

Breeding and Genetics: Genetics of Dairy Health Traits

34 Potential for inclusion of health data in international genetic programs. P. D. Miller*, *University of Wisconsin, Madison.*

Genetic selection programs for dairy cattle in many countries are reviewed, breeding goals are compared, and the degree of uniformity that exists and is required for international genetic programs for health traits is discussed. The most prevalent health disorders in dairy cattle are mastitis, infertility, lameness, milk fever, ketosis, metritis, and displaced abomasums. The manifestation of these disorders can be partly attributed to management and environmental factors, but there is evidence that each also has a genetic component. Health traits are genetically correlated with traits for which international genetic evaluations are routinely available from Interbull, including milk production, conformation, and udder health traits. Evaluations for longevity (length of herd life) are expected this summer. Genetic evaluations for female fertility traits are available in many countries and international evaluations are imminent. Effective selection using quantitative genetic approaches requires measurement and recording of phenotypes and frequent evaluation of candidates for selection. Producers use many different definitions to record health data and do not use a standardized format in on-farm or DHIA databases. Change will require significant time and effort by many people. Direct genotyping using DNA technologies offers potential for direct selection for genes causing health problems, but this is likely to be a slow and incomplete solution. Potential exists for genetic improvement of health in dairy cattle. Economic, social, and political forces will shape the changes that occur.

Key Words: Health, Genetic, International

35 Genetic basis and risk factors of infectious and noninfectious diseases in US Holsteins. I. Estimation of genetic parameters for single diseases and general health. G. Abdel-Azim¹, A. E. Freeman², M. E. Kehrli³, S. C. Kelm⁴, J. L. Burton⁵, A. L. Kuck¹, and S. Schnell¹, ¹*Cooperative Resources International, Shawano, WI*, ²*Department of Animal Science, Iowa State University, Ames*, ³*National Animal Disease Center-USDA-ARS, Ames, IA*, ⁴*Animal & Food Science Department, University of Wisconsin, River Falls*, ⁵*Michigan State University, East Lansing.*

Health data collected over a period of four years, 1996 to 1999, from 177 herds in Minnesota and Wisconsin were analyzed to establish genetic basis for infectious and noninfectious diseases. Three types of health traits were targeted, first, selected infectious conditions were fit together in a statistical model to identify animals that are superior in their general immunity for infectious diseases. Generalized immunity may be thought of as a combination of immune responses to a variety of immune system challenges. Second, single infectious and noninfectious diseases were analyzed separately. Third, infectious reproductive diseases as one category of related conditions and cystic ovary disease as one category of 3 related noninfectious ovary disorders were studied. Data were analyzed by a threshold model that included herd, year, season of calving, parity, sire, and cow as cross-classified factors. Days at risk and days in milk at the start of the trial were adjusted for by fitting the days as continuous covariates in the model. A heritability value of 0.202 ± 0.083 was estimated for generalized immunity. Heritability values of 0.141 and 0.161 were estimated for uterine infection and mastitis, respectively. Heritability of single noninfectious disorders ranged from 0.087 to 0.349. The amount of additive genetic variance recovered in the underlying scale of noninfectious disorders tended to 0 when combining together multiple conditions. Therefore, although the study is in favor of combining infectious diseases into categories of interest, we do not recommend the same approach for noninfectious disorders because of the different mechanisms controlling them.

Key Words: Disease Resistance, Generalized Immunity, Genetic Evaluation

36 Multivariate genetic parameters for health, reproduction, body condition score, and conformation traits in Swiss Holsteins. H.N. Kadarmideen*, *Statistical Animal Genetics Group, Institute of Animal Science, Swiss Federal Institute of Technology (ETH) Zurich ETH Zentrum (UNS), Ch-8029 Zurich, Switzerland.*

Data on body condition score (BCS), days to first service (DFS), non-return rate (NRR), somatic cell count (SCC), and 305-day yields of milk, fat and protein from 38,930 multiple lactation records of cows, daughters of 243 sires in 1830 herds were used to estimate genetic parameters. Single- and multi-trait repeatability animal models were used to estimate parameters based on restricted maximum likelihood methodology. Fixed effects in the model varied depending on the individual trait. Further, genetic relationships between 27 (linear and descriptive) type traits and functional traits (fertility and SCC) were estimated by regressing daughter type records on their sire estimated breeding values for functional traits, using the same data set. BCS had a moderate heritability (h^2) of 0.26 and fertility traits had low h^2 (0.12 for DFS and 0.06 for NRR). Heritability of SCC and milk production traits was 0.14 and around 0.30, respectively. BCS had favorable genetic correlations with fertility traits (-0.35 with DFS and 0.04 with NRR) suggesting that BCS could be considered in a fertility index. BCS had a favorable genetic correlation (r_g) with SCC, but not strong (-0.08). Selecting for milk production alone would lead to decline in genetic merit for functional traits considered here, as milk production has antagonistic r_g with fertility (range 0.12 to 0.27 with DFS and -0.12 to -0.24 with NRR), with BCS (-0.39 to -0.50), with SCC (0.10 to 0.15). Many type traits (especially udder traits) had a favorable genetic relationship with fertility traits and somatic cell counts whereas dairy character had an unfavorable genetic relationship. Results (genetic correlations) suggest that future selection indexes may include BCS (possibly also dairy character) as an indicator of fertility with appropriate (high) economic weights while including production traits with (less) optimal economic weights.

