then summarizes the main characteristics of agriculture in the EU-15. Thirdly, it provides an overview of the common agricultural policy CAP in the EU and of environmental regulations and directives. Finally, it discusses implementation of the EU Nitrate Directive in the Netherlands and Denmark. Systematic interference of governments with European agriculture started in the 19th century. Marked effects of policies on agriculture followed after the foundation of the EU with its CAP. Environmental issues in agriculture were addressed following the reform of the CAP in 1992 and following the implementation of various environmental regulations and directives from the 1980's and 1990's onwards. The EU Nitrate Directive has as yet the strongest influence on N and P in agriculture, especially through its objectives to designate areas vulnerable to nitrate leaching, to establish action programs and to establish a code of good agricultural practice. These measures must ensure that, for each farm, the amount of N applied via livestock manure shall not exceed 170 kg per ha per year. The Nitrate Directive was agreed to by all member states in 1991, but there are variations between member states in the interpretation, implementation and enforcement of the Nitrate Directive. Differences in the progress of implementation appear in part to be related to differences in the structure of agriculture, as shown by a comparison between Denmark and The Netherlands.

Key Words: Nitrogen, Nitrate, Europe

Breeding & Genetics: Dairy cattle breeding for nonproduction traits

509 Selection for mastitis in Norwegian dairy cattle.

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Clinical mastitis (CM) is the most frequent and costly disease in dairy production. Mastitis has been recorded through the health card system as an integrated part of the Norwegian Dairy Herd Recording System (NDHRS) since 1978, and includes recording of all veterinary treatments on individual cows. In 2002, 96% of the cows belonged to herds in the NDHRS. In Norway, antibiotics can only be prescribed by veterinarians, and it is compulsory to record diagnosis and treatment on the cow's health card. Information is then transferred to the NDHRS on routine basis. Mastitis has been included in the total merit index of Norwegian Dairy Cattle (NRF) since 1978, and the relative weight in the total merit index is currently 22%. In 2002, progeny testing for mastitis was based on an average of 210 daughters. Since 1990 there has been a favourable genetic trend for mastitis resistance. In 2002 the phenotypic average of CM (from 15 days prior to calving to120 days after first calving) was 11.5%. Results from a Norwegian selection experiment, including one group of cows selected for high protein yield (HPY) and one group selected for low clinical mastitis (LCM), clearly demonstrates the effect of direct and indirect selection on CM. After 3 cow-generations the genetic difference between LCM and HPY cows was 8.6 % CM. The genetic trend for the LCM cows, equivalent to a reduction of 0.9 % CM per year, shows that considerable selection response can be achieved for mastitis if sufficient selection pressure is put on the trait. If mastitis is ignored in the breeding program, selection for increased milk production will result in an unfavourable correlated response in CM. Results from the selection experiment indicate that an increase of 0.23 % CM per year may be expected as a correlated response. Genetic trends for the NRF population shows that with a broad breeding objective it is possible to obtain genetic improvement for health, fertility, and milk production simultaneously, despite unfavourable genetic correlations and low heritabilities for some of the traits.

