Breeding and Genetics:
Applications and Methods in Animal Breeding—Dairy I

130 The correlation analysis between Holstein body conformation traits and milk production traits in the Shanghai region. K. Zhu[1,2], G. L. Liu*[1,2], L. M. Huang[1], C. B. Zhang[2], and F. S. Fu[2], [1]*State Key Laboratory of Dairy Biotechnology, Shanghai Bright Holstan Co. Ltd., Shanghai, China,* [2]*Shanghai Dairy Breeding Center Co. Ltd., Shanghai, China.*

The objective of this study was to analyze the correlation between Holstein body conformation traits and milk production traits in the Shanghai region. In total, 871 Holstein cows were randomly chosen from 28 dairy farms in Shanghai at second stage of lactation as the object of our study. Five milk production traits, including 305-d milk yield, butter fat percentage, milk protein percentage, peak lactation days and peak milk production were obtained from dairy Herd Improvement (DHI) project of Shanghai Dairy Breeding Center. The quantitative values of 7 body conformation traits were recorded by 9-point methods and the model of multiple linear regressions was used here to analyze the correlation between the body conformation traits (as independent variable) and the milk production traits (as dependent variable). The results showed that the total score of body conformation were extremely significantly positively correlated with the 305-d milk yield, butterfat percentage, Peak milk production ($P < 0.01$), significantly positively correlated with the peak lactation days ($P < 0.05$), and weak correlation with the milk protein percentage (not significant). The body hindquarters capacity was significantly positively correlated with the milk yield. The cow hoofs character was extremely significantly positively correlated with the peak milk production, the butterfat percentage, and the milk protein percentage; and was significantly positively correlated with milk yield. The hip character was significantly positively correlated with the butterfat percentage. The lactation system and udder traits were significantly positively correlated with the peak lactation days. We concluded that the body hindquarters capacity, the hoofs character, the hip character, the lactation system and udder traits were the most important factors that influenced the milk production traits of Holstein cows. The identification and scoring of body conformation traits might provide significant guiding on screening high-yield, excellent producing Holstein cows as well as selection and assortative mating.

Key Words: Holstein cow, body conformation trait, milk production trait

131 Heterosis and effect of breed proportion for milk production traits in crosses between Danish Holstein, Danish Red, and Danish Jersey. E. Norberg*[1], K. Byskov[2], and M. Kargo[1,2], [1]*Centre for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark,* [2]*Knowledge Centre for Agriculture, Agro Food Park 15, Aarhus N, Denmark.*

During the last decade the use of systematic crossbreeding in dairy cattle herds has been increasing in Denmark. The aim of this study was to estimate the effect of breed proportion and heterosis on milk production traits. The study was based on records on milk yield (MY), protein yield (PY) and fat yield (FY) from 52,165 first lactation cows born in 2004 or later from 104 herds using systematic crossbreeding. More than 50% of the cows were crosses between Danish Holstein (DH), Danish Red (DR) and /or Danish Jersey (DJ) and the remaining were pure DH, DR or DJ. Cows with less than 45 DIM and/or a calving age below 18 or above 40 mo were omitted. The statistical model included a fixed effect of herd-year and calving month, a regression on calving age, a regression on the proportion of DH, DR and DJ genes, a regression on the degree of heterozygosity between DH and DR, DH and DJ and DR and DJ, a random genetic effect of the cow and a residual. Data was analyzed using AI-REML in the DMU package. The effect of breed proportions was estimated relatively to a pure DH. For MY, a pure DR was estimated to give 259 kg less than a pure DH, while a pure DJ gave 1838 kg less than a pure DH. For PY there was no significant difference between DH and DR. Danish Jersey produced 40 kg less PY than DH and 35 kg less than DR. There was no significant effect of breed proportion for FY between the 3 breeds. Heterosis was significant in all combination of breeds for all 3 milk production traits. Heterosis for crosses between DH and DR was estimated to 177 kg, 5.8 kg and 8.4 kg for MY, PY and FY, respectively. Corresponding figures for crosses between DH and DJ was 320 kg, 13.4 kg and 17.5 kg, while crosses between DR and DJ gave heterosis estimates of 380 kg, 14.3 kg and 20.2 for MY, PY and FY, respectively. The results obtained in this study demonstrate the existence of heterosis on milk production traits in crosses between the 3 Danish dairy breeds.

