

1012 Genotype by country interactions for growth traits in Charolais populations across four countries. K. A. Donoghue* and J. K. Bertrand, *University of Georgia, Athens GA.*

The importance of genotype by country interactions was evaluated for data from Charolais associations in Australia (AUS), Canada (CAN), USA and New Zealand (NZ). Data were composed of edited birth and weaning weight and postweaning gain records from the four countries. Only herds with more than 500 trait records, with an average contemporary group size greater than 9 animals, and that had trait records from progeny of 66 international sires were used in this study. Pairwise country samples were created that ranged from 20000 to 30000 trait records and a multiple trait animal model that considered each trait as a different trait in each country was used to estimate parameters in each pairwise analysis. Direct and maternal (in parentheses) estimated genetic correlations for birth weight for AUS vs. CAN, AUS vs. USA, USA vs. CAN, NZ vs. CAN and NZ vs. USA were 0.88 (0.86), 0.85 (0.82), 0.88 (0.82), 0.85 (0.83), and 0.84 (0.80), respectively. Direct and maternal (in parentheses) estimated genetic correlations for weaning weight for AUS vs. CAN, AUS vs. USA, USA vs. CAN, NZ vs. CAN and NZ vs. USA were 0.96 (0.91), 0.95 (0.90), 0.95 (0.91), 0.95 (0.92), and 0.95 (0.92), respectively. Direct estimated genetic correlations for postweaning gain for AUS vs. CAN, AUS vs. USA, USA vs. CAN, NZ vs. CAN and NZ vs. USA were 0.89, 0.91, 0.94, 0.90, and 0.91, respectively. Direct and maternal heritabilities were similar across all countries for birth and weaning weight, while direct heritabilities for postweaning gain in AUS and NZ were slightly lower than those in CAN and USA. The absence of genotype by country interactions observed in this study strongly indicates that a joint genetic evaluation for growth traits for Charolais populations could be conducted. A model that treated information from AUS, CAN, USA and NZ as one population, while adjusting for possible heterogeneous variances, could be implemented for this purpose.

Key Words: Genotype by Country Interaction, International Evaluation, Beef Cattle

1013 Evaluation of milk yield and udder characteristics in beef cows sired by high or low Milk EPD bulls. K. J. Stutts* and D. S. Buchanan, *Oklahoma Agricultural Experiment Station, Stillwater, OK.*

Maternal milk is an important influence on weaning weight that affects production efficiency in beef herds. The objective of this study was to evaluate High and Low Milk EPD sires for milk production and udder characteristics of their daughters. Cows used in this study were produced through the mating of Angus and Hereford bulls that differed in Milk EPD level to Hereford-Angus and Hereford-Angus-Brahman cows. They ranged in age from 7 to 11 yr old. All cows were bred by artificial insemination to South Devon bulls and calves were born in the spring from early February to early April. Milk production data were collected 7 times prior to weaning at 28 d intervals using the weigh-suckle-weigh method. The final milk production data corresponded to a 205-d weaning age for all calves. Udder measurements and scores were taken during periods 3 and 6 after complete removal of milk from the udder by suckling. Cows were restrained in a squeeze chute and visual conformation scores were given to each teat and the udder. Linear measurements were taken on the length of each teat, distance between the front teats, distance between the rear teats, and the diagonal distance from the left front to the right rear teat. Data were analyzed using least squares. Factors included in the model were breed, Milk EPD level, sex of calf, age of dam, and all two-way interactions. Age of calf was included as a covariate. High Milk EPD cows produced more milk than Low ($P < .05$), but there was not a difference ($P = .71$) in milk production between breeds. The interaction between breed and Milk EPD level was approaching significance ($P = .15$). Hereford sired cows had longer teat length ($P < .02$) and higher (more pendulous) udder scores ($P < .05$) than Angus. Low Milk EPD cows had slightly lower udder scores than High ($P < .10$). These results further confirm the utility of Milk EPD to predict milk production differences and provide only small evidence that there may be a negative effect on udder conformation for older High Milk EPD cows.