Key Words: Mastitis resistance, Selection, Norwegian dairy cattle

510 Associations of lactoferrin concentrations in milk with indicators of mastitis in dairy cows.

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Objectives were to determine levels of lactoferrin in milk and associations of lactoferrin with mastitis indicators. Milk samples were collected from 180 Holstein cows in the Iowa State University genetic research herd. For each cow, one 60 ml aliquot was evaluated for milk constituents by a commercial milk testing laboratory, and one 5 ml aliquot was frozen immediately for subsequent analysis for lactoferrin. Lactoferrin in milk was quantified by sandwich ELISA (Bethyl Laboratories, TX). A standard curve ranging from 7.8 - 500 ng/ml lactoferrin was used on each plate. Milk samples were diluted at 1:2000 (milk:diluent) in 10% Tween 20, 1% BSA, 50 mM Tris pH 8.0. Detection antibodies were conjugated with horseradish peroxidase. The substrate, 3,3',5,5'-tetramethyl-benzidine, was used to detect the bound detection antibodies. Samples were read in a microtiter plate at a wavelength of 450 nm. Detailed mastitis treatment records for 2002 were acquired and used to determine incidence of mastitis, number of days treated, and mastitis severity for individual cows. Projected mature equivalent fat corrected milk (FCM) and lactation average somatic cell score (SCS) were obtained from Dairy Herd Improvement records. Means for mastitis incidence, days treated, and lactation average SCS were .94, 19.3, and 3.2, respectively. Several chronic cows skewed results for days treated consequently this variable was transformed using the natural log function. Mean lactoferrin was .336 mg/ml (SD = .222 mg/ml). Highest FCM was associated with lowest concentration of lactoferrin in milk. Lactoferrin levels were lowest for youngest cows ($P < .01$). Stage of lactation was not important for lactoferrin concentration when cows with 10 or fewer days in milk were eliminated from the analysis. Correlations of mastitis indicators with lactoferrin and SCS measures were similar and indicated that highest days treated was associated with highest lactoferrin and highest SCS ($P < .05$). Correlation of lactoferrin and lactation average SCS was .36. In this small data set, heritability for lactoferrin was considerably higher than estimates for SCS related measures. Lactoferrin may be useful for genetic selection to control increases in mastitis that accompany selection for high yields.

Key Words: Lactoferrin, Mastitis, Somatic cell score

511 Measure of the impact of somatic cell count on longevity of Holstein and Jersey cows using survival analysis.

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Survival analysis through a Weibull proportional hazards model was applied to evaluate the effect of somatic cell count (SCC) on survival of 1,892,919 Holstein and 250,835 Jersey cows with first calving from 1990 to 2000 in the United States. Herds were divided in 5 levels for Holsteins (2 replicates per level) and 3 levels for Jerseys by average somatic cell count. Survival was defined as days from first calving until culling or censoring corrected for 305-d mature equivalent milk production. Our model included time-dependent effects of herd-year-season, parity-stage of lactation and within-herd-year quintiles for mature equivalent milk production, as well as the time-independent effect of age at first calving. Different rho and gamma parameters for the Weibull distribution were estimated for each of the herd levels. SCC was divided into 15 classes and its impact on functional survival, after accounting for all other factors listed above, was evaluated. Survival analysis methodology allowed a nonlinear relationship between SCC and longevity. Average censoring and failure time decreased as average SCC level of the herd increased. Results showed differences between levels of herds in the risk of culling; cows in the high SCC class had 3.4, 2.7, and 2.3 for Holsteins and 4.0, 2.9 and 2.2 for Jerseys times higher risk of being culled than cows in the average SCC class in herds with low, medium and high average SCC, respectively. This suggests stricter culling for SCC in herds with low average SCC. Cows in the lowest class for SCC also showed higher risk of culling than cows in the average SCC class, particularly in herds with high average SCC.

Key Words: Survival analysis, Somatic cell count, Longevity

512 Effect of synchronization protocols on genetic parameters of reproductive traits in dairy cattle.

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Genetic evaluation for female reproduction is one strategy for improving performance. Many producers utilize synchronization of ovulation or estrus to manage reproduction. Our objective was to examine the effects of synchronization protocols on parameter estimates of days to first breeding (DFB). Data were collected from producers participating in an AI progeny testing program, and utilizing DC305 herd management software to record reproductive treatments and events. Analysis was performed on 13,134 records from 42 herds. Data were split into