Key Words: heterosis, breed effects, milk production

132 Genetic parameters for body condition score and body weight in Canadian Holsteins. A. Sewalem*[1], R. Cue[2], K. Wade[2], H. Delgado[2], D. Lefebvre[3], R. R. Lacroix[2], J. Dubuc[4], and E. Bouchard[4], [1]*Agriculture and Agri-Food Canada, Guelph, ON Canada,* [2]*Department of Animal Science, McGill University, Montreal, QC, Canada,* [3]*Department of Research and Development, Valacta, Centre d'Expertise en Production Laitière, Bellevue, Québec, Canada,* [4]*University of Montreal, St-Hyacinthe.*

The objective of this study was to characterize and determine the association between body weight (BW) and body condition score (BCS) in Canadian dairy Holsteins. Body weight was calculated from a heart girth circumference measurement and then converted to an estimated body weight (kg). A total of 75,443 BW and 22,899 BCS records were obtained from first lactation first records of Holstein cows that calved between 2002 to 2008. The average BW was 601.6 ± 34.1 kg. Body condition score was recorded by producers using a subjective scale of 1 to 5 (0.13, 16.51, 72.35, 10.79, and 0.23%, respectively). The data were analyzed using a multiple-trait animal model, including fixed effects for herd, calving year, calving season, age at first calving; linear and quadratic regressions of days in milk; and random effects for animal and residual. The data was analyzed using DMU software. Results yielded a heritability for BW and BCS of 0.19 ± 0.01 and 0.17 ± 0.16, respectively. The genetic and residual correlations between BW and BCS were low (0.195 ± 0.06 and 0.23 ± 0.01, respectively). A subsequent analysis of these data will be carried out using a random regression approach by including all available records.

Key Words: body weight, body condition score, genetic parameter

133 Lactation profile and genetic parameters of locomotion score and lameness in dairy cattle. A. Kougioumtzis[1], G. E. Valergakis[1], G. Oikonomou[1,2], G. Arsenos[1], and G. Banos*[1,3], [1]*Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Thessaloniki, Greece,* [2]*College of Veterinary Medicine, Cornell University, Ithaca, NY,* [3]*SRUC/Roslin Institute, Edinburgh, UK.*

Lameness greatly concerns the dairy cattle industry because of its high prevalence and associated costs. This study aims to investigate the profile and genetic parameters of lameness before and after calving and throughout lactation in primiparous Holstein cows. The study was carried out in a large commercial in Greece and included 237 cows that calved between 2008 and 2010. Cows were locomotion scored weekly on a 5-point scale, starting 6 weeks before calving and throughout lactation. Cows with a score greater than or equal to 2 were considered lame. These records were matched with weekly body condition score, liveweight and milk yield. Total number of repeated records amounted to 9,643. Traits were analyzed with bivariate random regression models that included the effects of year-season of calving, country of origin, calendar month, barn, calving age, a fixed regression on week from calving, and random regressions on week from calving associated with the additive genetic profile and the permanent environment of cow. Fixed curves for the 2 traits illustrated an increase in their relative levels up to mid-lactation. Weekly estimates of genetic variance were highest before calving and during the 4 weeks following calving and then decreased gradually; all estimates were statistically greater than zero ($P < 0.05$) demonstrating the presence of genetic factors that control the animal's capacity for uninhibited movement and resistance to lameness. Consistent with the genetic variance, heritability estimates were highest before calving and decreased with lactation stage; average estimates were 0.39 ± 0.06 and 0.26 ± 0.06 for locomotion score and lameness, respectively. Statistically significant ($P < 0.05$) genetic correlations were found of weekly locomotion score and lameness with body condition score ranging from −0.31 to −0.65 and from −0.44 to −0.76, respectively. It is concluded that locomotion score and lameness are amenable to improvement with genetic selection and body condition score can be used as an auxiliary trait for this purpose.