Key Words: Beef Cattle, Milk Production, Udder Characteristics

ASAS/ADSA Breeding and Genetics: Genetic Parameters of Dairy Cattle

1014 Possibilities for genetic improvement of fertility in US dairy cattle. K. A. Weigel*¹ and J. S. Clay², ¹*University of Wisconsin, Madison*, ²*Dairy Records Management Systems, Raleigh, North Carolina.*

Interest in improving conception rates has skyrocketed in recent years. Direct costs of poor fertility include increased semen costs, veterinary costs, days open, and involuntary culling. Indirect costs include reduced genetic progress due to a larger number of repeat inseminations and an increased proportion of pregnancies to genetically inferior natural service bulls. Selection for male (service bull) fertility is possible using Estimated Relative Conception Rate data from Dairy Records Management Systems. Service bulls are evaluated for 70-day non-return rate on first inseminations. Evaluations for all bulls with at least 300 inseminations in the past three years are published. Sire evaluations for female (daughter) fertility are not yet available, but a system is under development. Female fertility can also be measured as 70-day non-return rate; in this case male and female fertility can be analyzed jointly using a maternal effects model. Days to first insemination can also be evaluated, but measurements may be biased by the use of heat synchronization products. In a pilot study, male and female fertility were evaluated as 70-day non-return rate using 8.03 million insemination records from 1995 to present. The range in daughter fertility PTA for Holstein sires was roughly 10%, similar to the range in service bull fertility solutions. The correlation between male and female fertility solutions of Holstein sires was 0.02, and the correlation between female fertility and PTA milk was 0.09. Therefore, it will be possible to improve conception rates with little or no loss in genetic merit for milk yield by practicing secondary selection for male and female fertility. Fertility evaluations can be improved by increasing the quantity and quality of DHI insemination data, by utilizing repeat service data, and by considering models that account for the binary nature of the data.

Key Words: genetic selection, fertility, dairy cattle

1015 Effect of heat stress on Non-Return rate in Holstein cattle. O Ravagnolo and I Misztal*, *The University of Georgia, Athens, GA.*

The objective of this study was to examine the relationship between reproductive traits and heat stress. Non-return rate at 45 days (NR45) was analyzed in a fixed effect model that included Temperature Humidity Index from a nearby weather station as a measurement of heat stress. Data consisted of 150,200 first inseminations at first and later parities of 110,860 Holstein cows from 550 herds in Georgia, Tennessee and Florida with weather information from 16 weather stations. THI on the day of the insemination, 2 days prior, 5 days prior, 10, 20 and 30 days after insemination were studied as independent variables. THI on the day of insemination showed the highest effect on NR45, followed by 2 days prior, 5 days prior and 5 days after insemination, but no relationship was found with THI at 10, 20 and 30 days after insemination. NR45 showed a decrease of 0.005 per unit increase in THI on the day of insemination for THI > 68. First and later parities presented similar thresholds but responded differently to increase in THI, with NR45 being significantly lower and more susceptible to increases of THI in cows in their first parity than in later parities (0.008 vs. 0.005 decrease per unit THI). Threshold for sensitivity to heat stress changed with the states, with FL, GA, TN having thresholds of 66, 70 and 70 respectively. The decrease in NR45 per unit increase of THI was 0.006, 0.005 and 0.007 for FL, GA and TN respectively (or a total of 0.07, 0.07 and 0.10). On the TN data only, the final fixed effect model used was $NR45 = \text{Herd}(\text{Year}) + \text{Month}(\text{Year}) + \text{age}(\text{parity}) + \text{days in milk} + 100\text{d milk} + \text{THI} + \text{error}$. Animals with more than 150 DIM had a 0.16 lower NR45 than animals with less than 60 days in milk at insemination. Lower milk producing animals showed 0.08 higher NR45 than higher producing animals. A difference of 0.10 in NR45 was observed between THI lower than 70 and THI 84. This variation in NR45 due to THI changes is sufficient to merit further studies to examine genetic components for heat tolerance for this trait.