Key Words: Reproduction, Body condition score, Genetic correlations

37 Estimation of genetic parameters for health traits in large commercial herds using data recorded in on-farm herd management software programs. N. R Zwald* and K. A Weigel, *University of Wisconsin, Madison.*

The objective of this study was to estimate genetic parameters for clinical mastitis, lameness, metritis, ketosis, and displaced abomasum using data recorded on commercial dairy farms. Disease incidence data were recorded in one of three herd management programs: DC305, PCDART, or DHIPLUS. Data were collected directly from 141 herds that participated in the Alta Genetics Advantage progeny test program, and Dairy Records Management Systems provided data from an additional 160,264 cows in 438 herds that routinely recorded health disorders. Incidence rates on were: 14.1%, 10.4%, 5.4%, 4.9%, 2.2%, for mastitis, lameness, ketosis, metritis, and displaced abomasum respectively. In the genetic analysis, herds were required to have a recorded incidence rate of $>1\%$ for ketosis, metritis, and displaced abomasum and $>3\%$ for mastitis and lameness. After removal of herds with incomplete reporting and cows with unknown sires or sires with < 5 daughters, data included: Clinical mastitis: 441 herds, 143,592 cows and 4505 sires Lameness: 228 herds, 79,413 cows, and 1109 sires Displaced abomasum (DA): 326 herds, 106,998 cows, and 2165 sires Metritis/Retained Placenta: 471 herds, 148,885 cows, and 2162 sires Ketosis: 133 herds, 44,335 cows, and 730 sires A threshold sire model was used. The model for early metabolic disorders (metritis, ketosis, and DA) was response = HYS + Lactation + sire. A three-trait model, treating occurrences of disease in each of the first three lactations as separate traits, was used for mastitis and lameness. This model was response = HYS+ stage of lactation + sire. Heritability estimates ranged from 0.06 to 0.11. Cases of ketosis, metritis, and DA were combined in an analysis of early metabolic health. Due to the binary nature of these traits, relationships between traits, and low incidence rates combining traits into an early metabolic health index has great potential for implementation in a selection program.

Key Words: Early Metabolic Disorders, Progeny Test, Genetic Parameters

38 Health parameters in F1 Jersey x Holstein, backcross (Jersey x Holstein) x Holstein, and pure Holstein calves. C. Maltecca* and K. Weigel, *Department of Dairy Science, University of Wisconsin, Madison.*

The present study is part of a larger project that aims to detect quantitative trait loci (QTL) affecting health, fertility, calving ease, and milk composition in a crossbred Holstein x Jersey cattle population. Fecal and respiratory scores and birth weights were recorded for F1 Jersey x Holstein, backcross (Jersey x Holstein) x Holstein, and pure Holstein calves on two farms. Fecal and respiratory scores were measured on a five-point scale of severity. Ninety two pure Holstein calves (41 females and 51 males) and 31 F1 Jersey x Holstein calves (15 females and 16 males) were from a commercial dairy in Wisconsin, while 60 pure Holstein calves (31 females and 29 males) and 35 crossbred calves (15 females and 20 males) were from the University of Wisconsin experimental herd. Mean Fecal scores were 1.36 (\pm 0.37) and 1.49 (\pm 0.38) for Holstein calves in the commercial and experimental herds, respectively. Corresponding means were 1.22 (\pm 0.16) and 1.44 (\pm 0.24) for F1 Jersey x Holstein calves and backcross (Jersey x Holstein) x Holstein calves, respectively. Mean respiratory score were 1.03 (\pm 0.01) and 1.10 (\pm 0.09) for Holstein calves on the commercial and experimental farms, respectively, and 1.04 (\pm 0.02) to 1.18 (\pm 0.12) for F1 and backcross calves, respectively. Mean birth weights for calves from multiparous dams in the experimental herd were 42.7 (\pm 3.3) and 39.2 (\pm 6.7) for Holstein males and females and 40.2 (\pm 7.4) and 41.2 (\pm 3.3) for backcross males and females, respectively. Mean birth weights for the commercial herd were 45.1 (\pm 6.4) and 42.0 (\pm 6.4) for Holstein males and females and 35.7 (\pm 3.4) and 31.4 (\pm 3.9) for backcross males and females, respectively. Differences between pure Holstein, F1 Holstein x Jersey, and backcross (Holstein x Jersey) x Holstein calves for scours and respiratory score were not significant.

