of increased milk yield and persistency, greater fertility later in lactation, and reduced labor associated with timed-AI protocols. The economically optimal VWP for an individual cow is obtained when expected future cash flows are maximized. An existing model that optimizes breeding and replacement decisions was adjusted. Major adjustments were: 1) weekly instead of monthly stages, 2) separation of the performance of the cows currently in the herd from the performance in the next lactation and of replacement heifers. This allowed for more accurate representations of individual lactation curves and risk of pregnancy. Insemination values, defined as the difference in future cash flows between breeding a cow this week compared to waiting and making the optimal breeding decision 3 weeks later, were calculated. A negative insemination value is the positive value of the delay of the VWP. Inputs for a Holstein herd in the US were used in the model. Estrus detection rate and conception rate were set at 40%. Minimum VWP was set at 42 DIM. Lactation curves were calculated by Best Prediction for 25,000 ME milk. Milk yield for 10 first lactation cows

currently in the herd were incremented by 0 to +9 kg/d. Insemination values at 42 DIM (INS42) decreased from \$45 to -\$47 by greater milk yield. Optimal VWP increased for cows producing  $\geq +5$  kg/d (range 49 to 133 DIM). When both estrus detection rate and conception rate were 50%, INS42 were on average \$21 lower. The VWP for cows producing  $\geq +4$  kg/d increased (range 63 to 182 DIM). Increased persistency (+0.08 kg/d after peak) reduced INS42 by \$40, increasing the VWP for cows producing  $\geq +2$  kg/d (range 49 to 224 DIM). In conclusion, the optimal VWP increased with greater milk yield, greater persistency, and greater risk of pregnancy, and therefore was different for individual cows in the first lactation.

**Key Words:** Voluntary waiting period, Economics, Optimization

**159 Optimal breeding and replacement decisions for dairy cows when heifer supply is constrained.** A. de Vries\*, *University of Florida, Gainesville.*

Objective of this study was to develop a model that optimizes breeding and replacement decisions for dairy cows when heifer supply is constrained. Herd resource constraints, such as a limited supply of heifers, make optimal breeding and replacement decisions for individual cows dependent on decisions for other cows in the herd. The presence of herd constraints requires that optimal decisions need to be determined simultaneously for all cows in the herd. Previous approaches provided complex and approximate solutions, while exact solutions for realistic problems have not been developed. In this study, the dairy cattle breeding and replacement problem under heifer supply constraints was modeled as a network consisting of nodes, arcs, and side constraints, and solved with the Interior Point algorithm in SAS procedure Netflow. To illustrate the model, data on lactation curves, milk prices, heifer prices, feed cost, labor cost, fixed cost, risk of involuntary culling, and risk of pregnancy for conditions in Florida were used. Heifer supply was varied as a fraction of the number of available slots on the dairy farm. The network formulation resulted in 35,758 nodes, 79,947 arcs, and 43,124 side constraints. Proc Netflow typically used approximately 6 minutes to solve the problem, with the vast majority of the time spent on preprocessing the data. Approximately 40 iterations of the Interior Point algorithm were needed, depending on the constraints. When the supply of heifers was not constrained, profit / slot per year was \$396.76 and 100% of the slots were filled with cows. Per year, 45.93% of slots received a replacement heifer. Forced entry of more or fewer heifers reduced profit. Not all slots were filled if the supply of heifers was considerably limited. Cows were kept longer when heifer supply was more limited. The maximum profit / slot per year was not associated with the greatest milk yield / slot per year. In conclusion, the network formulation solves the dairy cattle breeding and replacement problem under herd constraints for individual cows at a realistic level.

**Key Words:** Network, Optimization, Culling

**160 Protections available for intellectual property in the dairy artificial insemination industry.** E. Ogden and K. Weigel\*, *University of Wisconsin, Madison.*

