tory Services Division, *Guelph, Ontario, Canada*.

Meat colour is an important characteristic of pork quality but quantitative selection requires sacrifice of animals. Meat colour and single nucleotide polymorphisms (SNPs) of exon 14 and partial codon sequences of SLC44A3 gene of 500 pigs were used to examine the association of this gene with meat colour and change of colour during storage. Significant differences ($p \leq 0.01$) were found among breeds for subjective colour (NPPC; Scale 1-6). Duroc (4.45±0.07) and Lacombe (4.49±0.09) had significantly darker loins than other breeds: Yorkshire (4.16±0.07), Landrace (3.94±0.08) and crossbreds (3.98±0.06). Females (4.25±0.05) were darker on average than castrates (4.16±0.06). Thirteen SNPs were found in the SLC44A3 gene. Four of the 13 SNPs were in the coding region but only one resulted in an amino acid change. Three SNPs at base pair (bp) positions of 234, 381 and 386 were selected for analysis based on the following criteria: minor allele frequency above (5%) and no confounding with other SNPs. Defining the haplotypes of the three SNPs revealed four different haplotype alleles in the sampled pigs. SNP at bp 386 showed significant association with NPPC colour ($p \leq 0.05$), and a significant effect of haplotypes was also found within breeds ($p \leq 0.05$). Loin colour (Minolta CIE L*, a*, b*) was recorded on days one, four and seven post-mortem, and colour differences calculated. The greatest change in L* was observed during dark storage (days 1 to 4) with little change during storage in light (days 4 to 7). A significant difference between L* values as well as change in L* was observed among breeds ($p \leq 0.05$) and gilts tended to remain darker than castrates.

Key Words: meat colour, SLC44A3 gene, pork

419 Estimation of the IGF2 effect on backfat and lean muscle depth in Canadian Landrace. M. Jafarikia*, B. Sullivan, L. Maignel, and S. Wyss, *Canadian Centre for Swine Improvement*, *Ottawa, ON, Canada*.

IGF2 is a paternally expressed gene located at the distal tip of porcine chromosome 2. Allelic variation of this gene is associated with 15-30% of the phenotypic variation in muscle mass and 10-20% of the phenotypic variation in backfat thickness. Canadian Landrace with approximately one million records was used to investigate the proportion of the phenotypic variance in backfat thickness and muscle mass explained by IGF2. The genetic variance was estimated as $\sigma_{IGF2}^2 = 2pq\alpha^2$ where σ_{IGF2}^2, p, q and α represent IGF2 variance, frequency of paternal A, frequency of paternal G and allele substitution effect respectively. The traits under study included backfat and lean muscle depth adjusted to 100 kg live weight. The statistical models included the probability of inheriting the IGF2 allele from sire as a covariate along with contemporary group and sex as fixed effects. The GLM procedure of SAS was used for the analysis. In order to determine the paternal allele origin, a genotyping probability software was developed to estimate the paternal allele probabilities of all the animals in the pedigree using information from a limited number of genotyped animals from recent generations. The numbers of AA, AG and GG genotypes were 456, 304, 38, respectively. Using the homozygote genotypes (AA, GG), the total number of known paternal alleles was 494. The number of animals with known paternal alleles increased to 36,371 after using the genotyping probability estimation software. The estimated paternal A over G allele substitution effects were -1.28 mm and +2.05 mm and the estimated variances were 0.61 mm^2 and 1.55 mm^2 for backfat and lean muscle depth, respectively. The estimated variances were 14% and 11% of the observed phenotypic variance of backfat and lean muscle depth, respectively. The observed variance for backfat corroborated the range reported in previous studies but for lean muscle depth, a lower variance was found than the range reported in previous studies on other swine populations.

Key Words: IGF2, variance, backfat and lean muscle depth

420 Proximal promoter of the pig HMGCR gene: Structural and functional study. A. Cánovas*[1], R. Quintanilla[1], J. M. Reecy[2], M. Marquiés[3], and R. N. Pena[1], [1]*IRTA. Genetica i Millora Animal.*, *Lleida, Spain*, [2]*Iowa State University*, *Ames*, [3]*INDEGA. Universidad de León*, *León, Spain*.