three subsets: all first breedings (ALL), non-synchronized first breedings (NSYN), and synchronized first breedings (SYN). DFB was truncated to range from 25 to 300 d, with overall mean 73.9 d and SD of 26.9 d. NSYN data consisted of 7760 records with mean 73.0 d and SD 31.1 d. SYN data consisted of 5374 records with mean 75.2 d and SD 19.3 d. Only the earliest parity for each cow was included. Both animal and sire models were used to estimate genetic parameters. Fixed effects for both models were herd-year-season, parity, and calving age. Random effects were animal or sire. SYN was included as a fixed effect in the models of ALL. Variances were calculated using the REMLF90 program of Misztal. Heritabilities may be higher in SYN than in NSYN, ranging from 0.024 to 0.080 (Table 1). Variances were substantially lower in SYN records (Table 1). The SYN and NSYN data should be analyzed as different traits, or may be combined with an adjustment for heterogeneous variances.

	Sire var.	Sire model Residual var.	Heritability	—	Animal var.	Animal model Residual. var.	Heritability
ALL	4.914	469.1	0.041	—	30.95	442.5	0.065
NSYN	3.729	624.4	0.024	—	33.52	593.8	0.053
SYN	2.218	181.9	0.048	—	14.82	169.3	0.080

Key Words: Days to first breeding, Heritability, Synchronization

513 The effect of using body condition score and dairy character as indicators for genetic resistance to diseases in Danish Holstein.

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The aim of this study was to investigate the genetic relationship between body condition score (BCS), dairy character (DC), mastitis and other diseases than mastitis in first parity Danish Holsteins in order to explore the possibilities for using BCS and DC for indirect selection for disease resistance. The data set included 30,470 records on conformation scores and 366,286 on diseases. Mastitis was defined in the period from #10 to 50 days from calving (MS50) and other diseases were defined in the period #10 to 100 days from calving (OD100). Both traits were bivariate. These definitions are adapted from the current Danish evaluation system. A multivariate linear sire model was fitted and (co)variances were estimated using REML. The fixed effects were herd-year-season and age in months at calving for all traits. In addition fixed effects of classifier and regression on days in milk at classification was included for BCS and DC. The accuracy of an index for disease resistance with direct (OD100) and indirect (BCS and DC) information sources with different size of progeny group was estimated. By including DC as an indicator for diseases, the accuracy of the index for diseases increased especially when the progeny group was small and even when direct information on diseases was included. Using BCS as an additional indicator of diseases did not increase the accuracy. Breeding for cows with less DC is a way to achieve a cow genetically more resistant to diseases.

Trait	BCS	DC	OD100	MS50
BCS	0.25 (0.027)	-0.37 (0.01)	-0.05 (0.002)	0.008 (0.007)
DC	-0.60 (0.06)	0.22 (0.025)	0.03 (0.007)	0.010 (0.007)
OD100	-0.21 (0.10)	0.44 (0.09)	0.022 (0.004)	0.011 (0.007)
MS50	-0.15 (0.09)	0.22 (0.09)	0.31 (0.07)	0.036 (0.004)

Heritabilities (diagonal), genetic (below diagonal) and residual (above diagonal) correlations.

Key Words: Body condition score, Dairy character, Disease resistance

514 Comparison of First-Parity Holstein, Holstein-Jersey crossbred, and Holstein-Normande crossbred cows for dystocia and stillbirths.