Key Words: Heat Stress, Non-return rate, Holstein

1016 Analysing survival score and calving interval as a measure of fertility in Holstein Friesian cows in seasonal calving herds. V.E. Olori*¹, T.H.E. Meuwissen², and R.F. Veerkamp², ¹*Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland*, ²*Institute for Animal Science and Health, ID-Lelystad, Lelystad, The Netherlands*.

In a grass-based production system with seasonal calving, fertility is of major economic importance especially as a delay in conception can lead to culling and a shift in calving pattern. Calving interval (CI) information is readily available from milk records, analysing it presents a problem however as it can only be derived for cows that conceive and calve again. Therefore, calving interval should be treated as a censored trait, with survival to the next lactation (SU) being the censoring variable. These two traits are analysed in this study with a multivariate model to account for the non-random scoring of the CI. Genetic parameters and breeding values (EBVs) for CI and SU were estimated with a sire model for 1st lactation Holstein Friesian cows in Ireland. SU was pre-adjusted for milk yield within HYS. Milk yield was included as a third trait in the analysis because of the large effect it has on both CI and SU. The residual covariance could not be estimated because CI was only known for cows with a SU score of 1 thus this covariance was assumed to be 0. The h^2 was 0.04 for CI and 0.01 for SU with a genetic correlation of -0.28. Genetic standard deviation was 4% for SU and 7 days for CI. EBVs for about 1000 bulls with at least 20 daughters, ranged between -3.28% and 4.22% for survival rate and between -8 and 15 days for CI indicating a difference of about 8% and 23 days between the best and worst bulls. Inter-quartile range was 1.4% and 3.3 days for SU and CI respectively. The current model is expected to recover most of the genetic variation in fertility that can be recovered from calving dates, and future extensions, i.e. use of linear type trait or additional lactations for survival, appear straightforward. These traits now form part of the national index for selecting dairy cows and bulls in Ireland.

Key Words: Cow Fertility, Calving Interval, Survival rate

1017 Correlations among body condition score change, body condition score, production and reproductive performance. C. D. Dechow*¹, G. W. Rogers¹, and J. S. Clay², ¹*Pennsylvania State University*, ²*Dairy Records Management Systems*.

The objectives of this study were to estimate correlations among body condition score change (BCSCH), body condition score (BCS), production and reproductive performance. Producer-recorded BCS were obtained from Dairy Records Management Systems in Raleigh, NC through the PCDART program. Body condition scores were available at both calving (C) and postpartum (PP) for 7,424 cows in first lactation and 6,092 cows in second lactation. An additional 13,196 cows in first lactation and 10,053 cows in second lactation had BCS at C or PP only. Body condition score change was defined as BCS at C minus BCS at PP. Mature equivalents (ME) for milk, fat and protein, days to first service (DFS) and services per conception (SPC) were available. Heritabilities and correlations were estimated assuming bi-variate animal models using Average Information REML. Models included herd-year-season, age at calving, prior calving interval and random animal effect. Non-productive traits were analyzed with and without ME milk as a covariable. Initial correlations between BCS and BCSCH were obtained using all available observations. Additional estimates were obtained through pedigree linkages only by not allowing cows with BCSCH information to contribute BCS observations. Heritabilities estimates for BCSCH ranged from 0.02 to 0.07. Genetic correlation estimates between BCSCH and BCS at C ranged from -0.11 to -0.48. Genetic correlation estimates between BCSCH and BCS at PP ranged from -0.56 to -0.99. Phenotypic correlations between BCSCH and BCS were near 0.54 at C and -0.65 at PP. Genetic correlations between BCSCH and production traits ranged from 0.17 to 0.50. Genetic correlations between BCSCH and DFS ranged from 0.29 to 0.68. Selection for yield appears to increase BCS loss in early lactation by reducing BCS PP. More loss in BCS was correlated with an increase in DFS.

Key Words: Body Condition Score Change, Heritability

1018 Calving disorders of Holstein cows selected for large versus small body size. B.J. Heins*, L.B. Hansen, A.J. Seykora, and G.D. Marx, *University of Minnesota, St. Paul*.

