

195 Differences in genetic parameters for production traits and somatic cell scores estimated using a multiple trait random regression test day model in the Italian Holstein population. A.B. Samore*^{1,2}, F. Canavesi¹, S. Biffani¹, P. Boettcher³, and J. Jamrozik⁴, ¹ANAFI, Italy, ²Wageningen University, The Netherlands, ³IDGVA-CNR, Italy, ⁴CGL, University of Guelph, Canada.

Genetic parameters for a multiple test day random regression model, that Italy is planning to implement for routine genetic evaluation in the future, need to be estimated for production and somatic cell scores. The lactation model now used in Italy accounts for heterogeneity of genetic variance across herds. A similar adjustment could be still necessary when using a test day model. A first data set was randomly sampled by herd number including 82,368 test day (TD) records from 5,675 cows without regards to production level. Low (52,527 TD) and high (71,986 TD) production data sets were created by randomly sampling herds differing for milk production by more than two standard deviations. Genetic parameters were estimated using an animal model and including the fixed effect of herd-test day, and the random effects for permanent environment, animal, and residual. The shape of lactation was modelled using the function of Wilmink (1987) as: $W(t) = w_0 + w_1 t + w_2 \exp(-0.05t)$. The residual covariances differed across 4 stages in each lactation. In total the model estimated 666 genetic, 666 permanent environmental, and 120 residual (co)variances for each data set. A Bayesian approach, as described in Jamrozik et al. (1998), was used to obtain the means of the posterior distributions for all parameters of the model. Heritabilities ranged from .15 to .38 depending on trait and parity. A wide range of values was found for correlations between traits and parities. Interesting null or slightly favourable correlations were reported between somatic cell scores and production traits (on average -.10), also in first lactation (from -.02 to -.04), in the first data sets. Differences in parameters were found for different levels of milk production and will be considered to define the adjustment for heterogeneity of variances across herds in the official test day model evaluation procedure.

Key Words: Genetic parameters, Italian Holstein, Test day model

196 Nonparametric Bayesian Analysis Of Test Day Milk Yield Data. R. Rekaya*¹, ¹Dept. of Animal and Dairy Science, University of Georgia.

The practice of hierarchical modeling has increased in the last decade both in applied statistics and in animal breeding, in part, as a result of development in Markov Chain Monte Carlo methods (MCMC) to overcome the computational complexity. In hierarchical models, as with all parametric models, specification of distributions for parameters and often hyper-parameters is required. Usually a considerable uncertainty is associated with those distributions leading to inevitable concerns about the sensitivity of the resulting inferences to the assumed forms of component distributions. Hence, a nonparametric or semi-parametric modeling that avoids the prior specification of distribution forms is a logical choice to assess such uncertainty. Dirichlet process prior represents the

cornerstone of modern nonparametric Bayesian modeling by allowing in a relatively easy way, the relaxation of the parametric assumptions. A total of 3,214 test day milk yield records from 341 cows with complete lactations were analyzed using a parametric and a nonparametric hierarchical model. A three stage hierarchical model was assumed, where the first stage describes the conditional distribution of the data. Wood's incomplete gamma function was used. At the second stage, the joint distribution of the lactation curve parameters was assumed to be normal in the parametric case and unknown with a Dirichlet process prior for the nonparametric model. Posterior means of heritability for the three parameters of the lactation curve were 0.24, 0.27 and 0.14 using the parametric model and 0.16, 0.32 and 0.14 using the nonparametric model. Those changes were behind the Monte Carlo errors. Non-negligible changes were observed also for the genetic correlations between the lactation parameters. The posterior mean of the precision parameter of the Dirichlet process was 5.7. This small value does not support the normality assumption for the distribution of the lactation curve parameters used in the parametric case.

Key Words: Nonparametric, Dirichlet, Milk

197 Changes of genetic correlation between milk production and body size over time in Holsteins using random regression models. S. Tsuruta*¹, I. Misztal¹, T. J. Lawlor², and L. Klei², ¹University of Georgia, Athens, GA, ²Holstein Association USA Inc., Brattleboro, VT.

The objective of this study was to investigate changes of genetic correlations between milk production and body size traits with random regressions on year. Genetic parameters for production traits (milk, fat, and protein yields), linear type traits (stature, strength, body depth, and thurl width), and the body size composite (BSC = stature \times 0.50 + strength \times 0.25 + body depth \times 0.15 + thurl width \times 0.10) in Holsteins were estimated using bivariate (production and type) random regression models. About 40,000 first lactation cows with linear type scores obtained from Holstein Association USA Inc. and with 305-d production records obtained from USDA-AIPL were used in this analysis. Some of the protein records were missing. The first order Legendre polynomial for additive genetic effects was included in the models as linear random regression on year at calving. Heritability estimates for BSC increased over the years, ranging from 0.30 to 0.44. The genetic correlations between milk yield and BSC were positive and constant (0.09 to 0.10). The genetic correlations between fat yield and BSC increased in the 1980s but were stable (around 0.10) in the 1990s. The genetic correlations between protein yield and BSC were also positive, but decreased from 0.15 to 0.10 in the 1990s. The genetic correlations between milk yield and each linear type trait were all positive and relatively stable over time; especially, those for body depth were higher (0.14 to 0.16) than for other linear type traits. These results indicate that the trend of larger cows producing more milk has not changed for the last 20 yr.

