T83 Evaluation of the addition of urea to refrigerated raw milk on the crude protein, milk fat, lactose, and total solids contents determined by mid-infrared spectrometry. E. G. Esteves[1], M. M. O. P. Cerqueira*[2], L. M. Fonseca[2], M. O. Leite[2], M. R. Souza[2], C. F. A. M. Penna[2], R. Rodrigues[2], and L. R. Abreu[3], [1]*Ministry of Agriculture*, *Brasília, Distrito Federal, Brasil*, [2]*Federal University of Minas Gerais*, *Belo Horizonte, Minas Gerais, Brasil*, [3]*Federal University of Lavras*, *Lavras, Minas Gerais, Brasil*.

To detect the effect of fraudulent addition of urea to refrigerated raw milk, 32 samples of milk from 32 samples of milk from bulk tanks were collected at different dairy farms. A control sample and 3 test samples added with different levels of urea (0.0723, 0.1445 and 0.2891 wt%) were made. Both, the bulk tank and the test samples were analyzed to determine the crude protein, lactose, milk fat, and total solids contents by mid-infrared spectrometry. The crude protein, lactose, and total solids contents increased in 0.110, 0.17, and 0.140 wt%, respectively, on a 0.2891 wt% of urea added to milk. On the same conditions, the milk fat content decreased in 0.032 wt%. The equations of linear regression among the urea levels added (in wt%) and the crude protein and the total solids contents (both in wt%) were established. The changes on refrigerated raw milk composition submitted to the addition of urea detected by mid-infrared spectrometry analysis show that this fraudulent addition can increase the profits of the dairy farmer when milk payment is applied by the dairy industry.

Key Words: urea, milk composition, mid-infrared spectrometry

T84 Cheese whey compositional analysis using infrared spectroscopy. F. A. Pinto[1], L. A. Clementino[1], D. L. S. Oliveira[1], L. R. Abreu[2], L. M. Fonseca*[1,3], R. Rodrigues[1,3], M. O. Leite[1,3], and M. M. O. P. Cerqueira[1,3], [1]*Federal University of Minas Gerais/Escola de Veterinária/DTIPOA*, *Belo Horizonte, MG, Brazil*, [2]*Universidade Federal de Lavras/DCA*, *Lavras, MG, Brazil*, [3]*Laboratory for Milk Quality Analysis*, *Belo Horizonte, MG, Brazil*.

Compositional analysis of whey is necessary for its best utilization. To perform physicochemical analysis, infrared spectroscopy techniques are useful, as they are fast and precise. The objective of this research was to evaluate infrared spectroscopy for measurement of cheese whey composition from typical Brazilian cheeses. Twenty-one samples of whey from Minas padrao cheese and 22 samples of whey from Prato cheese were analyzed, using standard methods and a filter infrared equipment (Combisystem 2300, Bentley). The results for fat, protein and total solids using infrared instrument based on filters and standard methods were compared by Friedman test for related samples. The mean values are presented in Table 1.

The differences between results from both methods were significant. The pasteurization process can affect the results, as compounds formed during heating may interfere with infrared spectrum readings, and the whey samples used for equipment calibration were made from raw milk. After a linear transformation of the results with curve approximation, measurement of whey composition from Minas padrao cheese by infrared and standard methods were statistically equivalent. Therefore, results show that it is necessary to perform an equipment calibration for cheese whey analysis using infrared equipment based on filter. However, for whey from Prato cheese, even after transformation, the difference was significant. This whey has a water excess, as showed by the high freezing point. Moreover, it has a dye that is added for typical orange color during Prato cheese production. Water and pigment may affect the absorption of infrared radiation by the whey constituents. Therefore, infrared spectroscopy based on filters can be used for component analysis of whey from Minas padrao cheese, as long as a calibration adjustment is used. For Prato cheese whey, the infrared method based on filters did not provide accurate results.