Key Words: Calves, Backcross, Health

39 Application of a finite mixture model to somatic cell scores of Italian goats. P. Boettcher*¹, D. Gianola², G. Pisoni³, C. Vimercati³, M. Rinaldi³, and P. Moroni³, ¹IBBA-CNR, Segrate, Italy, ²University of Wisconsin, Madison, ³University of Milan, Milan, Italy.

Mastitis infection usually results in high concentrations of somatic cells (SCC) in the udder of affected animals. Data on SCC from infected and uninfected mammary glands can be viewed as drawn from many statistical distributions with different means and, possibly, different variances. Information on bacterial infection is often not available to indicate the distributions from which a given data point originates, but an analysis with finite mixture models can account for this uncertainty by assigning each record to a given distribution with a certain probability. The objective was to apply such an analysis to data for SCC in dairy goats. Data were 1378 test-day records of SCC and presence of bacteria in each of the udder halves of 92 primiparous goats in five Italian herds. The approach regarded all observations from a given udder half as arising from the same distribution. The fit of a single component (standard) model with mixtures of two or three distributions was examined. From a biological standpoint, a two-component model would be appropriate if observations from healthy and infected udder halves were from two different distributions and a three-component (or more) model would be appropriate if bacterial species differed in their effect on SCS. The two-component model was able to separate distributions that differed in mean by 0.89 SCC (log 2), or approximately 0.30 standard deviations. The proportions of the "low" and "high" SCS components were approximately 60 and 40%, respectively. The ability of the analysis to assign observations to different distributions according to bacterial presence was tested. A clear association with bacterial infection was observed. For example, observations from udder halves with no bacterial infection were assigned to the component with a low mean SCS with a probability of 65%. In contrast, udder halves with bacterial presence at eleven test days were assigned to the high group with a 70% probability. The three-component model was unable to distinguish separate distributions. Application of a mixture model in genetic evaluations may improve selection programs based on EBV for SCC.

Key Words: Somatic Cell Score, Goats, Mixture Model

40 Test day model evaluation for production traits and somatic cells score for the Italian Holstein. F. Canavesi*, S. Biffani, and F. Biscarini, *ANAFI Via Bergamo 292,26100, Cremona, Italy.*

In the past three years the Italian Holstein association in cooperation with Canadian Dairy Network (CDN) has been working toward the development of a random regression test day model evaluation for milk, fat, protein and somatic cell score (SCS). The model is a multiple trait, multiple lactation test day animal model with fixed effects of herd-test day-parity. A Legendre polynomial of 4th order is used to fit the fixed effect of age-parity-region-season and the random effects of the animal and of the permanent environmental effect. Heritability for production traits is on average 0.30 the same parameter used for the official evaluation based on lactation records. Heritability of SCS is 0.17 in first, 0.21 in second and 0.25 in third lactation respectively, much higher than the present 0.08 value used for genetic evaluation based on first lactation test day records with a repeatability test day model. The correlation with the official sire production proofs is around 0.97 for yield traits and 0.70 for SCS. For cow proofs the correlation is around 0.92 for production traits and 0.69 for SCS. The first official publication is expected before the end of 2004.

Key Words: Test Day Model, Genetic Evaluation, Random Regression

41 Crossbreds of Normande-Holstein, Montbeliarde-Holstein, and Scandinavian-Holstein compared to pure Holsteins for production and SCS during the first 150 days of first lactation. B. J. Heins, L. B. Hansen*, and A. J. Seykora, *University of Minnesota, St. Paul.*