Holsteins selected for large versus small body size since 1966 were evaluated for edema, retained placenta, dystocia, and stillbirths from the Northwest Outreach and Research Center, Crookston, of the University of Minnesota. Edema scores (1 as none to 5 as severe), placental scores (1 as cleaned normally to 5 as prolapsed), dystocia scores (1 as no assistance to 5 as pulled), and stillbirths (0 for alive or 1 for dead) were recorded for 1228 Holstein cows from 1985 to 2000 (born from 1983 to 1999). Records were for 542 first lactations, 320 second lactations, and 366 third or later lactations, and the three lactation groupings were analyzed separately. Investigated were effects of body size line, year of calving, body weight within line, age, sex of calf, and time of calving on the dependent variables: edema score, placenta score, dystocia score, and stillbirths. The large versus small size lines did not differ significantly for edema, retained placenta, or dystocia. However, there was a tendency for edema to increase with body weight within size line. Mean scores were 2.5 for edema, 1.3 for placenta, and 2.2 for dystocia. For dystocia, only sex of calf was significant ($P < .001$) for all lactation groupings. For first calving, the least squares mean for calf sex was 3.4 for males and 2.8 for females. Mean score for dystocia for the entire herd (both body size lines) tended to run higher than the national average and this might have resulted in higher stillbirth rates of calves. The correlation of dystocia and stillbirths was .32 and was highest for first calving. The unadjusted mean for stillbirth rate across all parities and both body size lines (14% for the large line and 10% for the small line) was 12%. The greatest incidence of stillbirths was for first-lactation cows at 23%. Incidence of stillbirth was 3% for second parity and 6% for third and higher parities. For first calving, the body size lines differed significantly ($P < .05$) for stillbirths, with least squares means of 29% for the large line and 22% for the small line. There was no significant trend with time for any of the four traits across the 16 years.

Key Words: body size, dystocia, stillbirths

1019 Genetic parameters for stillbirth in Dutch Black-and-White dairy cattle. A. Harbers*, L. Segeren, and G. De Jong, *CR Delta, Arnhem, The Netherlands*.

Data on stillbirth are recorded in the Netherlands but are not used for a genetic evaluation. Aim of this study was to estimate genetic parameters for stillbirth as a prerequisite for a genetic evaluation. Data included 1 million records of first parity (PAR 1) and 2.8 million records of higher parity (PAR ≥ 2) cows from 1994 onwards. Four different traits (first vs. higher parities and stillbirth as a direct vs. indirect effect) were considered. Heritabilities were estimated using a model with age at calving, parity, year of birth, month of birth, and herd by 2-year period as fixed effects. Random effects were included for sire (direct effect) or maternal grandsire (maternal effect) and residual. Breeding values for indirect effects were computed as maternal effect - 0.5 × direct effect. Genetic correlations were derived from breeding values of bulls adjusted for reliability. Unadjusted means are higher for first parities than for higher (11.4% vs. 5.3%). No phenotypic trend in stillbirth over time was found. Heritabilities range from 0.01 to 0.05. Stillbirth in PAR 1 has only a moderate correlation with stillbirth in PAR ≥ 2 (0.52-0.73), especially for the direct effect. The correlation between direct and indirect effects are -0.07 and -0.02 for PAR 1 and PAR ≥ 2 , respectively. Predicted transmitting abilities (PTA) of bulls range from -7% to +7% for both direct and indirect effects in PAR 1. In PAR ≥ 2 , PTA's range from -3% to +3% for direct and indirect effects. The results indicate that genetic variability for stillbirth exists, but heritabilities are low. Genetic correlations indicate that stillbirth in PAR 1 differ from stillbirth in PAR ≥ 2 . Genetic correlations between direct and indirect effect indicate that both traits can be improved independently. Based on these results a routine genetic evaluation of stillbirth in the Netherlands will be implemented in 2001.

Key Words: Stillbirth, Genetic parameters, Dairy cattle

1020 Timeliness of progeny testing through artificial insemination and percentage of bulls returned to service. H.D. Norman*¹, R.L. Powell¹, J.R. Wright¹, and C.G. Sattler², ¹Agricultural Research Service, USDA, Beltsville, MD, ²National Association of Animal Breeders, Columbia, MO.