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First-parity Holstein, Holstein-Jersey crossbred, and Holstein-Normande crossbred cows calving from June 2001 to December 2002 were compared for dystocia and stillbirths from six California herds. Dystocia scores ranging from 1 (no assistance) to 5 (hard pull) and stillbirths (1 for alive and 0 for dead) were recorded for 1268 Holstein cows, 243 Holstein-Jersey cows, and 66 Holstein-Normande cows. Cows were bred to Brown Swiss, Holstein, Jersey, Montbeliarde, Normande, and Scandinavian Red sires. Investigated were effects of calf sex, breed composition of cow, age at calving, breed of service sire, sire of calf within breed composition, and herd. For dystocia, sex of calf, and herd were significantly different (P<.01). The least squares mean for calf sex were 1.71 for males and 1.35 for females. Breed composition of dam did not differ significantly, however, there was a tendency for less calving complications for the crossbred cows compared to Holsteins. Mean scores were 1.59 (H) 1.46 (HxJ), and 1.54 (HxN). Brown Swiss sired calves (1.64) differed significantly (P<.05) from Jersey sires (1.32), and Brown Swiss sires differed (P<.02) from Holstein (1.67) sires. For stillbirths, calf sex, age at calving, and breed of sire were significantly different (P<.01). Male calves (14%) had higher stillbirths than females (3%). Holstein sires had the highest rate of stillbirths (15%), and rates for the other breeds of sires were 8% for Brown Swiss, 8% for Jersey, 12% for Montbeliarde, 4% for Normande, and 6% for Scandinavian Red sires. Holstein sires differed significantly from Normande (P<.05) and Scandinavian Red (P<.01) sires. Montbeliarde differed significantly (P<.05) from Scandinavian Red sires. Although not significantly different, Holstein cows had 12% stillbirths, Holstein-Jersey cows had 9% stillbirths, and Holstein-Normande cows had 6% stillbirths.

Key Words: Crossbreeding, Dystocia, Stillbirths

515 Effect of mating Holstein females to Holstein versus Jersey AI sires on fertility, dystocia, calf weight, and retained placenta.

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First services from AI were recorded on 270 Holstein cows and on 181 Holstein heifers. One half of cows and heifers were mated to Holstein AI sires and the other half were bred to Jersey AI sires. Cows and heifers were randomly assigned to either a Holstein or Jersey service sire, except coefficients of inbreeding were not allowed to surpass 6.25% for mating of Holstein sires to Holstein females. First service conception rates did not differ by breed of service sire for lactating cows. For virgin heifers, Holstein sires had significantly higher first service conception rates than Jersey sires (P<.01). From September 2001 to January 2003, 135 Holstein and 152 Holstein-Jersey crossbred calves were born at the University of Minnesota research herds at the St. Paul campus and at the West Central Research and Outreach Center, Morris. Dystocia was scored with a range of 1 (no assistance) to 5 (hard pull). Mean dystocia score was 1.65. Independent variables for analysis were herd, parity (1st versus 2nd and later), sex of calf, and breed of sire. Differences between Holstein and Jersey sires were significant for dystocia score, calf weight, and retained placenta (P<.05). Least squares means for Holstein and Jersey sires, respectively, were dystocia score, 1.94 versus 1.32; calf weight, 43.5 kg versus 35.6 kg; and retained placenta, 6.5% versus 1.0%. Stillbirth rate was 8.6% for Holstein sires and 6.7% for Jersey sires, but not significantly different (P>.05).

Key Words: Crossbreeding, Dystocia, Fertility

516 Genetic correlation estimates among body condition score, dairy form, days open and production traits for US Holsteins.

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The objectives of this study were to estimate genetic correlations among body condition score (BCS), dairy form (DF), days open (DO), ME milk, ME fat and ME protein production. Body condition score and DF obtained from the Holstein Association USA Inc. were merged with DO and production data from the Animal Improvement Programs Laboratory at USDA. Edits applied to the data included: a valid BCS observation, a minimum of 20 daughters per sire, a minimum of 10 cows per herd-classification visit (HV) or herd-year-season of calving (HYS), age between 24 and 60 months at classification, less than 336 days in milk (DIM) at classification and minimums of 25 days open and 4,537 kg of ME milk. Only one record per cow was used and DO greater than 250 were set to 250. The final data set included 166,222 records. Fixed effects were age within lactation group, 5th order polynomials of DIM and HV for BCS and DF, age within lactation group and HYS for production traits and lactation number and HYS for DO. Random sire and error were included for all traits and all analyses were performed with AS-REML. Heritability estimates ranged from 0.04 for DO to 0.30 for ME protein. The genetic correlation estimate between BCS and DO was