Key Words: Genetic correlation, Body size, Random regression

Dairy Foods

Whey Proteins: Structure, Production, Function, and Future

198 β -Lactoglobulin: Properties, Structure and Function. L. Sawyer*, *The University of Edinburgh.*

β -Lactoglobulin (BLG) is the major whey protein of ruminant species. It is present also in the milks of many, but not all, other species. Its amino acid sequence and 3-dimensional structure show that it is a member of the lipocalin family that includes a widely diverse series of molecules most of which bind small hydrophobic ligands and may act as specific transporters, as does serum retinal binding protein. BLG appears to bind a wide range of ligand molecules but it is still unclear whether this is its physiological function. During heat treatment in milk processing plants, BLG is believed to be a major initiator of aggregation and hence fouling of heat-exchangers. It has also been linked to milk allergy. In reviewing the physicochemical properties of the protein, emphasis will be placed upon those studies that give insight into the behaviour during unfolding and denaturation under a variety of conditions. Further, by considering the lipocalin family in general, and in particular the species

distribution of BLG, some speculation as to the physiological function can be made.

Key Words: β -Lactoglobulin, Structure

199 Heat-induced reactions involving β -lactoglobulin and other milk proteins in milk, whey, and model systems. L. K. Creamer*¹, G. A. Manderson¹, Y-H. Hong², P. Havea¹, Y-H. Cho³, H. Singh⁴, A. Bienvenue⁵, and R. Jimenez-Flores⁵, ¹NZDRI, Palmerston North, New Zealand, ²Chonnam University, Kwanju, Korea, ³Mass. General Hospital, Boston, MA, USA, ⁴IFNHH, Massey University, Palmerston North, NZ, ⁵DPDC, Calpoly, San Luis Obispo, CA, USA.

Heat treatment of milks is an essential step in modern dairy processing and the effects can be far-reaching in terms of product functionality and the heat-induced gelation of whey protein concentrate (WPC) solutions is important in functional food applications. Heating WPC solutions or milk beyond pasteurisation causes some of the individual whey proteins

form aggregates and to aggregate with the other whey proteins. Studies using various kinds of two-dimensional polyacrylamide gel electrophoresis (PAGE) analysis as the major tool with simple solutions of pure whey proteins confirmed that β -lactoglobulin (β -Lg) was the most important whey protein in these aggregations. A previously unknown group of intermediates, the non-native β -Lg monomers, was of particular interest and some characteristics of these and other early heat-induced intermediates were determined. The changes in the positions of the disulphide bonds in β -Lg as a consequence of heat treatment were identified from mass spectroscopy-based analyses. \otimes Heated mixtures of α -lactalbumin (α -La) and β -Lg were found to contain 1:1 disulfide-bonded dimers as well as non-native monomers, dimers, trimers, etc. of both α -La and β -Lg. The findings from this and other model systems were then tested in WPC solutions using one- and two-dimensional PAGE. \otimes In heat-treated milk the whey proteins interact to form disulfide bonds with the casein micelles and κ -casein (κ -Cn) is the most significant casein in this reaction and β -Lg was the most important whey protein in this reaction. In a model system, κ -Cn and β -Lg formed 1:1 aggregates as well as large polymeric aggregates. A heat-induced complex of β -Lg and κ -Cn was isolated from a heated mixture of casein micelles and β -Lg by chromatography. Analysis of this complex identified a number of novel disulfide bonds between β -Lg and κ -Cn. \otimes These results have shown that β -Lg is critical to the heat-induced changes in both milk and WPC, and have led us to re-evaluate the likely mechanism for the initial changes within β -Lg in response to heat-treatment.

Key Words: β -Lactoglobulin - κ -casein complex, Non-native β -lactoglobulin monomers, Heat-induced β -Lg - α -La complex

200 Functional properties of whey proteins. M. Britten*, FRDC, Agriculture and Agri-Food Canada, St-Hyacinthe, Qc., Canada.