HMGCR is the rate-limiting enzyme in the biosynthesis of cholesterol. We have studied the role of the HMGCR gene in pig lipid metabolism by means of expression and structural analysis. Animals came from a high intramuscular fat commercial Duroc line used in the production of fine quality cured ham. The experiment was based on a half-sib design, generated by mating five parental boars with 385 females and using only one male offspring per litter. We characterized the mRNA expression profile of the porcine HMGCR in six tissues involved in lipid metabolism. HMGCR is expressed at high levels in the duodenum and back fat. In contrast, heart and liver had lower HMGCR mRNA expression levels. In addition, we amplified the proximal promoter (600 bp) of this gene and identified two SNP at positions -239 and -16 bp. In silico analysis of the distal and proximal promoter SNPs revealed that they may potentially affect the binding of myogenic bHLH family members (e.g. myoD, myogenin, myf5 and myf6), and Ets-2 family members, respectively. The pig HMGCR promoter region exhibited a high level of conservation (72 to 86% sequence identity across species) with conserved motifs for several transcription factors. Futhermore, we evaluated the interaction between HMGCR:c.-239G>T promoter SNP and promoter activators and inhibitors in hepatic (HepG2) and muscle (C2C12) cell lines. In C2C12 and HepG2 transfected cells, we observed that insulin (1 μM), increased the transcriptional activity of the HMGCR G allele promoter, whereas 25-hydroxycholesterol (12.5 μM) also inhibited the transcriptional activity of the G allele promoter. Our findings indicate that HMGCR may play an interesting role in the genetic variability of lipid and cholesterol metabolism in pigs.

Key Words: pig, meat quality, lipid metabolism

Dairy Foods: Dairy Foods 1

421 Value-added components derived from whey. W. Modler*, *Agriculture Canada (formerly, Centre for Food & Animal Research, Ottawa, Ontario, Canada)*, *Kemptville, Ontario, Canada*.

Initially, whey products, such as roller dried whey powder, had poor functionality and limited food product application. Technological advances in evaporation and spray drying, along with the development of demineralization and electrodialysis technology, led to further improvements in functionality in whey-based powders. The next generation of products consisted primarily of WPC and WPI prepared primarily through the development of membrane technology, particularly microfiltration. More recently, improvements have provided cleaner separations, improved membrane performance and durability. In addition, nanofiltration and microfiltration have provided additional tools for whey processors for

producing and modifying the functionality of whey-based ingredients. These technological developments have diversified ingredient selection and expanded their use in frozen desserts, snack foods, beverages, processed meats, fermented dairy products, processed cheese foods/spreads, baked goods and confectionary. More recently emphasis has been placed on the isolation of the major proteins in whey for use as gelation agents (beta lactoglobulin) and nutritional supplements (alpha lactalbumin). In addition, good progress has also been made in the isolation, characterization and production of bioactive components from whey, now termed nutraceuticals. The components of interest include both major and minor proteins, enzymes, peptides, lipids/lipoproteins, vitamins and minerals. Selected components of this group have been shown to reduce hypertension, sarcopenia, cancer, osteoporosis and modulate immune function. This paper will highlight the development and application of the value-added products derived from whey, with emphasis on the food and nutraceuticals industry. Future technological challenges could include the isolation, purification and characterization of pharmaceutical components from whey.

Key Words: whey, functional foods, nutraceutical

422 Optimizing the recovery of protein during microfiltration of preconcentrated whey. C. Marella*, L. E. Metzger, and K. Muthukumarappan, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