-0.33. The genetic correlation estimate between DF and DO was 0.51. The genetic correlation estimate between BCS and DO was -0.10 when DF was included as a covariable and the genetic correlation estimate between DF and DO was 0.49 when BCS was included as a covariable. Genetic correlation estimates among BCS and production traits ranged from -0.20 to -0.30, whereas genetic correlation estimates among DF and production traits ranged from 0.41 to 0.52. These genetic correlations can be used to help develop appropriate weights for an index that includes days open evaluations. Using dairy form evaluations as an indicator trait would increase the accuracy of days open evaluations for newly proven bulls.

Key Words: Body condition score, Dairy form, Days open

517 Seasonality of days open in US Holsteins.

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The objectives of this study were to establish a pattern for the seasonality of Days Open (DO) by state and region within the US and to present statistics on regional trends for DO. Data included 6,871,265 records from 1998 to 2001. Fixed effects in the model included region, herd, year and month of calving (MOC), parity, milk-class, region*MOC, herd*MOC, year of Calving*MOC and parity*MOC. Results showed that DO were longest for March/April and shortest for September/October calvings for all regions, years and parities. Regional mean DO were 156 (Southeast), 145 (Midwest), 142 (Northeast), 143 (Northwest), and 140 (Southwest). Mean DO by state ranged from 135 (AZ) to 161 (FL). States with DO $>$ 150 included: KY, OK, TX, and most parts of the Southeast. Monthly variations by state ranged from 7 (OR) to 64 (AR, MS). States with monthly variations $>$ 40 d were AZ, MO, AR, OK, TX, GA, SC, NC, MS, AR, TN, AL and LA. Regularity of calving was computed as the ratio of calvings in months with the least and most calvings. Regularity varied from 0.16 (LA) to 0.88 (MA). It was below 0.4 for AZ, TX, OK and all of Southeast. Exceptions in the general patterns were FL, where regularity was higher and variations of DO were lower than in adjacent states, and in CA, where, despite hot weather, regularity was high and variations were low. Studies on the effect of heat stress on days open in the Southeast are limited by the small number of cows compared to other regions and by low fraction of cows bred during the peak of heat stress. Therefore, such studies could use data from all regions associated with hot weather including lower Midwest and parts of Southwest.

Key Words: Days open, Seasonality, Month of calving

518 A new genetic evaluation for calving ease in the Italian Holstein.

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The first genetic evaluation for calving ease was published around 1992. Data collected by milk recording agencies define calving difficulty based on 5 classes: A for easy calvings, B for calvings that required the assistance of one person, C for caesarean birth, D for difficult calving and E for embriotomy. These data were linear transformed on a scale from 0 to 100. Breeding Values were calculated using a sire model that included the environmental effects of herd-year and age-sex-month of calving. The new evaluation is based on the same data, edited for a higher standard of quality. The model used is a threshold model analysing three classes of difficulty: A, B and C and over. Environmental fixed effects in the model are: year-month, province-year, sex-parity-age. Herd year is an environmental random effect. Heterogeneity of variance is considered in the model for sex, province and year. Genetic random effects in the model are sire and maternal grand sire. Heritability estimates are 0.07 for direct sire effect and 0.027 for the maternal effect. Genetic correlations were 0.20 and -0.53 for sire-maternal grand sire and direct-maternal respectively. Correlation with breeding values computed using the old linear model were around 0.83 mainly due to data editing. The new model will be used for the official genetic evaluation before the end of year 2003.

