

Evolution of milk calcium content during the year

Catherine Hurtaud, Muriel Johan, Ségolène Leurent, Yves Gallard, Luc Delaby

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HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés. than that of fat and total solids. Excellent ratio of prediction to deviation (RPD) value was observed for protein, while RPD for fat, lactose, total solids and non-fat solids were acceptable. It was concluded that near infrared transflectance spectrum would be capable of in milk composition determination.

Table 1. Parameters of milk composition model

			Calibration			Validation			
Milk composition	Pre- treatment	PC	Predicted Y vs. measured X	RMSE	R ²	Predicted Y vs. measured X	RMSE	R ²	RPD
Protein	No	9	Y =0.969x +0.114	0.036	0.98	Y=0.960x +0.148	0.045	0.97	4.97
Fat	No	6	Y =0.916x +0.383	0.177	0.93	Y=0.910x +0.410	0.197	0.92	3.06
Lactose	MSC	12	Y =0.928x +0.362	0.029	0.96	Y=0.911x +0.448	0.042	0.91	3.15
Total solids	SNV	5	Y =0.922x +1.093	0.219	0.92	Y=0.915x +1.188	0.234	0.91	3.41
Nonfat solids	SNV	11	Y =0.940x +0.569	0.067	0.94	Y=0.927x +0.695	0.077	0.92	3.54

Key Words: near-infrared transflectance spectrum, milk composition

W8 Evolution of milk calcium content during the year. C. Hurtaud*¹, M. Johan¹, S. Leurent², Y. Gallard², and L. Delaby¹, ¹INRA-Agrocampus Ouest UMR 1348 PEGASE, Saint-Gilles, France, ²INRA Domaine du Pin-au-Haras, Exmes, France.

Calcium content is regarded as being relatively stable in cows' milk during lactation. However, results from commercial herds, have suggested that changes in milk calcium (Ca) content can occur. The objective of this experiment was to compare the characteristics of milk (especially milk Ca content) based on low input grass based systems compared with corn silage based systems, across 2 breeds of dairy cows (Holstein, HO vs. Normande, NO). The experiment took place on the INRA experimental farm of Le Pin-au-Haras. Sixty dairy cows were observed from calving to drying off. Two feeding systems were compared. The Intensive system (IS) was designed to maximize individual performance, with a high energy diet (in winter, corn silage with 30% concentrate; in spring, summer and autumn periods, pasture with 4 kg/d of concentrate supplemented with corn silage from July). The Grass system (GS) was designed to decrease inputs (in winter, conserved grass with no concentrate; in spring, summer and autumn, pasture with no concentrate). The experimental design was a continuous design. No significant interaction was detected between feeding system and breed for milk yield and composition. During the whole year, GS treatment reduced milk yield (-5 kg/d), with no significant effect on protein and total Ca contents. The NO cows produced less milk, but with higher protein and total Ca contents. During winter, GS treatment reduced milk yield, protein and total Ca contents. Milk Ca content decreased from January to June and rapidly increased after July irrespective of breed. During May and June, HO milk had a Ca concentration below the French limit of 1.2 g/L of the European health allegation of milk for consumption. There was a significant effect of stage of lactation and month on Ca content. Month included numerous significant factors such as maximum daily temperature, day length and radiance duration. This study clearly showed that both cow genotype and lactation stage affects milk Ca content. However, the lactation stage did not explain all the seasonal variations of milk calcium content observed in this trial.

Key Words: milk, dairy cow, calcium

W9 Quantitative analysis of supercritical carbon dioxide (sc-CO₂) treated β -lactoglobulin tryptic peptides. C. Kembel* and R. Jimenez-Flores, *California Polytechnic State University, San Luis Obispo*.

Whey protein is an abundant source of biologically active peptides that have a diverse set of functional properties. One limitation in the production of novel peptides is the native folding of the proteins secondary and tertiary structure. B-Lactoglobulin is a barreled protein with a hydrophobic core capable of binding other proteins. Due to its abundance in whey, it represents an important source of bioactive peptides. We present a method with the potential for the production of novel bioactive peptides from whey. Supercritical CO₂ is known to change protein conformation due to its hydrophobic properties, high diffusion coefficient, low viscosity, and low surface tension. Because β-Lactoglobulin contains a large hydrophobic core where binding sites are present, sc-CO₂ treatment is likely to expose these hydrophobic sequences. These sequences are normally confined to the interior of the protein away from enzymatic attack under normal conditions. Therefore upon exposure to sc-CO₂, these sequences were shown to be more susceptible to trypsin hydrolysis. This method increases the potential for the production of novel peptides. Minor changes in the temperature of the sc-CO₂ treatment induced subsequent conformational changes resulting in different peptides. Variable conditions (pH, temperature, and pressure) sc-CO₂ was shown to yield unique fingerprints by SDS-PAGE. Capillary electrophoresis was then used to discern the peptide profiles of the sc-CO₂ treated peptides as well as native peptides. Distinct differences in peptide profiles were noted. Subsequent analyses will include HPLC-MS to determine peptide sequences and quantity differences in peptide treatments.

Key Words: supercritical CO₂, whey protein, bioactive peptide

W10 AFM imaging and analysis of phospholipid monolayers. J. Cuthbert^{*1}, S. Gallier², D. Gragson¹, and R. Jimenez-Flores¹, ¹California Polytechnic State University, San Luis Obispo, ²Massey University, Palmerston North, New Zealand.

Membrane structure analysis in biological systems is fundamental for understanding its relationship with function. Membrane analyses still relies on observations of the physical phenomena of its components in model systems. Dairy foods are complex systems that incorporate parts of colloidal properties with emulsions. The emulsion in a dairy system is unique due to the presence of the milk fat globule membrane (MFGM). This membrane is composed of phospholipids and proteins, and it has an important biological function in the initial stages of mammals' lives, and in humans it has an important nutritional role throughout their life. In our work to elucidate the structure/function relationship of the MFGM, we are exploring some structural aspects of its phospholipids. Therefore, in this work we present how the properties of the phospholipid/protein monolayers found in milk fat globules were investigated using atomic force microscopy (AFM) in a model system with phospholipids extracted from raw milk and either β-casein or β-lactoglobulin. Slides of the phospholipid and phospholipid-casein monolayer films were prepared as models from a Langmuir trough. The aim was to determine if the monolayers would form liquid-ordered domains or alternatives. Our observations indicate that this technique distinguishes liquid ordered domains in AC contact mode. In this mode, the cantilever oscillates above the surface. It is gentle enough to image phospholipid monolayers without damage. When the tip approaches the surface, the sample's intermolecular and electrostatic forces change the cantilever's amplitude and phase angle. As the cantilever is affected by surface forces, a piezoelectric scanner adjusts its height. The monolayer