Progeny-test (PT) programs of US artificial-insemination (AI) organizations were examined to determine timeliness, PT daughter distribution, and future use of PT bulls. Means, standard deviations (SD), and deciles for bull age at semen distribution, PT daughter birth, and PT daughter calving were calculated by breed (Ayrshire, Brown Swiss, Guernsey, Holstein, and Jersey) for bulls entering AI service since 1959. Mean Holstein bull age at semen distribution (16 mo) changed little over time, but SD decreased from 4 mo in the 1960s to 2.4 mo in the 1990s. Most bulls (80%) had semen released by 18 mo. Mean Holstein bull age at PT daughter birth and calving declined by 4 mo from the 1960s to the 1990s to 29 mo and 56 mo; SD decreased from 6 to 3 mo. Usually for other breeds, bulls were older at PT daughter birth and calving, and SD were larger. Mean Holstein bull age when 80% of PT daughters had been born declined from 36 mo in the 1960s to 31 mo in the early 1990s; for other breeds, bulls were older (36 to 41 mo). Mean Holstein bull age when 80% of PT daughters had calved declined from 65 mo in the 1960s to 59 mo in the 1990s; for other breeds, bulls were older (62 to 70 mo). Percentage of first-lactation Holstein cows that were PT daughters increased over time to 14%. For Holsteins, percentage of herds with five first-lactation records or more that were usable for evaluation but with no usable PT records decreased from 85% in 1965 to 39% in 1998, whereas percentages increased from 11 to 38% for herds with from 1 to 19% PT records and from 1 to 5% for herds with >50% PT records. Percentage of Holstein PT bulls returned to AI service declined from >50% for bulls with PT entry in 1965 to about 15% for bulls with PT entry around 1990; for other breeds, about 20% of recent bulls returned to service. More rapid sampling and increased selection intensity of PT programs have lead to more rapid genetic progress.

Key Words: Artificial insemination, Progeny test

1021 Adjustment for heterogeneity of genetic variance across herds in the Italian Holstein Friesian. F. Canavesi*¹, M. del P. Schneider¹, M. Cassandro², A. Bagnato³, and A. B. Samore¹, ¹ANAFI, Italy, ²University of Padova, Italy, ³University of Milan, Italy.

Heterogeneity of genetic and residual variances exists across herds in the Italian Holstein Friesian population. Residual standard deviations varied from 30 to 35 kg for protein yield and genetic standard deviations across classes varied from 20 to 24 kg. Consequently, heterogeneity of heritability (.30-.34) was observed. The official procedure for genetic evaluation in Italy pre-adjusts for phenotypic within herd variability. This procedure standardizes the residual variance but not the genetic, leaving unchanged the difference in heritability across herds and leading to possible bias in genetic evaluations if daughters of bulls are not randomly distributed across herds. Two methods to account for heterogeneity were tested: a multiple trait approach and a pre-adjustment that takes into account increase of heritability according to herd variability. Methods were compared in terms of sire rankings with the official genetic evaluation. Data used were from the February 1999 official evaluation. The multiple trait approach classified herds into categories of variability and lactations from different categories were considered as different traits. The genetic pre-adjustment of data followed the approach currently applied in the US for its official genetic evaluation. Heritability was assumed to increase with increased within herd variability. Both methods led to a greater representation of bulls in the top list from herds with lower genetic variability (+2/3 bulls) and the difference in kg of protein decreased by 1 kg on average. The multiple trait approach produced a less accurate comparison between generations of bulls, by overestimating older bulls. This result had also an impact on international comparison. Pre-adjustment of genetic variance heterogeneity across herds is now being considered to improve the quality of genetic evaluation procedures in Italy.

Key Words: Heterogeneity of variance, Genetic evaluation, Italian Holstein

1022 Simultaneous accounting for heterogeneity of (co)variance components in genetic evaluation of type traits. N. Gengler^{1,2}, G. R. Wiggans*³, J. R. Wright³, and T. Druet^{1,2}, ¹Gembloux Agricultural University, Gembloux, ²and National Fund for Scientific Research, Brussels, Belgium, ³Agricultural Research Service, USDA, Beltsville, MD.