The cost of semen has declined due to fierce competition and the ease of erasing competitive advantages by buying sons of competitors' sires. It is difficult for breeding companies to recoup research and development costs, but intellectual property law could be of value. Copyright law protects ideas, but facts such as DNA sequences can't be copyrighted. Trade secret law protects valuable information, but

secrets can be lost by reverse engineering, and it would be difficult to keep DNA information secret. A trademark designates a product's origin, and these have been applied to laboratory animals, so a name or prefix could be trademarked. A patent allows the owner to exclude others from using or selling an invention, and many innovations are patentable, including DNA sequences. The exact sequence and defined utility are required, so patenting a whole genome would be difficult. Process claims can protect methods to create genetically modified animals, but traditional breeding methods are not novel. Patentability rests on whether an innovation is a product of man or nature, not if it is inanimate or living, so plants, animals, and microbes have been patented. A patentable animal must express a DNA sequence that is not naturally occurring, not merely a sequence that is discovered as useful. Due to these limitations, contractual licensing may be the best option. A seller can license a product, rather than sell it outright. In exchange for letting a purchaser use the product, the seller restricts its field of use. This allows the seller to keep the product out of competitors' hands and to use price discrimination. Price discrimination keeps costs low for those who can't impact the seller's ability to recoup expenses and puts the burden on those who can. Acceptance can involve a signed contract or specific conduct, such as opening of a shrink-wrap license (for software). Such restrictions are applicable to the dairy genetics industry. By restricting the reselling of a unit of semen or the resulting calf, a company could keep its genetics out of competitors' hands and use price discrimination in the marketplace.

**Key Words:** Intellectual property, Genetics, License

**161 Genetic analysis of milk urea nitrogen and lactose and their relationships with production traits in Canadian Holstein cattle.** F. Miglior<sup>1,2</sup>, A. Sewalem<sup>1,2</sup>, J. Jamrozik<sup>3</sup>, D. M. Lefebvre<sup>4</sup>, and R. K. Moore<sup>4</sup>, <sup>1</sup>*Agriculture and Agri-Food Canada - Dairy and Swine Research and Development Centre, Lennoxville, QC, Canada*, <sup>2</sup>*Canadian Dairy Network, Guelph, ON, Canada*, <sup>3</sup>*Centre for the Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada*, <sup>4</sup>*Programme d'Analyse des Troupeaux Laitiers du Québec, Ste-Anne-de-Bellevue, QC, Canada*.

The Programme d'Analyse des Troupeaux Laitiers du Québec (PATLQ) has been collecting data in Quebec dairy herds on lactose since 2001 and milk urea nitrogen (MUN) since 1997. While data on MUN is also being collected in other Canadian provinces, testing for lactose concentration in Canada is currently done exclusively in Quebec by PATLQ. Concentrations of MUN are measured at Canadian DHI labs by infrared technology. Several studies have already reported associations of MUN and lactose with fertility, health and/or energy balance traits in dairy cows. The objective of this research was to estimate heritabilities of MUN and lactose in the first three parities, and their genetic relationships with milk, fat, protein and SCS in Canadian Holsteins. Multiple-trait random regression test-day animal model and the Gibbs sampling method were used for parameter estimation. Regression curves were modelled using Legendre polynomials of order four. Data were a random sample of test day records (60,645 records from 5022 cows) extracted from the original data set, which included 1,183,725 records from 235,760 Holstein cows. A total of six 4-trait analyses, which included MUN and/or lactose (yield or percentage) with different combinations of production traits, were performed. One chain of 100,000 cycles was run for each 4-trait analysis and the first 10,000 samples were discarded as a burn-in. Average daily heritabilities were moderately high for MUN (0.384 - 0.414), lactose kg (0.466 - 0.539), and lactose percentage (0.478 - 0.508). Lactose kg was highly correlated with milk yield (0.979). Lactose percentage

and MUN were not genetically correlated with milk yield. Research is underway to assess the relationships between MUN and lactose with fertility traits.

**Key Words:** Milk urea nitrogen, Lactose, Variance component estimation

**162 Blood metabolite profiles in dairy cattle selected for differences in milk component production.** M. Westall\* and D. Moody Spurlock, *Iowa State University, Ames*.