Normande-Holstein (NxH) crossbreds (n = 171), Montbeliarde-Holstein (MxH) crossbreds (n = 194), and Scandinavian-Holstein (SxH) crossbreds (n = 120) were compared to pure Holsteins (H, n = 294) for milk, fat, and protein production and SCS during the first 150 days of lactation of first lactation. Cows were housed in seven commercial dairies in California and calved from June 2002 to December 2003. Dependent variables for analysis were test-day observations from DHI. All Holstein sires and all Holstein maternal grandsires were required to have an NAAB sire code to assure they were A.I. sires. Normande, Montbeliarde, and Scandinavian crossbreds were all daughters of A.I. sires via imported semen. Independent variables were breed (H, NxH, MxH, SxH), random effect of sire within breed, random effect of cow within sire and breed, stage of lactation (4-30 d, 31-60 d, 61-90 d, 91-120 d, 121-150 d), herd-year-season (3-mo seasons within the seven herds), age at calving (linear, months), milking frequency (2X, 3X), and PTA of Holstein maternal grandsire (linear). Breed was significant for all traits. Least squares means for fat plus protein were 2.03 kg (H), 1.90 kg (NxH), 2.05 kg (MxH), and 2.18 kg (SxH). Relative to production of pure Holsteins on a percentage basis, differences were -6% (NxH), +1% (MxH), and +7% (SxH). Least squares means for SCS were 2.13 (H), 2.40 (NxH), 2.33 (MxH), and 1.88 (SxH).

Key Words: Crossbreeding, Production, SCS

42 Accuracy and stability of national and international somatic cell score evaluations. R. L. Powell*, A. H. Sanders, and H. D. Norman, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Most research on accuracy of dairy bull genetic evaluations has been with yield traits. This report focuses on somatic cell score (SCS) evaluations. International evaluations through Interbull (IB) have been available since May 2001. February 2004 U.S. and IB SCS PTA were matched with U.S. and IB PTA from May 2001 (US04, IB04, US01, and IB01, respectively) for 14,821 Holstein bulls. All four evaluations were required for each bull. Over the three years, the means were essentially the same (increased 0.001) in each system (U.S. and IB). Correlations of 0.96 and regressions of later on earlier PTA of 0.99 were nearly as expected. Bulls adding substantially to numbers of U.S. daughters had mean increases in PTA of about 0.01 and regressions of nearly unity but correlations between earlier and later PTA were about 0.04 lower than expected considering reliabilities. The US01 and IB01 PTA were compared as predictors of US04 where IB01 PTA included data from at least one other country. As expected, US01 was the better predictor where it contained essentially the same daughters as US04, but IB01 was better when U.S. daughters increased at least 25%. Mean PTA difference

from US04 was closer to zero, standard deviation of the differences was smaller, and correlations were higher. The advantage in correlation from IB01 increased with the amount of new U.S. data in the 2004 evaluation. Both U.S. and IB evaluations were stable on average, increasing in mean only slightly. Regressions were essentially unity in both systems. Correlations were less than expected by about 0.01 overall and lower by 0.04 for subsets with substantial added data. Inclusion of foreign data in addition to U.S. data improved the prediction of later U.S. SCS evaluations.

Key Words: Genetic Evaluation, Somatic Cell Score, Interbull

43 Genetic component of heat stress. S. Oseni, I. Misztal*, S. Tsuruta, and R. Rekaya, *The University of Georgia, Athens.*

A norm reaction model was used to estimate the genetic parameters of days open (DO) and pregnancy rate (PR) under heat stress. Data included DO records for GA, TN and NC. Pregnancy rate was computed as $PR = \min\{1, 1/[(DO-50)/21-1]\}$. PR, unlike DO, assigns greater weight to smaller DO records. Fixed effects model included herd-year-month of calving, age of the cow, and a regression on 305-d milk yield. The norm-reaction model additionally included the effect of animal with random regression on a heat index, which was normalized solutions to months of calving from the fixed model; residual variance was assumed to be a function of the heat index. The shape of the heat index for DO (PR) was close to sinusoidal (triangular) function with the highest value in April (May) and the lowest value in October (October). For DO and PR, genetic and residual variances and heritabilities were highest for spring calvings and lowest for fall calvings. For DO (PR), the variance associated with the highest level of heat index was 33% (33%) of the genetic variance of the regular effect. Genetic correlation between regular and heat stress effects for DO (PR) was 0.67 (-0.65). As a validation process, DO was computed with the model above, without the heat stress index and the months of calving grouped into four seasons treated as multiple traits. In general, the genetic and residual variances of the multiple trait model followed those of the norm-reaction model for DO.

