

Breeding and Genetics: Breeding for Milk Quality and Test-Day Model Applications

611 Quantitative trait loci for milk-fat composition in Dutch Holstein Friesians. A. Schennink*¹, W.M. Stoop¹, H. Bovenhuis¹, J.M.L. Heck², P.D. Koks¹, M.H.P.W. Visker¹, and J.A.M. van Arendonk¹, ¹*Animal Breeding and Genomics Centre, Wageningen University, Wageningen, the Netherlands*, ²*Dairy Science and Technology Group, Wageningen University, Wageningen, the Netherlands*.

This study is part of the Dutch Milk Genomics Initiative and aims at the characterization of genes involved in milk-fat synthesis and milk-fat metabolism. Previous research has shown substantial genetic variation in milk-fat composition: heritabilities were high (0.42-0.71) for short- and medium-chain fatty acids (C4-C16) and moderate (0.22-0.42) for long-chain fatty acids (C18 and longer). A genome-wide scan was conducted to map quantitative trait loci (QTL) affecting milk-fat composition in Dutch Holstein Friesian dairy cattle. The mapping population consisted of 7 half-sib families containing 849 cows in a daughter design. A total of 1378 single nucleotide polymorphisms (SNP) were typed covering all 29 autosomes, to construct a 2829 cM genetic linkage map. The phenotypes under study were 56 milk-fat composition traits, including saturated, mono-unsaturated, poly-unsaturated, and conjugated fatty acids, unsaturation indices, fat percentage and fat yield. A regression interval mapping approach was used to estimate effects and positions of the QTL. In addition to QTL on chromosomes 14 and 26, at which the genes coding for diacylglycerol acyltransferase 1 (DGAT1) and stearoyl-CoA desaturase 1 (SCD1) are located, QTL were detected on several other chromosomes. QTL were detected for short- and medium-chain fatty acids, as well as for long-chain fatty acids. Our results will enable marker assisted differentiation and marker assisted selection, in order to optimize milk quality and to develop innovative dairy products. Prior to implementation of these QTL in breeding programs, additional work is needed to fine map the chromosomal locations and select positional candidate genes influencing milk-fat composition.

Key Words: Milk-Fat Composition, Dairy Cattle, Quantitative Trait Loci

612 Genetic parameters of saturated and monounsaturated fatty acids estimated by test-day model in Walloon dairy cattle. H. Soyeurt*¹, C. Bastin¹, P. Dardenne², F. Dehareng², and N. Gengler^{1,3}, ¹*Gembloux Agricultural University, Gembloux, Belgium*, ²*Agricultural Walloon Research Centre, Gembloux, Belgium*, ³*National Fund for Scientific Research, Brussels, Belgium*.

The contents of saturated (SAT) and monounsaturated (MONO) fatty acids in milk vary through the lactation. The aim of this research was to estimate the genetic parameters for these groups of fatty acids in bovine milk using multi-trait random regression test-day models. The relationship between these fatty acids and the milk production traits was also studied as well as the effects of season and stage of lactation. The model included as fixed effects: herd x date of test, class of 15 days in milk, class of age. Random effects were herd x year of calving, permanent environmental, additive genetic, and residual effects. Since October 2007, all spectra generated by milk recording in the Walloon part of Belgium were collected. The contents of SAT and MONO were estimated by mid-infrared spectrometry. First results were obtained from 100,841 test-day records from 11,626 Holstein heifers. The season and stage of lactation influenced the contents of SAT and MONO in milk

and milk fat. The heritability estimates of SAT and MONO in fat were higher at the beginning of the lactation. The negative energy balance of cows could explain this variation. The values of heritability were also higher at the end of lactation. The genetic and phenotypic correlations among studied traits varied also through the lactation. This study confirms the genetic variability of fatty acids and suggests a possible relation between the contents of SAT and MONO in milk fat and the energy balance of cows.

Key Words: Fatty Acid, Genetic Parameter, Dairy Cattle

613 Genetic parameters of stearoyl coenzyme-A desaturase 9 activity estimated by test-day model. V. M.-R. Arnould*¹, N. Gengler^{1,2}, and H. Soyeurt¹, ¹*Gembloux Agricultural University, Gembloux, Belgium*, ²*National Fund for Scientific Research, Brussels, Belgium*.