Long term selection for increased milk production in the US dairy industry has contributed to a decline in fitness traits. The objective of this study was to evaluate energy mobilization in cows selected for high versus average production of milk components. We hypothesized high producing cows would show greater mobilization of body energy reserves, potentially contributing to compromised fitness traits. Cows were randomly chosen to represent selection lines from the Iowa State University research herd that have been selected for high (HFP) versus breed average (AFP) fat plus protein PTA since 1986. Twenty-eight HFP and 22 AFP cows balanced for first and later parities were used. Blood samples were taken weekly from week 1 to 12 post partum, and monthly through week 24. Body condition scores (BCS) and body weights were taken at the time of blood collection. Serum was analyzed for glycerol, non-esterified fatty acids (NEFA) and creatinine concentration. Data were analyzed for each week of lactation using a model that included fixed effects of line, parity and their interaction, and a random effect of cow within line and parity. Preliminary production data project a non-significant difference between AFP and HFP cows for energy corrected milk (23,679 versus 24,164 lb, respectively). BCS for HFP cows were less than for AFP cows at weeks 16 and 20 ( $P < 0.05$ ). Body weights did not differ between lines throughout the experiment. Serum creatinine for AFP cows was less than for HFP cows at weeks 2, 3 and 4 ( $P < 0.05$ ). Glycerol concentrations for AFP cows were greater than for HFP cows at weeks 16 and 20 ( $P < 0.05$ ). NEFA did not significantly differ between lines. In contrast to our hypothesis, differences in glycerol concentration indicate greater mobilization of adipose tissue by AFP than HFP cows in mid lactation. However, this difference may be a reflection of total body fat. The significant difference between lines for creatinine concentration was unexpected, and suggests a potential difference in the tissue origin of mobilizable energy between cows selected for differences in milk component production.

**Key Words:** Energy mobilization, Fat, Muscle

**163 Effects of accounting for heat stress on genetic evaluation of US Holsteins for milk by a test day model.** J. Bohmanova<sup>1</sup>, I. Misztal<sup>1</sup>, S. Tsuruta<sup>1</sup>, H. D. Norman<sup>2</sup>, and T. J. Lawlor<sup>3</sup>, <sup>1</sup>*University of Georgia, Athens*, <sup>2</sup>*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*, <sup>3</sup>*Holstein Association, Brattleboro, VT*.

The purpose of this study was to quantify the effect of heat stress on genotype by environment interaction among different regions of the United States. The national data consisted of 55.5 million first parity test-day (TD) milk yield records on 5.8 million Holstein cows. Subsets of the national data were from the Northeast (NE) with 12.5 million TD records on 1.3 million cows, and from the Southeast (SE) with 3.5 million TD records on 0.36 million cows. Meteorological data from 202 public weather stations were matched with herds based on distance. Daily mean temperature-humidity index (THI) was calculated

from temperature and relative humidity records three days prior to TD. The first model that lacked the effect of heat stress included fixed effects of herd-test date, age at calving class, frequency of milking, and DIM x season class, and random genetic additive (regular breeding value) and permanent environmental effects. The second model that accounted for heat stress included two additional random regressions on degrees of heat stress ( $t = \max[0, \text{THI} - 72]$ ), one for additive genetic (heat breeding value) and one for permanent environmental effect. Breeding values (BV) were computed by BLUP90IOD. Correlations involved sires with at least 300 daughters in regions being compared. When heat stress was ignored, the correlations of regular BV between NE and SE were 0.86. When the heat stress was considered, the correlation increased by 0.01. The correlation between heat BV for NE x SE was 0.72. Heat stress effect as applied explains only a fraction of differences in sire ranking between SE and the NE. The real impact of heat stress may be higher because THI as used accounts only for a fraction of variability due to heat and low correlations are in part due to limited accuracies.

**Key Words:** Genetic evaluation, Heat stress, Genotype x environment interaction

**164 Estimation of genetic parameters of test day milk yields for Holsteins in Khorasan province of Iran.** J. Eslami<sup>1</sup>, H. Farhangfar<sup>\*2</sup>, and H. Naeemipour<sup>2</sup>, <sup>1</sup>Zabol University, Zabol, Iran, <sup>2</sup>Birjand University, Birjand, Iran.

In this research a total of 72187 monthly test day mil yields obtained from 8652 first lactation Holsteins calved from 1993 to 2003 in Khorasan province of Iran was used to estimate genetic parameters using single trait, repeatability and random regression test day animal models. In the random regression test day model orthogonal legendre polynomials of 4th order was used to take account of additive genetic and permanent environmental variation during lactation among individual animals. Heritability estimates of test day milk yields ranged from 0.11-0.25 and 0.10-0.24 for single and random regression test day models respectively. In the repeatability test day model the heritability estimate of monthly test day milk yields was found to be approximately 0.16. The results obtained showed that the second part of the lactation course was more heritable than the first part of the lactation. Repeatability of test day milk yields was 0.64. Genetic correlations among adjacent test day milk yields were high and decreased as the interval between them increased. The genetic

correlations between months 1 and 10 and between months 9 and 10 were the lowest and highest respectively.