Key Words: Genetic evaluation, Calving difficulty, Threshold model

519 Characteristics of genetic evaluations for daughter fertility in relation to other fitness traits.

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Considerable attention is being focused on cow fertility because of the initiation of genetic evaluations for daughter pregnancy rate (DPR) in February 2003. In order for a new trait to be accepted, the industry needs to understand its characteristics. Properties of DPR evaluations were compared with those of evaluations for other fitness traits introduced during the last decade. For cows born during 1988, 1993, and 1998, predicted transmitting abilities (PTA) for DPR averaged 0.9, 0.5, and 0.4%, respectively, which reflected a negative genetic trend. Cow PTA for somatic cell score (SCS) also had a small unfavorable trend, but cow PTA for productive life (PL) has been improving. Mean reliability (REL) for cow PTA DPR is nearly as high as REL of PTA for PL and SCS even though based on a lower heritability (0.04 for DPR compared with 0.085 for PL and 0.10 for SCS), partly because of additional observations on fertility in later lactations or because of its lower repeatability. For 1988, 1993, and 1998 birth years, cow REL DPR was 32, 32, and 30%, respectively, compared with REL PL of 33, 32, and 31% and REL SCS of 32, 35, and 34%. For artificial-insemination (AI) bulls born during 1984 through 1988 ($n = 6037$), 1989 through 1993 ($n = 7247$), and 1994 through 1998 ($n = 5425$), PTA DPR averaged 0.1, 0.0, and -0.2%, respectively. Similar to cow PTA, bull PTA SCS showed a small unfavorable trend (3.11, 3.11, and 3.13), whereas PTA PL have been improving (-0.47, 0.01, and 0.14 mo). Mean bull REL DPR were 67, 67, and 59%, respectively; mean REL PL were 67, 67, and 61%, and mean REL SCS were 68, 73, and 69%. Effects of birth year and AI sampling organization on bull PTA DPR was examined. Birth year accounted for 2.6% of variation in DPR; AI sampling organization accounted for additional 0.3%. Those same effects accounted for 5.8 and 0.1%, respectively, of PL variation and for 1.1 and 0.4% of SCS variation. For bulls in active AI service, no differences were found between AI sampling organizations for DPR, although an effect was found for PL and SCS. Based on REL alone, reservations about using PTA DPR in selection programs because of its limited accuracy appear to be unwarranted.

Key Words: Daughter pregnancy rate, Productive life, Somatic cell score

520 Definition of traits and comparison of models for genetic evaluation of cow fertility.

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Cow fertility and longevity traits often have distributions similar to coin tosses that are repeated if tails are observed. Methods to evaluate repeated binomial observations were compared by simulation. Dependent variables included 21-d pregnancy rate, length of time to achieve pregnancy, and log of length of time. Pregnancy rate and average number of 21-d opportunities required to achieve pregnancy are reciprocals, but the product-moment (linear) correlation of true transmitting abilities was -0.987 rather than -1.00 because of curvature. An evaluation of pregnancy rate in which lactations received more weight if the cow required more cycles to become pregnant was preferred slightly to an unweighted evaluation but was not more accurate than evaluation of days open. Of the several models of analysis compared in simulation, none had an accuracy advantage of $>$1% over the others. With actual days-open data, heritability decreased from 4.1 to 3.0% when the upper limit on days open was increased from 150 to 305 d, probably because heritability of days to first breeding is higher (6.6%). The economic benefits of very early pregnancy are not as great as the costs of delayed pregnancy. Thus, breeding dates up to 250 d (rather than 150 d) are used routinely so that the more severe fertility problems are identified. As compared with days open or calving interval, pregnancy rate can be computed sooner, cows that do not become pregnant are included more easily, and larger rather than smaller values are desirable. Pregnancy rate can be obtained from days open using a nonlinear formula, pregnancy rate = 21/(days open – voluntary waiting period + 11), or by a linear approximation, pregnancy rate = 0.25(233 – days open), obtained from the derivative of the nonlinear formula evaluated at the mean. Voluntary waiting period is the initial phase of lactation during which no inseminations occur (assumed to be 60 d) and the factor of +11 adjusts to the middle day of the 21-d cycle. With either formula, 154 days open

converts to a pregnancy rate of 20% and 133 days open to a pregnancy rate of 25%.