Dairy and beef products account for a large part of fat intake in human nutrition and therefore can be linked to dietary diseases. The stearoyl Coenzyme-A desaturase 9 (delta-9) gene was identified as a potential functional candidate gene affecting milk fat composition in dairy cattle. The objective of this research was to estimate the genetic parameters of delta-9 activity indicator traits and to study the relationship between delta-9 activity as described by these indicator traits and common milk production traits. A total of 126,331 test-day records were obtained from 14,259 Holstein (> 84% Holstein gene) heifers belonging to 105 herds. The studied traits were milk yield, percentages of fat and protein, content of monounsaturated fatty acids, and 3 ratios reflecting the delta-9 activity (C14:1/C14:0; C16:1/C16:0 and C18:1/C18). The used model was a multiple-trait random regressions test-day model and included as fixed effects: herd x date of test, class of age, and month x year. Random effects were herd x year of calving, permanent environmental, additive genetic, and residual effects. The fatty acid contents were estimated by mid-infrared spectrometry. Delta-9 activity varied within year and lactation. The obtained heritability estimates of delta-9 as well as the genetic and phenotypic correlation varied also through lactation. This study suggests potential improvements of delta-9 activity and subsequently milk fat composition can be achieved by animal management but also by breeding and animal selection.

Key Words: Delta-9 Desaturase, Genetic Parameters, Dairy Cattle

614 Relationship between lactoferrin, minerals, and somatic cells in bovine milk. H. Soyeurt*¹, V. M.-R. Arnould¹, D. Bruwier¹, P. Dardenne², J.-M. Romnee², and N. Gengler^{1,3}, ¹*Gembloux Agricultural University, Gembloux, Belgium*, ²*Agricultural Walloon Research Centre, Gembloux, Belgium*, ³*National Fund for Scientific Research, Brussels, Belgium*.

Selection for increased mastitis resistance is hampered by lack of available data. Currently, somatic cell count or score are proven indicators. However, it should be a priority to increase the number of available indicator traits for mastitis resistance. The aim of this research was to study the relationships among potential indicator traits as lactoferrin content, concentrations of major minerals in milk (calcium, Ca; sodium, Na; phosphore, P), and somatic cell count. First, 3 calibration equations

were developed using partial least squares regressions to predict the contents of Ca, Na, and P in milk by mid-infrared spectrometry. A total of 1,609 milk samples were collected between March 2005 and May 2006 for 475 cows from 6 dairy breeds. Based on their spectral variability, 100 samples were selected using a principal components approach. The contents of these minerals were estimated by emission spectrometry (ICP-AES). The ratio of standard deviation to standard error of cross validation obtained for the equations predicted the contents of Ca, Na, and P were superior to 2 suggesting the use of these equations in this research. Second, the relationship between lactoferrin, minerals and somatic cells was studied using a random regressions multi-trait animal test-day model. A total of 57,973 milk samples were collected from 94 herds between April 2005 and January 2008 during milk recording in the Walloon part of Belgium.

Key Words: Minerals, Lactoferrin, Bovine Milk

615 Genetic variation in milk protein composition and the effects of genetic variants on the concentration of individual proteins. J. M. L. Heck*¹, A. Schennink², G. C. B. Schopen², H. J. F. van Valenberg¹, H. Bovenhuis², M. H. P. W. Visser², J. A. M. van Arendonk², and A. C. M. van Hooijdonk¹, ¹*Dairy Science and Technology, Wageningen University, Wageningen, the Netherlands*, ²*Animal Breeding and Genomics Centre, Wageningen University, Wageningen, the Netherlands*.

Milk protein composition determines, to a large extent, the nutritional value and technological aspects of milk. To determine the variation in protein composition the concentration of the six major milk proteins, α -lactalbumin (α -LA), β -lactoglobulin (β -LG), α_{S1} -casein (α_{S1} -CN), α_{S2} -casein (α_{S2} -CN), β -casein (β -CN) and κ -casein (κ -CN) was determined by capillary zone electrophoresis in individual milk samples of 2000 cows. This population was especially selected to be able to determine which part of the variation is caused by genetic effects or by factors as herd, stage of lactation, season and cell count. Heritability of every milk protein was determined using an animal model. Genetic variants of the main milk proteins were identified by DNA analyses and their effect on milk protein composition was determined.