**Key Words:** Genetic parameters, Test day models, Random regression

**165 Studies on drops of PTA from first to second crop for final score in Holsteins.** V. Koduru<sup>\*1</sup>, I. Misztal<sup>1</sup>, S. Tsuruta<sup>1</sup>, and T. J. Lawlor<sup>2</sup>, <sup>1</sup>The University of Georgia, Athens, <sup>2</sup>Holstein Association USA Inc., Brattleboro, VT.

Drops of PTAs for final score from first to second crop of daughters have been reported for Holstein sires. The objective of the study was to investigate whether the causes of these drops were different distributions of grade and registered animals in the subsequent crops. The PTAs were estimated from 2 datasets: data A (5,993,207 animals with classification year up to 2001) and data B (6,606,175 animals with classification year up to 2005). For the sires born between 1993 and 1996 (N=145) PTA drops were calculated as difference between PTAs estimated from data B (second crop) and PTAs estimated from data A (first crop). The basic single trait (ST) animal model included effects of herd-year-season-classifier (HYSC), age-year, stage of lactation-year, animal genetic, permanent environmental and residual effects. Modifications to the ST model included reduced weights for grade records and treating HYSC as random. A two trait model treated records of registered and grades as separate with animal effects considered correlated or not. The last model corresponded to separate evaluations for grade and registered cows with heritability of 31% for registered and 17% for grades, and the correlation between their additive effects was 77%. Separate analyses used data adjusted for heterogeneous herd variances. The mean and SD of first crop and second crop PTAs estimated with the basic ST model using unadjusted data, were 2.2 and 0.7, and 1.5 and 0.6 respectively. Mean difference of PTAs estimated with ST model was 0.69 and the drops were in the range of -2.1 to 0.3, with more drops (94%) than gains. Drops with the modifications to the ST model were 81% or higher. With a multiple trait model, the percentage of drops was 89 for registered and 80 for grade when genetic effects were assumed correlated, and 86 and 69 when they were not. The adjustment had little effect on the results. Drops of PTA from first to second crop for final score are mostly due to factors other than changing fractions of grades and registered.

**Key Words:** Final score, Holstein, PTA

## Dairy Foods: Cheese I

**166 Textural and rheological properties of cream cheese: effect of cream mix homogenization pressure and incubation temperature.** M. Brighenti<sup>\*1</sup>, S. Govindasamy-Lucey<sup>2</sup>, J. J. Jaeggi<sup>2</sup>, K. Lim<sup>2</sup>, M. E. Johnson<sup>2</sup>, and J. A. Lucey<sup>1</sup>, <sup>1</sup>University of Wisconsin, Madison, <sup>2</sup>Wisconsin Center for Dairy Research, Madison, WI.

The objective of this study was to determine the impact of cream mix homogenization pressure (HP) and incubation temperature (IT) on rheological and textural properties of cream cheese. A central composite experimental design and response surface methodology were used for data analysis. Cream cheeses were manufactured using different HP (100, 122, 175, 228, and 250 Bar) during the first stage of homogenization, while the pressure of the second step was constant (50 Bar). The IT used were 20, 21, 23, 25, and 26°C. Curds were

stirred at pH 4.7. Storage modulus (SM) values at 8°C were obtained by small amplitude oscillatory tests. Hardness was determined by texture profile analysis (TPA). A trained sensory panel used spectrum descriptive analysis to determine: firmness, stickiness, and difficulty to spread. Cream cheeses were analyzed 2 and 4 weeks after manufacture. For most samples, significant ( $P < 0.05$ ) differences were observed for hardness between 2 and 4 weeks, suggesting that there were changes in the structure of cream cheeses during storage. In most cases, samples became harder. Increasing IT significantly ( $P < 0.05$ ) decreased SM, hardness (TPA), and sensory firmness and difficulty to spread, while it increased stickiness. This effect may be due to an increase in hydrophobic interactions at higher IT that may cause contraction of the casein particles, which could reduce the contact area and decrease