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Table 1. Compositional analysis of cheese whey using standard methods and infrared spectroscopy

	Minas Cheese Whey		Prato cheese whey	
Component	Standard Methods	IR Spectroscopy	Standard Methods	IR Spectroscopy
Fat (g/100g±SD)	0.38±0.12	0.33±0.12	0.40±0.08	0.26±0.15
Protein (g/100g±SD)	0.78±0.08	0.67±0.11)	0.78±0.08	0.73±0.07
Total solids (g/100g±SD)	6.42±0.21	6.79±0.20	6.19±0.75	6.85±0.54
Ashes (g/100g±SD)	0.49±0.03	–	0.48±0.05	–
Chloride (g/100g±SD)	0.20±0.01	–	0.19±0.02	–
Freezing point (°C)	–0.507	–	–0.492	–

SD-standard deviation.

Key Words: cheese whey composition, infrared spectroscopy, infrared milk analyzer

T85 Comparison of Mojonnier and Gerber methods for analyzing the fat content of fermented milk beverages. E. H. P. Andrade, M. O. Leite, C. F. A. M. Penna, M. R. Souza, L. M. Fonseca*, and M. M. O. P. Cerqueira, *Federal University of Minas Gerais*, *Belo Horizonte, Brasil*.

The objective of this study was to compare 2 methods to estimate fat content in fermented milk beverages. The samples of fermented milk beverages were collected in large supermarket chains from Belo Horizonte, Minas Gerais, Brazil. Both methods are described in Brazilian legislation, but Mojonnier is the official method to analyze fat content in milk beverages and Gerber is the official method to analyze fat content in fluid milk. Gerber is a simpler and easier method to perform than Mojonnier method. Thirty samples of fermented milk beverages were analyzed using the 2 methods. There was no difference ($P > 0.05$) between Mojonnier and Gerber methods for fat content measurement in these samples. So, both of them could be used to measure the fat content in fermented milk beverages.

Key Words: fermented milk beverages, Mojonnier method, Gerber method

T86 Quantitative analysis of the distribution of fat globules in milk. G. Impoco[1], N. Fucà[2], and G. Licitra*[1,2], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*DACPA, University of Catania*, *Catania, Italy*.

This study aims at devising image analysis methods to quantify the distribution of fat globules in confocal laser scanning microscope

(CLSM) images. Milk was collected from a local farm and subject to eight different treatments. Ten images were recorded for each milk specimen using CLSM at 40X and classified according to five parameters (small globules count, large globules count, globule density, presence of clusters, and distribution homogeneity). Each image was classified through visual inspection by assigning a numeric score to each parameter. Visual evaluation provided qualitative, subjective information. Automatic quantitative analysis was performed onto the same images to obtain objective, repeatable estimates. Each image was partitioned into cells. For each cell, nine numerical descriptors were computed (e.g., number of globules in a cell, area covered by globules). For each descriptor, a measurement was obtained at each cell. The variances of such measurements over all cells were recorded. Nine descriptors were thus obtained for each image. Factor analysis on manual evaluation data revealed that count of small and large globules were strongly inversely correlated (−0.85), as well as density and homogeneity to the presence of clusters (−0.40 and −0.61, respectively). Density and homogeneity had a moderate correlation factor (0.66). Principal component analysis showed that the first three components accounted for 80% of the total variance in scores. Factor analysis was also performed on software measurements. As expected, several descriptors were highly correlated since they capture similar aspects of the images. After grouping correlated factors, numerical description was consistent with qualitative parameters. Automatic classifications turned out to be a good interpretation of manual annotations. This suggests that quantitative characterization of dispersed phases of fluids in CLSM micrographs is promising.

Key Words: image analysis, milk treatments, milk microstructure

T87 Evaluation of Sprint rapid protein analyzer for total protein analysis of Cheddar cheese. H. M. Zhang*, P. Salunke, J. K. Amamcharla, and L. M. Metzger, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