The results show large variation in concentration of all individual proteins and a large part of this variation was caused by genetic factors. Milk protein composition has a moderate to high heritability with heritabilities ranging between 0.3 and 0.8. Large variation in combination with high heritability offers great opportunities for changing milk protein composition. The screening of the main milk protein genes resulted, next to the detection of the common genetic variants (α -LA B, α_{S1} -CN B and C, α_{S2} -CN B, β -LG A and B, β -CN A1, A2, A3 and B, κ -CN A and B), into the detection of κ -CN E which was not previously detected in Dutch Holstein Friesian cows. We show that genotypes of β -LG, β -CN and κ -CN have major effects on the concentration of individual proteins and explain a considerable part of the genetic variation in milk protein composition.

This was likely the first study where the total and the genetic variation in detailed protein composition was determined on such a large amount of animals. The effect of genetic variants on all individual proteins, rather than on total protein or total casein, has not been reported frequently. The information resulting from this study shows the possibilities and limits of changing bovine milk protein composition.

Key Words: Milk Protein Composition, Heritability, Genetic Variants

616 Effect of casein genotypes on heritability of milk coagulation ability in Holstein Friesian cows. M. Cassandro*¹, R. Dal Zotto¹, M. De Marchi¹, A. Comin¹, S. Chessa², and G. Bittante¹, ¹*University of Padova, Legnaro, Padova, Italy*, ²*University of Milano, Italy*.

Cheese-making industry plays a fundamental role in Italy, where more than 75% of overall marketable milk is converted into cheese. Therefore, it is important to analyze the genetic aspects of milk coagulation properties (MCP) as coagulation time (RCT, min) and curd firmness (a30, mm). Aim of this study was to estimate the heritability for RCT and a30 estimated with or without the effect of casein genotypes (CSN2 and CNS3) included on the linear model. A total of 1,071 individual milk samples of Italian Holstein cows, daughters of 54 sires, reared in 34 dairy farms of Veneto region (Italy), were analysed for RCT and a30. Moreover, all cows were genotyped for CSN2 and CSN3 loci. Heritability of RCT and a30 traits were 0.25 and 0.15, respectively, without including the effects of CSN2 and CNS3 in the analysis. The use of casein genotypes effect in the model showed a lower heritability estimates (0.15 and 0.09, for RCT and a30, respectively). These results evidenced that MCP can be improved using genetic strategies and that casein genotypes might be considered as major genes for milk coagulation abilities.

Key Words: Milk Coagulation Ability, Genetic Parameters, Casein Genotypes

617 Modeling extended lactation curves in Italian Holsteins. R. Steri¹, F. Canavesi², E. Nicolazzi², G. Gaspa¹, and N.P.P. Macciotta*¹, ¹*Dipartimento di Scienze Zootecniche, Università di Sassari, Sassari, Italia*, ²*Associazione Nazionale Allevatori Frisone Italiana, Cremona, Italia*.

In several countries the average lactation length of dairy cattle has increased markedly in recent years, essentially due to reproductive failures but also to management strategies. The search for suitable mathematical models for extended lactations is of great importance both for genetic evaluations via Random regression Models, and for management decision, especially for the assessment of an economically convenient asymptotic level of production. In this work, 737,011 test day records for milk yield of 69,863 lactations of 45,521 Italian Holsteins (with about 46% of lactations >350 DIM) farmed in four provinces of the North of Italy, were modelled with six common lactation curve functions: Wood (WD), Wilmlink (WIL), Ali and Schaeffer (AS) multiple regression, fifth-order Legendre polynomials (LEG), quadratic (QSPL) and cubic splines (CSPL) with three knots. Moreover, data were modelled with the version of the Dijkstra model specifically suggested for extended lactations. As expected, functions with a larger number of parameters showed better fitting performances for individual patterns, with about 75% of curves showing an adjusted R-squared higher than 0.70 for AS, LEG, QSPL and CSPL. Moreover, fitting performances tend to increase with lactation length due to the larger number of data. Lactations curves exceeding 650 DIM and that showed adjusted R-squared greater than 0.75 when modelled by the modified Dijkstra function, separately by parity, in order to calculate some measures of technical importance. Days at peak were 75, 48 and 48 for first, second and third calving cows; peak yield were kg/d 32.7, 38.3, 39.9. Cumulative yield at 305 and 1000 DIM were different across parities: 9,177 vs 22,154 (1st parity), 9,846 vs 21,925 (2nd parity), 10,115 vs 21,875 (3rd parity). The estimated