Key Words: Genetic evaluation, Cow fertiltity, Pregnancy rate

521 Quality of data included in genetic evaluations for daughter pregnancy rate. P. M. VanRaden, M. E. Tooker*, A. H. Sanders, and G. R. Wiggans, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*.

National genetic evaluations of daughter pregnancy rate are based on data from 40 million lactation records of 16 million cows that calved since 1960. Up to five lactations are included per cow. Date pregnant is determined from several data sources. The most accurate information is last insemination date verified by birth date of next calf within 15 d of expected birth date. For lactations with no reported inseminations, date pregnant is obtained by subtracting mean gestation length (280 d for Holsteins) from next calving date. For lactations without next calving date, date pregnant is assumed to be the last insemination date unless the cow was subsequently examined and verified not pregnant, or was still milking in the same lactation more than 295 d after the last insemination. Last reported breeding date is used if the next lactation is initiated by abortion. A final data source is an owner report that the cow was sold because of infertility. Such cows are assumed to be nonpregnant and the last insemination date is disregarded. Records for pregnancy rate are considered to be complete at 250 d in milk (DIM), and pregnancy status after 250 DIM is not used. Date pregnant is set equal to 50 DIM for cows that become pregnant before 50 DIM. Some early pregnancy dates calculated from next calving date are inaccurate because of short gestations or unreported abortions. Therefore, lower and upper limits of 50 and 250 DIM, respectively, were applied after adjusting days open for season effects; 5 and 14% of records were affected. For Holstein calvings during 1998 and 1999, 57% had breeding date verified by calving date; 6% had next calf born with no previously reported breeding date; 5% had breeding date inconsistent with birth date of next calf; and 5% had the cow reported as sold for reproductive reasons. Although 19% of reported final breeding dates could not be verified because the cow was sold for reasons other than fertility, comparisons with birth date indicate that most farms report accurate breeding dates.

Key Words: Genetic evaluation, Fertility, Pregnancy rate

522 Use of early lactation days open records for genetic evaluation of cow fertility. M. T. Kuhn* and P. M. VanRaden, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*.

National genetic evaluation for female fertility was implemented in February 2003. The evaluations are reported as daughter pregnancy rate. Pregnancy rate is calculated from days open (**DO**) as (233 – DO)/4. Currently, records must have a minimum of 250 days in milk (**DIM**) to be included for genetic evaluation. Furthermore, DO is set to 250 for records that go beyond that upper limit. This research examined the possibility of using DO records prior to 250 DIM by predicting unknown records. The prediction model included the fixed effects of lactation and calving ease and linear regressions on age at calving, average of first three test day milk yields, previous DO, previous number of services, and days to first breeding. Quadratic effects of age and milk yield were also included. To assess the utility of the predictions, 10 DO groups were formed by defining the first group as 70 days or less and subsequent groups in 20 day increments. The final group was defined as $\geq$ 250-d. Each record was included in each group. Within group, y-hat was defined as actual DO if actual DO was $\leq$ the upper limit for that group or projected DO otherwise. Bias, standard deviation of prediction errors, and phenotypic correlations between y-hat and actual DO were calculated for each group. Genetic correlations were estimated for the groups with 90, 130, and 170 day upper limits. Bias ranged from 30 d (70-d group) to 0 d and was close to 0 d starting with the 110-d group. Standard deviation of prediction errors ranged from 49 d to 14 d. Phenotypic correlations increased from .41 (70-d) to .98 (250-d). Estimates of genetic correlations were 1 in all 3 groups examined. These results suggest that DO records can be utilized prior to the current 250-d requirement. Projected records require a weight less than one in genetic evaluation. Weights can be determined from correlations between actual and predicted records. Pregnancy confirmation code, now being collected, will also contribute to determination of weights.