Microfiltration processing is an integral part of filtration based manufacture of WPC and WPI and is utilized to remove lipid material from whey. Generally whey preconcentrated with ultrafiltration is subjected to microfiltration. During microfiltration about 25-30% of the protein is lost in the retentate along with the lipid materials. The objective of this research was to optimize the recovery of protein and determine if mineral chelating processing aids have an impact on protein recovery and fouling of microfiltration membranes. Experiments were conducted using whey preconcentrated by ultrafiltration to a volume reduction (VR) of 4.5. Initially three levels of VR (4, 5 and 6) and three levels of diafiltration (DF) (0, 50 and 100% of feed volume) were used during microfiltration. All the experiments were conducted in triplicate using a lab scale plate and frame membrane separation unit. A Polyvinyledene fluoride membrane of 0.5 μ pore size, transmembrane pressure of 10 kPa, pH of 6.2 and temperature of 25°C were used. Treatment combinations of 5VR x 100 DF and 6VR x 100DF resulted in maximum protein recovery of 84%. Subsequently the treatment combination 6VR x 100DF was used to conduct experiments with the addition of disodium phosphate (2.201 g/L), trisodium citrate (3.04 g/L) and sodium hexameta phosphate (3.1605 g/L). These quantities are sufficient to chelate all the Calcium (15 mM) present in the WPC. Addition of mineral chelating aids did not significantly ($P>0.05$) affect on the recovery of protein but resulted in significant ($p<0.05$) reduction in both overall and irreversible fouling. Addition of sodium hexameta phosphate resulted into the lowest overall and irreversible fouling resistances (0.67×10^{12}/m and 0.07×10^{12}/m respectively). The results from this study indicate that maximum recovery of protein can be obtained with VR of 6 and DF of 100%. Addition of sodium hexameta phosphate leads to reduced fouling during microfiltration.

Key Words: microfiltration, protein recovery, processing aids

423 Nanoparticulation of denatured whey protein by pH–cycling. M. Britten*, J. Houde, and H. J. Giroux, *Agriculture and Agri-Food Canada*, *St-Hyacinthe, QC, Canada*.

Nanoparticles are used for entrapment, protection and delivery of highly sensitive ingredients or bioactive compounds in food systems. Cross–linking of denatured whey protein through pH–cycling is proposed to develop nanoparticles with controlled size and properties. Whey protein soluble polymers were produced by heating at low ionic strength and neutral pH. Acidification was used to induce aggregation. The effect of aggregation conditions on the physicochemical characteristics and stability of nanoparticles was studied. Nanoparticles with a diameter varying from 40 to 300 nm were produced by modifying the aggregation pH, $CaCl_2$ concentration and the holding time at the aggregation pH before readjustment to pH 7.0. Nanoparticle size and dispersion turbidity increased with increasing maturation time while the concentration of accessible thiol groups decreased. Thiol–disulphide exchange reaction is likely responsible for the stabilization of nanoparticles. Size, turbidity and voluminosity of whey protein nanoparticles were controlled by aggregation conditions. The stability of nanoparticles in the presence of different dissociating agents (EDTA, urea, SDS and DDT) was evaluated and the results confirmed that the nanoparticles are mainly stabilized by disulphide bonds. Hydrophobic interactions seem also involved in the formation of nanoparticles. Whey protein nanoparticles obtained by pH–cycling is a promising approach for the protection and delivery of sensitive compounds such as aroma and nutraceuticals.

Key Words: whey protein, nanoparticle, thiol-disulphide

424 Development of an optical backscatter method for determining thermal denaturation of whey proteins during milk processing. A. M. Lamb*, M. Castillo, F. A. Payne, and Y. L. Xiong, *University of Kentucky*, *Lexington*.

The heat denaturation of whey proteins impacts the functional properties of milk. After denaturing, β-LG associates with κ-CN, which significantly impairs milk coagulation by creating a steric obstacle for κ-CN hydrolysis and by increasing the gel moisture retention. Correlations of the degree of β-LG denaturation to gelation time, gel firmness, and gel moisture content have been widely documented. The resulting high moisture and soft gels are undesirable for cheese manufacture but advisable in yogurt processing, as it aids in preventing one of its most frequent defects, wheying-off. Currently no inline technique is available for quantifying β-LG denaturation and aggregation with κ-CN in milk. The goal of this study was the development of an optical sensor method with inline potential for the determination of β-LG denaturation and subsequent association with κ-CN during milk heat treatment. Duration of thermal exposure at 80°C was the factor with 5 levels (3, 5, 7, 12, 25 min). The levels were chosen from preliminary kinetic calculations based on current literature findings. The samples were tested to determine the level of denaturation and protein association by SDS-PAGE, differential scanning calorimetry, and undenatured whey protein analysis before and after heat treatment. Samples also underwent light backscatter analysis for the correlation and validation of optical response to protein denaturation. The physical-chemical analysis performed indicated that denaturation represented a first order reaction, as expected. Light backscatter response was found to be proportional to heat treatment intensity, increasing as much as 4.5% after treatment. This suggests that light scatter could be used to determine the whey protein denaturation degree. Early prediction of the potential gelling strength of milk will allow milk batches to be used for their most suitable purposes. Successful development of this optic sensor technology

will aid in the decision-making process of dairy plants for the assurance of a high quality product.