asymptotic level of production in the tail of lactation was on average 10 kg/d but together with a marked variability.

Key Words: Dairy Cattle, Extended Lactations, Mathematical Models

618 Issues in modelling lactation curves with regression splines. N. P. P. Macciotta*¹, F. Miglior^{2,3}, A. Cappio-Borlino¹, and L. R. Schaeffer⁴, ¹*Università di Sassari, Sassari, Italia*, ²*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, ³*Canadian Dairy Network, Guelph, ON, Canada*, ⁴*CGIL, University of Guelph, Guelph, ON, Canada*.

Regression splines are a type of segmented regressions in which the curve is divided into different segments of the independent variable, joined at points named knots, each fitted with different polynomials. Cubic splines are becoming a model of interest for fitting individual lactations in random regression test day models for dairy traits whereas linear and quadratic splines have been proposed to fit growth curves. The main objective in spline modelling is to optimize the number and placement of knots. Non linear procedures allow for the estimation of knot position, treated as parameter of the function. In this study, lactation curves of Canadian Holsteins were modelled with splines of different order by using non linear procedures. Data were 285,340 test day records of Canadian Holsteins each with 10 records. Average curves of different parities (1 to 3) were modelled with linear, quadratic and cubic splines. Models with one, two and three knots were tested. Estimated knots positions were used to model individual curves by linear spline regressions. Fitting of average curves was high for all models considered (adjusted R-square > 0.98). By and large, the increase of the number of knots resulted in convergence problems. Only quadratic splines converged in all the three parities and for all the number of knots considered. The order of splines affected the knot position: for example when only one knot was fitted, the position was between 30-37 days in milk (DIM) for linear, 40-46 DIM for quadratic and 53-62 DIM for cubic splines, respectively. For increasing number of knots, their positions appeared more consistent for quadratic and cubic splines. When three knots were fitted, the first knot was between 10 and 26 DIM, the second between 23 and 59 DIM, the third between 60 and 252 DIM. Finally, no substantial increases of adjusted R-square was observed when increasing the number of knots or moving from quadratic to cubic splines in individual fitting, with about 60% of curves having an adjusted R-square greater than 0.6.

Key Words: Lactation Curve Modeling, Regression Splines, Knots

619 Improving stability of test day model bull proofs. F. Canavesi, S. Biffani*, E.L. Nicolazzi, and R. Finocchiaro, *ANAFI, Cremona, Italy*.

Test days are used for the official genetic evaluation in Italy since November 2004. They are used in a multiple trait multiple lactation random regression test day model. Since its introduction a larger variation on average was observed in bull proofs in comparison to the old repeatability model based on 305 days ME lactation records. In order to

improve proof stability several areas were investigated from definition of fixed effects to estimation of genetic parameters. Critical moments in bull proofs variation were the arrival of second and third lactation into the system.

In Italy progeny testing daughter data are coming into the genetic evaluation system at different times depending on efficiency of AI studs in distributing semen, efficiency of farmers in using young bulls doses, age at calving heterogeneity across regions. Therefore young bulls add daughters at every run and this may cause variation in bull proofs. A bull gets its official proofs when there are at least 30 daughters at 120 DIM in 30 herds but there were not limits set for second and later parities daughters. In January 2008 a new procedure was applied and now second and third parity daughters data can be used for bull evaluation only if they meet the following criteria: 5 daughters at 120 DIM in second lactation and 3 daughters at 120 DIM for third lactation. This improved stability of proofs from run to run on average by 10% and moreover reduced the number of bulls that were decreasing one run and increasing the next or viceversa due to the arrival of early and scarce data on second and third parity daughters.