The Kjeldahl method is widely used as a reference method for protein measurement of numerous dairy products including cheese. However, it is labor intensive, time consuming, and utilizes hazardous chemicals. A new protein analysis instrument called the Sprint rapid protein analyzer (CEM Corporation) was recently developed. This instrument utilizes an automated protein-tagging technology and is rapid, easy to operate, and does not utilize hazardous chemicals. In previous research we have demonstrated that the Sprint method is applicable for analysis of milk and cream samples. The objective of this study was to evaluate the applicability of the Sprint method for the analysis of Cheddar cheese. In this study 6 Cheddar cheese samples were analyzed for protein in duplicate using the Sprint method and the Kjeldahl method at 1 week, 3, 6, 9, and 12 mo on ripening. The protein content of each sample measured by Kjeldahl analysis remained relatively constant throughout ripening (mean difference between 1 week and 12 months was - 0.23%), whereas the protein content of each samples measured by the Sprint method decreased during ripening (mean difference between 1 week and 12 months was 2.68%). The average protein differences between the methods (Sprint – Kjeldahl) at 1 week, 3, 6, 9, and 12 month samples was 2.04, 1.34, 0.90, 0.11, and -0.79%. These results indicate that the Sprint method over estimated the protein content during early ripening and underestimates the protein content after extended ripening. As Cheddar cheese ages the level of intact protein decreases and the level of hydrolyzed protein increases. Since the protein-tagging technology utilized in the Sprint method is influenced by protein hydrolysis it is not surprising that the results of this method are influenced by the age of the cheese. In order to utilize the Sprint method for protein analysis of Cheddar cheese the level of protein hydrolysis in the cheese needs to be controlled.

Key Words: Sprint rapid protein analyzer, Cheddar cheese, total protein

T88 Determination of true proteins in dairy products: A comparative study between Kjeldahl and Sprint protein analyzer. D. Zhao*, V. Jai, and N. Y. Farkye, *California Polytechnic State University*, *San Luis Obispo*.

True proteins (TP) in milk play a major role in yield, functionality and nutritional value of dairy products and products containing dairy components. It is standard practice in milk procurement for milk processing plants to pay premium for protein content of milk. However, in the dairy industry, TP is of greater economic value than total protein content hence the need for rapid determination of TP is of significant interest. In this study, the Sprint Rapid Protein analyzer, SPR (CEM Corporation, Matthews, NC) was compared with the standard Kjeldahl method to measure the TP in selected dairy products. The SPR is based on the Orange G dye binding method that measures the TP directly unlike Kjeldahl in which TP is calculated as the difference between total nitrogen and non-protein nitrogen multiplied by 6.38. Cheddar and mozzarella cheeses, and milk protein powders such as whey protein concentrate 80, milk protein concentrate, milk protein isolate, whole milk powder, and non fat dry milk were analyzed for true proteins by both the methods and the results were compared. The results were not statistically different for Cheddar cheese ($P > 0.05$), Mozzarella cheese ($P > 0.05$) and the milk protein powders ($P > 0.05$). The repeatability within the samples for Cheddar cheese, Mozzarella cheese and milk powders were similar in both methods (standard deviation 0.02–0.42 from Kjeldahl; and 0.04–0.49 for SPR). The relative standard deviation for all the products measured in both the methods was always less than 2%. Therefore, the precision and accuracy in measuring true protein by SPR in dairy products is comparable to Kjeldahl. The SPR offers rapid (less than 5 min), easy determination of true proteins in dairy products. It can be a good alternative to Kjeldahl in a dairy processing plant where faster results are needed

Key Words: true proteins, Kjeldahl, Sprint rapid protein analyzer

T89 Application of FTIR spectra for early detection of spore contamination in fluid milk. J. C. Huber-Rockow* and R. Jimènez-Flores, *California Polytechnic State University*, *San Luis Obispo*.

FTIR is shown to be a useful tool for the analysis of spores in several food products and processes. This research aims to improve milk safety and processing practices through the development of a fast and reliable FTIR method to document and quantify the metabolic changes in spores in raw milk and milk after a germination-induction heat treatment. In this study, basic FTIR-ATR spectral analysis and principal component analysis properly differentiates 11 reference strains of *Bacillus* in their 1200–900 cm^{-1} fingerprint regions (*B. megaterium*, *B. subtilis* (2), *B. pumilus*, *B. licheniformis* (2), *B. coagulans*, *B. circulans*, *B. amyloliquefaciens*). Subsequently, using the whole spectra generated by the FOSS MilkoScan FT2, we successfully identified individual strains at different stages of heat-induced germination in a milk system, however no significant difference between strains was identified. Further analysis will improve differentiation between strain variability and natural variability of milk. Completion of this work will continue to highlight the utility of FTIR as a tool for safety and quality screening in the dairy industry.

Key Words: FTIR, spores, milk quality