In recent years, the use of whey proteins in formulated foods has increased. Health conscious consumers recognize their high nutritional value. Specific biological activities have also been attributed to whey proteins which makes them suitable ingredients for the formulation of functional foods. Along with a healthy image, whey protein provides foods with improved texture and overall quality. A better control of protein polymerization is however required to optimize their use. Heating a whey protein dispersion leads to polymer formation. The pH, calcium and protein concentrations during treatment determine aggregate size, shape and hydration. These characteristics influence their behavior in food systems. Controlled aggregation of whey protein is used to increase the viscosity and improve the mouth feel of liquid products. Added to cheese milk, whey protein aggregates are trapped in the curd and increase the yield, moisture and reduce firmness of cheese. In specific aggregation conditions, whey proteins form opaque dispersions and can be used as clouding agents in beverages. Gel formation is usually induced by heating native whey protein dispersions. However, it can also be obtained from polymerized whey protein dispersions by acidification or by the addition of salts. Use of polymerized whey proteins in yogurt formulations increases firmness and reduces syneresis. Whey proteins are also used in the preparation of emulsions and foams. They adsorb at interfaces and form a membrane which prevents emulsion coalescence or foam collapse. Whey protein membrane has also been shown to provide protection against lipid oxidation. The combination of interfacial adsorption and gel formation properties is used to produce solid-like emulsions and foams. This approach finds applications in baked foods or in the development of nutrient carriers. Whey protein polymerization offers new means to control food texture and stability. It should support the development of formulated food especially designed for health conscious consumers.

Key Words: protein polymers, gel formation, emulsions

201 Technological, functional and biological properties of peptides obtained by enzymatic hydrolysis of whey proteins. S.F. Gauthier* and Y. Pouliot, Centre de recherche STELA, Université Laval, Quebec, Canada.

The study of peptides released by enzymatic hydrolysis of whey proteins has been initially focussing at functional properties in model systems. Our first work showed that sequences 41-60 and 21-40 from β -lactoglobulin (β -LG) were responsible for improved emulsification properties in tryptic hydrolysates of β -LG. Further work showed that adding negatively charged peptides from chymotryptic hydrolysates of whey proteins could prevent phase separation of dairy-based concentrated liquid infant formulas, as a replacement of carrageenin. Hydrolysis of whey proteins using bacterial enzymatic extracts was also successful in improving heat stability of whey proteins in an acidic beverage. Recent work demonstrated the occurrence of interactions between peptides β -LG 102-105, β -LG 142-148 and the native β -LG. These latest results suggest that β -LG could be used as a carrier for bioactive peptides. Finally, the emerging functional foods and nutraceuticals have triggered the development of new knowledge on the biological activity of whey proteins. Whey proteins are recognized to comprise peptide sequences having ACE-inhibiting properties. Our work led to the development of whey protein enzymatic hydrolysate that has demonstrated antihypertensive properties when orally administered to SHR rats at a dosage of 75 mg/kg. Our work has shown that the enzymatic hydrolysis of whey proteins is not only improving their functional and technological properties but it is also providing powerful tools to exploit their full potential by generating bioactive peptides.

202 The quantitative analysis of whey proteins - where we are and where we are going. DE Otter* and EA Foegeding, North Carolina State University, Raleigh, NC.

As whey proteins become ingredients in more sophisticated nutraceutically and functionally based foods and dairy products it is imperative that they can be accurately quantified. My presentation will highlight some of the research presently being undertaken to address this issue and to suggest directions for future research.

Previous work has concentrated on quantifying the major whey proteins; α -lactalbumin, β -lactoglobulin, bovine serum albumin and immunoglobulin. There is however an increasing demand to also quantify the minor components, such as glycomacropeptide, lactoferrin and folate binding protein; the bioactivity of the different proteins/peptides; and the amount of native and denatured protein. Researchers are using a number of diverse methods for measuring the individual whey proteins. The idiosyncrasies of each method must be considered when quoting values for the individual proteins.

The cornerstone of any successful quantitative method is the availability of well-defined calibration standards. A wide array of analytical techniques such as nitrogen analysis, UV spectroscopy, PAGE, HPLC and CE has been used to characterise a set of whey protein standards. These techniques all have their individual limitations but when used together they give a good estimate of protein purity. An alternative method based on the unique amino acid 'fingerprint' of each whey protein has also been used to characterise the standards (Tsao et al., The Food Technologist, 28 (3), 94, 1998). Using an in-line nitrogen detector to accurately quantify the nitrogen content of specific HPLC peaks has further enhanced the characterisation. The identity and integrity of the proteins in these peaks has been verified by HPLC-mass spectrometry. Another important component of method development is method validation and accreditation. This usually involves an inter-laboratory comparison study under the auspices of an international organisation such as AOAC or IDF. The steps involved for an HPLC method for the quantification of bovine IgG that is currently going through this process will be described.

Key Words: Whey proteins, Quantitative analysis, Calibration standards

Extension Education and International Animal Agriculture The Impact of Governmental Policies on North American Animal Agriculture

203 Mexico: Agricultural policies, trade agreements and challenges for the animal scientist. M Garcia-Winder*¹, ¹T.C. Jacoby & Co.

The importance of the agricultural sector in Mexico is not only determined by the number of people living in rural areas (25% of total

population), or because of its contribution to GNP (6.3%), but also because it is a sector with higher poverty levels and in more need of development. The incorporation to GATT, was the beginning of profound transformations. As a consequence agricultural policies have been