The multi-trait canonical transformation genetic evaluation system for type traits was modified to estimate adjustments for heterogeneous variance (HV) simultaneously with estimated breeding values (EBV) for final score and linear traits. Heterogeneity, estimated for transformed traits, was regressed within parity toward population mean by fitting a model with fixed effects of mean final score for herd, size of contemporary group, appraisal month, and year-season and a random effect for interaction between herd and appraisal date. Method R was used to estimate variances for the heterogeneity model within each EBV iteration. For 2497 bulls that had been used for artificial insemination, correlations between HV-adjusted and February 2001 official evaluations ranged from 0.981 for suspensory ligament to 0.996 for dairy form. Annual trend for bull EBV was lower with HV adjustment than for official evaluations for all traits except teat length (0.073 points less for dairy form to 0.020 points more for teat length) with the largest percentage reduction (26.4%) for front teat placement. Mean absolute values of differences between HV-adjusted and official evaluations and standard deviations (SD) of those differences generally increased as reliabilities increased to about 80% but decreased slightly for reliabilities of >90%. Mean differences were largest for bulls born from 1985 through 1994 and bulls with daughters with lowest mean final scores. Mendelian sampling (evaluation minus mean of parent evaluations) was calculated for cows born from 1984 through 1998. Mendelian-sampling SD with HV analysis declined less over time than for official evaluations. For regression of SD on birth year, slope from the HV analysis ranged from 21% of slope for official evaluations for rear udder height to 76% for rump angle. Type evaluations of Ayrshires, Brown Swiss, Guernseys, Jerseys, and Milking Shorthorns will be adjusted for HV to enable more accurate selection decisions.

Key Words: heterogeneous variance adjustment, type evaluation

1023 Evaluation of classifiers that score type traits and body condition score using common sires. R. F. Veerkamp¹, C. L. M. Gerritsen¹, E. P. C. Koenen², A. Hamoen², and G. De Jong*², ¹Institute of Animal Science and Health, ID-Lelystad, The Netherlands, ²NRS, Arnhem, The Netherlands.

Subjective visual assessment of animals by classifiers is undertaken for several different traits in farm livestock, e.g. linear type classification, body condition score, or carcass conformation. One of the difficulties is the effect of an individual classifier. To ensure that classifiers rank animals consistently, i.e. the repeatability between classifiers and within classifier, training sessions are required. In this study genetic links across routinely scored records are used to validate scoring of individual classifiers. Absence of a unity correlation between classifiers might be due to poor repeatability between classifiers. Eighteen classifiers of the NRS scored 18 traits, and body condition for 91,589 first lactation heifers, daughters of 601 sires. Genetic correlation of each individual classifiers with all other classifiers grouped were estimated in a series of bivariate analysis. Likelihoods were compared between two models with the genetic correlation either estimated or fixed at unity. Classifiers that scored a large number of animals (ca. 7,500) had a relative large part of the genetic correlation significantly different from unity as these were estimated with large precision. Estimates from classifiers that scored a few animals (ca. 1000) were sometimes low due to sampling. Therefore, a genetic correlation ≤ 0.90 that was significantly different from unity was used as criteria to mark traits for individual classifiers. On average each classifier had 3.3 traits marked, ranging from 0 to 9. Overall feet and legs, rump width, central ligament, and foot angle received most marks (12 to 6 classifiers), but there was agreement (i.e. no mark) for body condition score, stature, rump angle, teat length, overall udder, and teat placement. It is concluded that these simply and cheaply to obtain marks can be used in training sessions to improve the quality of the scoring system.

Key Words: Genetic correlations, Body condition score, Type classification

1024 Evaluations for final score at different ages. L. Klei^{*1}, S. Tsuruta², I. Misztal², and T. J. Lawlor¹, ¹Holstein Association USA, Inc., Brattleboro, VT, ²University of Georgia, Athens, GA.