Dairy Foods: Chemistry

45 Utilization of front face fluorescence spectroscopy for rapid analysis of process cheese functionality. S. K. Garimella Purna*, L. A. Prow, and L. E. Metzger, *University of Minnesota, St. Paul.*

The purpose of this study was to evaluate the feasibility of front face fluorescence spectroscopy (FFFS) to predict the functional properties of process cheese spreads. A total of 27 different commercial samples from three different manufacturers were used in this study. Each sample was analyzed using tube melt test and dynamic stress Rheometry (DSR). The tube melt data is a measure of cheese flow in mm, whereas the DSR data was used to calculate the melt temperature (temperature at $\tan\delta = 1$). Additionally fluorescence spectra of tryptophan (excitation: 290nm; emission: 305-400 nm) were collected on each sample at 20°C using a front face accessory. Six replicates were taken from each sample and six scans were performed on each replicate. After collection the curves were normalized and the mean curve was baseline corrected. Multivariate statistical analysis was used to correlate the fluorescence data with the functionality data. In the initial analysis two samples with large spectral and concentration residuals were eliminated from the calibration set. The calibration models were developed using partial least square regression (PLS). The analysis included preprocessing using mean centering and verification using cross validation. A correlation coefficient of 0.90 and 0.82 between the fluorescence spectra and the functionality data was obtained for the DSR and tube melt respectively. The regions from 309-315 nm and 355-395 nm of the tryptophan spectra had highest correlation to DSR; while the tube melt data had the highest correlation between 334-348 nm. Examination of the tryptophan spectra indicated that an increase in the melt temperature measured by the DSR resulted in a blue shift in the spectra. These spectral shifts have been related to the protein conformational changes due to change in the environment of tryptophan residues present in the protein. These results indicate that the melt properties of process cheese spreads are related to molecular structure that can be measured using FFFS.

Key Words: Fluorescence, Process Cheese, Functionality

Genetic correlations of spring with summer, and fall with winter were 0.97 and 0.98, respectively. Genetic correlations between spring/summer and fall/winter were around 0.8. The norm reaction model for DO allows inexpensive but limited genetic evaluation of fertility under heat stress. Results of such an evaluation may strongly depend on the editing criteria and on the details of the model.

Key Words: Days Open, Pregnancy Rate, Heat Index

44 Use of peeling and reverse peeling to estimate the power to map a recessive disease gene. L. R. Totir*, R. L. Fernando, and J. M. Reecy, *Iowa State University, Ames.*

Animal pedigrees containing individuals that exhibit the phenotype of a recessive disease (e.g. dwarfism) can be used to map the causative recessive disease gene by performing a genome scan. When planning a linkage study, however, it is important to know beforehand the number of animals that must be genotyped and the marker density needed to have sufficient power to locate the disease gene. Conditional on the observed disease phenotypes, reverse peeling can be used to sample genotypes at the disease locus and at two flanking marker loci. Given the sampled genotypes and the observed disease phenotypes, peeling can be used to compute the logarithm of the likelihood ratio (LOD score). By replicating this process, the power to detect the disease locus can be estimated by calculating the frequency of samples where the LOD score is larger than 3. This strategy was applied to an Angus cattle pedigree of 39 animals including six affected individuals. For this pedigree we studied the behavior of the power to map a disease gene as a function of the number of animals genotyped, and the size of the marker interval. It was determined that, for this pedigree, the power to map a disease gene was larger than 90 percent for marker intervals equal to or smaller than 15 cM. This strategy can be used to design genome scans to map disease genes with adequate power.

Key Words: Power, Peeling, Recessive Disease Gene

46 Modified milk vs. producer milk samples for calibrating infrared (IR) milk analyzers: which gives the best validation performance? K. E. Kaylegian*¹ and D. M. Barbano^{1,2}, ¹Dept. of Food Science, Cornell University, Ithaca, NY, ²Northeast Dairy Foods Research Center, Ithaca, NY.

Nine IR milk analyzers were calibrated with modified milk samples and nine different IR analyzers were calibrated with producer milk samples. No single lab had more than two instruments. The population of instruments represented three different manufacturers, several different models, and FTIR and filter based instruments. The validation study was replicated three times with different calibration and validation samples. Labs that calibrated analyzers with producer samples used their normal calibration samples and procedures. Modified milk samples (n = 14) were made from pasteurized gravity separated cream, skim milk UF retentate and permeate, lactose, and water. Validation samples (n = 12) were raw individual producer milks. Both the modified milk calibration set and the producer milk validation set were preserved with dichromate and analyzed by all labs using chemical reference methods (ether extraction, Kjeldahl, and oven drying) to produce all lab mean reference values. Validation of individual instruments was assessed by the mean difference (MD) and standard deviation of the difference (SDD) between the IR predicted values and all lab mean reference chemistry values. Comparison of the two calibration sample types was done using Euclidian distance plots. The range of MD for fat, true protein, and total solids tests on the validation set across labs was reduced by 30% or more for analyzers calibrated with modified milks vs those calibrated with producer milks. In general, the SDD was lower for analyzers calibrated with modified milks vs those calibrated with producer milks.

Key Words: Infrared Milk Analysis, Calibration, Validation