Key Words: light backscatter, optical sensors, protein denaturation

425 Use of whey protein fractions as a fat substitute for sausage. A. C. B. Ferreira[1], W. L. M. Santos[1], L. M. Fonseca*[1,2], and R. L. Bradley Jr.[3], [1]*Federal University of Minas Gerais (UFMG), School of Veterinary Medicine, Department of Food Technology and Inspection*, *Belo Horizonte, MG, Brazil*, [2]*Laboratory of Milk Quality Analysis, UFMG*, *Belo Horizonte, MG, Brazil*, [3]*University of Wisconsin, Department of Food Science*, *Madison*.

Special attention has been given to the excess of calories and fat ingestion, mainly for health reasons. As consequence, there is a growing interest for products with low fat content. This work had as objective to evaluate the physico-chemical and sensorial quality of pork sausages, manufactured with whey protein concentrate (WPC) or protein concentrate with high level of β-lactoglobulin (called hereof β-lactoglobulin; US Patent n. 6,900,290), as substitutes of the fat. The sausages were manufactured in the Laboratory of Meat Technology of the DTIPOA/ School of Veterinary Medicine-UFMG. Seven treatments were used, six containing different levels of addition of WPC, or β-lactoglobulin and a group control containing 20% of fat (three treatments containing 10% of fat and three different levels of WPC, that is, 0.2%, 0.5% and 1.0%, and three treatments containing 10% of fat and three different levels of β-lactoglobulin that were, 0.1%, 0.3% and 0.6%). Each level of treatment was repeated in five batches, with two times of evaluation, in the day of production and after a period of seven days of storage at 4°C. The samples were analyzed for protein (g/100g), fat (g/100g), ashes (g/100g), chlorides (g/100g), water content (g/100g), and for the determination of the caloric value (Kcal/g), water activity (Aw), pH, texture (Kgf), and loss after cooking (g/100g). Analyses were done in the first week of production and after seven days of storage. Results for protein, fat, caloric value and moisture content presented statistical difference between the group control and the other treatments ($p \leq 0.05$). The other analyses results were not different among the treatments and between the two weeks of evaluation ($p \geq 0.05$). Additionally, the sensorial analyses results showed that there was no difference among the different treatments with the level of fat substitution used in this experiment ($p \leq 0.05$). The milk proteins were efficient for the fat substitution in pork sausages, in the treatment levels for the present experiment, complying with the Brazilian legal requirements, in addition to maintain the sensorial quality.
Acknowledgements: FUNDEP/UFMG; FAPEMIG; CNPq; CAPES.

Key Words: whey protein concentrate, β-lactoglobulin, reduced fat

426 Influence of casein on flux and passage of serum proteins (SP) during microfiltration (MF) using polymeric spiral wound (SW) membranes at 50°C. J. Zulewska*[1], M. Newbold[2], and D. M. Barbano[2], [1]*University of Warmia and Mazury*, *Olsztyn, Poland*, [2]*Cornell University*, *Ithaca, NY*.