The objective of this study was to investigate genetic evaluations for final score (PTAT) at different ages. Breeding values were predicted with a random regression model (RRM) and with the current national genetic evaluation model (NE), a repeatability model. RRM included fixed effects for management group and stage of lactation; fixed regressions on age at classification; additive genetic and permanent environmental effects with random regressions on age; and random residual effects. Correlations between PTATs from RRM at various ages and NE ranged from 0.89 to 0.99. PTAT genetic trends for sires and registered cows from RRM at 24 and 60 months of age were similar to those obtained from NE. Trend for grade cows from RRM was lower at 60 month of age than NE trend. The correlation between PTAT of sires and the average age of daughters tended to be positive indicating that daughters of high type bulls are scored more often. Bulls whose genetic evaluation improves as the age of daughters increases tend to have higher genetic evaluations for traits associated with increased longevity. For example, sires with the largest positive difference between PTAT at 60 and 24 months of age had an udder composite evaluation that was 2.7 points higher than those with the largest negative difference in PTAT at the two ages. Proportion of registered cows in the data set decreased from over 80% for cows born in 1981 to 55% for cows born in 1997. Registered cows have mostly two or more scores while grade cows tend to have only a single score at an early age. Declining numbers of scores at later ages may result in selection of sires whose daughters are superior at an early age but age poorly. Evaluation for final score by the random regression model allows identifying bulls whose daughters are superior at an early age and mature gracefully.

Key Words: Holstein, Final Score, Random Regression

1025 Genetic correlations of pathogen-specific clinical mastitis with milk yield and somatic cell score. Y. de Haas^{*1}, H.W. Barkema², and R.F. Veerkamp¹, ¹Institute for Animal Science and Health, ID-Lelystad, The Netherlands, ²Animal Health Service, Drachten, The Netherlands.

Several pathogens play a crucial role in the type of clinical mastitis (CM), and since the etiology of each mastitis-causing pathogen is different the question can be raised whether selection for yields affects all pathogens equally, and if selection for lower somatic cell counts improves resistance to all pathogens equally. Therefore, the objective of this study was to quantify genetic variation for overall and pathogen-specific CM and to estimate genetic correlations with milk yield and somatic cell score. Data from 274 Dutch herds recording clinical mastitis over an 18-months period were used. Analyzed pathogens were *Staphylococcus aureus*, coagulase negative staphylococci, *Escherichia coli*, *Streptococcus dysgalactiae*, *Streptococcus uberis* and other streptococci. The data set contained 47,563 lactations of 28,695 cows of different parities. Cases of overall and pathogen-specific CM were treated as binary traits

in AS-REML. In total, 5,950 lactations with at least one case of CM were included, and in 5,780 cases the mastitis-causing pathogen was classified. Variance components for the sire, maternal grandsire, and permanent environmental effect were estimated using generalized linear mixed models with a logit-link function. Heritabilities ranged from 0.02 to 0.10 for pathogen-specific CM. Genetic correlations of overall CM with milk yield and somatic cell score at 150 days were 0.69 and 0.63, respectively. However, these genetic correlations differed per mastitis-causing pathogen. For instance, the incidence rate of clinical *E. coli* mastitis was slightly unfavorably correlated with 150d milk yield (0.13), but stronger with 150d SCS (0.74). Whereas the genetic correlations with clinical *Str. dysgalactiae* mastitis were 0.70 and 0.16, respectively. Therefore, current selection practices (using milk yield and somatic cell count) will have different effects on the incidence rates of each pathogen.

Key Words: Genetic correlations, Clinical mastitis, Pathogens

1026 Genetic evaluation of episodes of short and long duration of elevated somatic cell scores. X. Li, M. M. Schutz^{*}, A. P. Schinckel, and D. L. Lofgren, Purdue University.