Key Words: Stability of Proofs, Test Day Model, Accuracy of Proofs

620 Genetic parameters for milk, fat and protein in Holsteins using a multiple-parity test day model that accounts for heat stress. I. Aguilar*^{1,2}, I. Misztal¹, and S. Tsuruta¹, ¹*University of Georgia, Athens, GA*, ²*Instituto Nacional de Investigación Agropecuaria, Las Brujas, Uruguay*.

Data included 585,119 test-days (TD) in first to third parity for milk (M), fat (F) and protein (P) from 38,608 Holsteins in GA. Daily temperature humidity indices (THI) were available from public weather stations. Models included a repeatability test-day model (MREP) with a random regression on heat stress index (HIS), and a test-day random regression model (MRRM) using linear splines with 4 knots and HSI, which was defined as THI over 22C from the 3rd day before the TD from a weather station closest to the farm. Knots for splines in MRRM were placed at 5, 50, 200, and 305 days-in-milk (DIM). Random effects were additive and permanent environment in MREP and additive, permanent environment and herd-year for MRRM. Additionally, models included herd test day, age, milking frequency and DIM classes as fixed effects. In MREP and for M, F and P, the phenotypic variance increased by 50-60% from 1st to 2nd parity and additionally by 12-15% in 3rd parity. The regular genetic variance increased by 30-40% from 1st to 2nd parity but slightly declined in 3rd parity for M and P. The heat stress variance doubled from 1st to 2nd parity, and additionally increased by 20-100% in 3rd parity. The genetic correlations between parities in the regular animal effect were ≥ 0.84 , but they were ≥ 0.96 between 2nd and 3rd. The genetic correlations between parities in the heat-stress effect were $\geq 0.56-0.79$. The genetic correlations between regular and heat stress effects across parities and traits were between -0.30 and -0.47. With MRRM, the variance of the heat stress effect was about half of that with MREP. The most negative (-0.42) genetic correlation for milk between regular and heat stress effects was at 50-200 DIM for 1st parity and at 200-305 DIM for parities 2-3. Genetic variance of heat stress strongly increases with parity. It is inflated with MREP due to timing of lactations to avoid the peak production during heat stress.

Key Words: Heat Stress, Variance Components, Multiple Lactations

621 An alternative model to accommodate very large numbers of traits in random regression test-day models. N. Gengler*^{1,2}, ¹*Gembloux Agricultural University, Gembloux, Belgium*, ²*National Fund for Scientific Research, Brussels, Belgium*.

Computing capability has continued to increase following Moore's law allowing the use of full multitrait models in many cases. However there are still situations where current computing algorithms need to be optimized. One of these is large scale multitrait random regression models (MT-RRM), the type suitable for type traits and milk components where potentially 30 and more traits are analyzed together using several random regression effects. An equivalent model to a MT-RRM can be defined as a complete repeated records model where the different traits are standardized according to residual variances or records are weighted accordingly. Trait-specific or across trait fixed effects can be defined. Trait-specific random effects need to be used; however definition of random effects does not need to be identical for all traits. This equivalent model is also an excellent base to use rank reduction as the

potentially large number of random effects (effects x number of traits x number of regressions) can be reduced dramatically based on (co)variance structures among them. Adapted variance component estimation strategies can be used based on REML and Gibbs sampling algorithms. Alternative solving algorithm such as the use of sequential estimation of regressions and effects on regressions can be easily adapted to this framework. This equivalent model has also the practical advantage that it allows for easier models where some traits have been recorded for a long period (e.g., stature, milk, fat, protein) and other traits are recent and have much more sparse data (e.g., rear legs rear view, different fatty acids in milk fat). This can be done by a full or partial transformation of records of different traits to repeated records. This alternative model approach should make MT-RRM practical for many traits and trait groups under selection in dairy populations, today and in the future.

Key Words: Mixed Model, Equivalent Model, Rank Reduction