Key Words: genetics, locomotion, lameness

134 Multi-trait analysis of bovine leukosis incidence, somatic cell score, and milk yield in US Holstein cattle.

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Bovine leukosis (BL) can be defined as a retroviral disease caused by the bovine leukosis virus (BLV) which affects only cattle. Positive BL dairy cows produce less milk and have more days open compared with those that are negative. In addition, the virus also affects the immune system and causes a weak response to vaccines in infected animals. The objectives of this study were to estimate the heritability for BL incidence and its genetic correlations with BL, milk yield (MY) and somatic cell score (SCS). Results of a commercial ELISA assay used to detect BLV antibodies in milk samples were obtained from Antel BioSystems Inc. (Lansing, MI). The data included continuous milk ELISA scores and binary milk ELISA diagnosis as well as MY and SCS for 11,554 cows from 112 dairy herds across 16 US states. Continuous and binary ELISA results were analyzed jointly with MY and SCS using linear and threshold animal models, respectively. Estimates of heritability obtained with the 2 approaches were very similar and around 8%, indicating that there is a non-negligible genetic component underlying BL disease incidence. Estimated genetic correlations of BL incidence with MY were 0.14 and 0.17 using the threshold and linear model, respectively, whereas with SCS such correlations were 0.17 and 0.20. In summary, results of this study indicated that selection could be used to improve resistance to BL in Holstein cattle. In addition, selection for increased MY may also increase BLV susceptibility, such that higher infection rates may be expected in high-performing dairy herds. Nevertheless, selection for reduced SCS may increase the resistance to BLV. Hence, simultaneous selection for improved MY and BLV resistance using an appropriate index may lead to improvement of both traits.

Key Words: bovine leukosis, multi-trait analysis, heritability

135 Effect of genetic selection for Johne's disease resistance on the prevalence in dairy cattle using an epidemiological model.

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Johne's disease in dairy cattle is an important issue in the dairy industry. Genetic variation exists therefore genetic selection could be an additional approach to control this disease. The objective was to study the effect of different selection strategies on the prevalence of john's disease taking epidemiological aspects into account, using deterministic simulation. Three strategies were compared: (1) dam-selection, i.e., selection of cows only based on their ELISA test (current test and cull surveillance program); (2) sire-selection, i.e., using only the top 80% of the sires based on their EBV for resistance; (3) combining both strategies. Three parameters in the model were affected by genetic selection: length of latent period, susceptibility and length of susceptible period. The effect of selection on the parameter under selection was 'translated', using an epidemiological model, to an effect on prevalence to assess the effect of a selection strategy. For dam-selection, responses to selection for Johne's disease resistance were small, irrespective of the parameter that was varied in the model. For sire-selection, responses to selection were much larger for all 3 parameters that were varied. The largest effect was observed for length of susceptibility period, followed by susceptibility and then length of the latent period. Sensitivity analysis of the parameters showed that this ranking did not depend on the disease prevalence. The conclusion of this simulation study was that genetic selection for Johne's disease resistance on the sire level could contribute to the control of the disease.

Key Words: Johne's disease, genetic-epidemiological model, selection response

136 Genetic analysis of processed in-line mastitis indicator data.

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The aim of this study was to estimate heritability of elevated mastitis risk (EMR), a trait derived from in-line measurements of cell counts expressing risk of mastitis on a continuous scale, and its genetic correlation with in-line somatic cell counts. Log-transformed somatic cell counts (SCC; n = 855,181) based on in-line measurements (OCC, DeLaval, Sweden) in automatic milking systems were collected from 2007 to2013 in 7 herds from a total of 1986 first and second parity cows (5 to 305 d in milk). Only data from the lactation with most measurements was used from each cow. A bio-model based on exponential smoothing of the SCC values followed by factor analysis for estimation of the latent variable EMR was used. Finally, EMR was expressed as a continuum on the interval [0;1] using sigmoid transformation. Thus, an EMR value close to zero indicates low risk of mastitis and a value close to one indicates high risk of mastitis. The EMR values were summarized for each cow using the log-transformed median EMR. A second trait

was defined as the median of the log-transformed SCC values from 5 to 305 d in milk. A bivariate animal model was used for estimation of co-variance components for the 2 traits. The fixed part of the model included herd and parity. Estimates of heritability were 0.08 (SE = 0.04) and 0.14 (SE = 0.05) for EMR and SCC, respectively. The genetic correlation between the 2 traits was 0.97 (SE = 0.08). The high genetic correlation indicates that the 2 traits are influenced by common genes, as expected because EMR values are based on SCC measurements. The heritability of SCC is reduced when SCC measurements are processed into EMR values but with similar standard errors. The EMR values are useful in a management context for early mastitis detection and health surveillance; however the present results suggest that SCC values are preferable to EMR values for estimation of breeding values.

Key Words: mastitis, genetic parameter, dairy cow