Long or short episodes of elevated somatic cell scores (SCS) may indicate different causes of mastitis and may be under different levels of genetic control. The objectives of this study were to estimate genetic and phenotypic parameters of short and long episodes of elevated SCS, and to compare preliminary Predicted Transmitting Abilities (PTA) of sires for lactation means of SCS and short and long episodes. Two random subsets of Holstein Dairy Herd Improvement Association test-day records represented 70,369 lactations of 51,433 cows and 79,890 lactations of 57,357 cows, respectively. Occurrence of short and long episodes of elevated SCS within a lactation were binomial traits defined by two methods. Method 1 defined short episodes (S1) as test-day SCS increasing by 2 or more units to above 5 and then declining by 2 or more units to below 5 on consecutive test days. Long episodes (L1) were defined when no decrease of 2 occurred for the subsequent test day. Method 2 defined short (S2) and long episodes (L2) similarly, but used the within-herd residual standard deviation of a lactation curve for 30 stage of lactation classes in place of the constant threshold of 5. Genetic components of variation for lactation means of SCS and the incidence of short and long episodes were analyzed using single- and multiple-trait animal models. Heritabilities of lactation SCS (LSCS) and adjusted lactation SCS after removing episodes of short duration (ALSCS) were around 0.10. Heritability estimates were near 0 for S1 and S2, and near 0.04 for L1 and L2. Genetic correlation of LSCS with S1 and S2 averaged 0.902 and 0.945, respectively. Phenotypic correlations were low, about 0.197 and 0.239 for S1 and S2, respectively. Current selection for decreased SCS appears to be consistent with genetic improvement for lower incidence of short episodes of elevated SCS. Low heritability of short episodes may preclude genetic progress from direct selection. The PTA for LSCS and ALSCS were similar giving further evidence that episodes of short duration may be under little genetic control.

Key Words: Mastitis, Somatic Cell Scores, Genetics

ASAS/ADSA Physiology: Estrous Synchronization

1027 Use of ECP in a presynchronized timed artificial insemination protocol for lactating dairy cows. E. R. Jordan^{*1}, S. M. Pancarci², M. J. Schouten³, and W. W. Thatcher², ¹Texas A and M University, ²University of Florida, ³Schouten Dairy, Hico, TX.

To test whether ECP could replace the final GnRH in a timed artificial insemination (TAI) protocol, lactating dairy cows were grouped by week of calving and assigned to treatments on alternating weeks. All cows were presynchronized using two PGF₂α (Lutalyse[®]; Pharmacia Corp., Kalamazoo, MI; 25 mg, im) treatments 14d apart (35±3 and 49±3d postpartum). Cows in both groups received a treatment of GnRH (Cystorelin[®]; Merial Ltd., Iselin, NJ; 100µg, im) on d0 (63±3d postpartum). Seven days later (70±3d postpartum) PGF₂α was administered. Cows assigned to TAI (n=157) received a second GnRH at experimental d9 (72±3d postpartum) and were artificially inseminated 24 hr later (73±3d postpartum). Cows in the ECPsynch group (n=164) received ECP (ECP[®]; Pharmacia Corp., Kalamazoo, MI; 1 mg, im) on experimental d8 (71±3d postpartum) and were artificially inseminated 48 hr later (73±3d postpartum). Pregnancy was verified 37-44d after insemination

by rectal palpation. Health records of cows were recorded and included in the data analysis. Stage of the estrous cycle at initiation of the treatment protocol and prior cyclicity was determined based on previous observed estrus. Statistical analyses included stepwise logistic regression analysis to determine significant variables and the general linear model of SAS. The treatment by estrus interaction was significant (P<.01). The pregnancy rate for the cows in estrus was 32.8±8.2% (n=28) for TAI and 40.4±4.1% (n=107) for ECPsynch, but 26.8±3.8% (n=129) and 6.6±5.7% (n=57), respectively for cows not observed in estrus. Fewer cows on TAI than ECPsynch expressed visual signs of estrus (P<.01). The pregnancy rate for cows initiating the synchronized regime between d5 and 12 of the estrous cycle was higher than for cows at other stages of the cycle or at an unknown stage (P<.02). Based on these results, pregnancy rates at first synchronized insemination after the voluntary waiting period will be similar for cows receiving either ECP or GnRH as the ovulatory hormone for timed insemination.

Key Words: Timed artificial insemination, ECP, ECPsynch