Key Words: Genetic evaluation, Cow fertility, Prediction

Food Safety: On farm food safety: Assessment of costs, tools and management

523 Economic assessment of food safety in the dairy chain. N. Valeeva*, M. Meuwissen, and R. Huirne, *Wageningen University, Wageningen, the Netherlands*.

As a result of the increased demand for food safety, a number of quality assurance regulations have been introduced all over the world. However, little is known about the costs and efficiency of implementing such regulations, especially with regard to the entire chain. The objective of this research was to develop a mathematical programming model to identify measures for increasing the level of food safety in the dairy production chain in a cost-effective manner. The chain included compound feed production and its transport, the dairy farm itself, transport of raw milk, processing, delivery of (pasteurized) milk, and the retailer and catering sectors. The model focused on two main groups of hazards: microbial (*Salmonella, E. coli, M. paratuberculosis* and *S. aureus*) and chemical (antibiotics and dioxin). In collecting input data for the model, special attention was given to the costs of the various measures and the effectiveness of these measures in increasing the food safety level. Costs included implementation and maintenance of these measures (including interest and depreciation costs). Effectiveness was measured by adaptive conjoint analysis as the relative contribution of each measure to the food safety level. An electronic questionnaire was completed by 67 experts from industry, research, extension and farming who evaluated the measures in four steps. Linear regression analysis was then performed to determine the relative contribution (i.e. so-called utility level) of each measure. Respondents were consistent (R-squared > 0.8) with respect to their individual responses. Relative contributions and cost estimates were used in the mathematical model to determine the optimal set of measures for various food safety levels. Results showed that the dairy farm (42%) and dairy processing (24%) stages are most important for reducing microbial hazards. In contrast, the compound feed (43%) and dairy farm (39%) stages are most important for reducing chemical hazards. Overall, an increase in the higher levels of food safety was associated with a steep non-linear increase in costs.

Key Words: Food safety, Dairy chain, Economics

524 Bactericidal efficacy of quaternary ammonium compounds against species of bacteria isolated from feces of dairy cattle. A. A. Sawant*, N. V. Hegde, S. C. Donaldson, K. B. Buck, and B. M. Jayarao, *Pennsylvania State University, University Park, PA*.

Quaternary ammonium compounds (QAC) are widely used as disinfectants in dairy, meat-packing, and food processing industry. QACs have been shown to be more effective against gram-positive than gram-negative bacteria. In a dairy setting, gram-negative organisms are the major microflora in the environment. There is very little information on the MIC_{90}values of gram-negative bacteria of dairy origin to QACs. A study was conducted to assess the susceptibility of gram-negative bacteria isolated from feces of lactating cattle to QACs. Gram-negative bacteria including *Escherichia coli* (n=186), *Citrobacter koseri* (n=14), *Enterobacter aerogenes* (n=3), *Klebsiella oxytoca* (n=3), and *Pseudomonas* spp. (n=6) were examined for their susceptibility to cetyltrimethylammonium bromide (CTAB), benzalkonium chloride (BKC), and benzyldimethylhexadecyl ammonium chloride (BDAC). The MIC_{90} modal values for *E. coli* were 60μg/ml for BKC (range 30 - >80), 60μg/ml for CTAB (range 50-700), and 400μg/ml for BDAC (range 100 - >800). *Pseudomonas* spp. showed high MIC_{90} values for BKC ($\geq$80μg/ml), CTAB ($\geq$700μg/ml), and BDAC ($\geq$700μg/ml). *Citrobacter koseri*, *E. aerogenes*, and *K. oxytoca* showed MIC_{90} $\geq$30μg/ml for BKC, $\geq$300μg/ml for CTAB, and $\geq$600μg/ml for BDAC, respectively. The presence of *qacE* gene in *E. coli* was detected in 80 of 186 (43%) of the *E. coli* isolates. The *qacE* gene was also detected in other species except *E. aerogenes*. Results of the study suggested that: (1)