The objective was to determine the influence of casein on flux and passage of SP during MF using polymeric SW membranes at 50°C. Flux, percentage and rate of SP removal from skim milk and casein-free skim milk using polymeric SW membranes were compared. Skim milk was pasteurized (72°C, 16 s), cooled and split into 2 batches. One batch (620 kg) was MF 3X at 50°C using 0.1 micron ceramic (1.7 m^2) uniform transmembrane pressure (UTP) membranes, to produce casein-free skim milk (UTP MF permeate). Casein-free skim milk (380 kg) was recycled for 65 min using 0.3 micron polymeric (polyvinylidene fluoride, 20.5 m^2) SW membrane, the system was flushed with water, then skim milk (1106 kg) was MF at 3X bleed-and-feed at 50°C. The percentage SP removal was determined by the mass of SP [((TN-NPN)-(TN-NCN))*6.38] in permeate divided by the mass of SP [((TN-NPN)-(TN-NCN))*6.38] in skim milk multiplied by 100 where SP was determined using Kjeldahl. This process was replicated 3 times. Flux, percentage SP removal, and rate of SP removal for casein free skim milk and skim milk were significantly different: 80.2 vs. 17.2, ($kg/m^2/h$), 59.5 vs. 35.2%, and 0.40 vs. 0.06 ($kg/m^2/h$), respectively. The presence of casein in skim reduced flux by 4.7 times and increased the rejection of SP. The rate of SP removal ($kg/m^2/h$) from casein free skim milk is 7 times that of skim milk with the same membrane and processing conditions. The presence of casein in a feed stream decreases the efficiency of polymeric membranes. The membrane performance on casein free skim milk demonstrates the potential that could be achieved with polymeric membranes, if casein fouling could be reduced. Approaches that could be investigated to reduce casein fouling in MF for separation of casein and SP are: membrane configuration (spiral-wound vs. flat-sheet), cross-flow velocity, retentate flow channel volume, and membrane surface characteristics. If casein fouling was reduced, the area of SW membranes and the time required to process a given volume of skim milk and produce a defined composition MF permeate could be decreased.

Key Words: serum protein, casein, microfiltration

427 A non-pasta filata Mozzarella cheese making method using CO_2: Cheese composition and yield. L. Li[1], M. Newbold[2], and D. M. Barbano*[2], [1]*South China University of Technology*, *Guangzhou, China*, [2]*Cornell University*, *Ithaca, NY*.

A new Mozzarella cheese making method was developed using CO_2 to control calcium-protein equilibria during cheese making. Our goal was to develop a lower cost method of producing full-fat Mozzarella with acceptable functionality for pizza baking without using any added starch or phosphates to retain moisture and fat during baking. About 2000 to 2500 ppm of CO_2 was injected into pasteurized skim milk and this was blended with the appropriate amount of cream without added CO_2. Fat content of the cheese was controlled by adjusting the casein to fat ratio in the milk. The pH of the milk plus CO_2 mixture at the beginning of cheese making was between 5.9 and 6.0, which increased coagulation firmness and reduced rennet use by 50 to 70%. Coagulation, cutting, and cooking times and temperatures were very similar to those used for Cheddar cheese manufacture. Final moisture content of the cheese was controlled using the relationship between the temperature of the whey and the pH of the curd in a stirred curd process. When the curd reached the target pH (5.1 to 5.35), the whey was drained and the curd was dry salted. The salted curds were chopped to uniform size (about 5 to 10 mm), sprayed with a hydrophopbic surface coating, and individually quick frozen. The experiment demonstrated the ability to control moisture in the range from 52 to 58%, with a fat on dry basis of >45%. Salt retention in the curd can be controlled by temperature conditions during salting and was between 90 and 99.5%. Fat recovery in the cheese was higher (about 94 to 95%) than a typical pasta-filata manufacturing process (about 85%). Higher fat recovery and higher moisture produced actual yields (12 to 13.5 kg/100 kg of milk) without any fortification with nonfat milk solids. The new process eliminates Cheddaring, stretching, molding, brine salting, block packaging, and shredding equipment when the intended use of the cheese is for food service pizza. The frozen cheese is slow thawed at refrigeration tem-

perature and put directly on a pizza for baking.

Key Words: CO_2, mozzarella, yield

428 A non-pasta filata Mozzarella cheese making method using CO_2: Cheese functionality. L. Li[1], M. Newbold[2], and D. M. Barbano*[2], [1]*South China University of Technology, Guangzhou, China*, [2]*Cornell University, Ithaca, NY*.

A new method of Mozzarella cheese making was developed using CO_2 as a processing aide to control calcium-protein equilibria and deliver a full-fat Mozzarella with acceptable functionality for pizza baking without using any added starch or phosphates to retain moisture and fat during baking. Two versions of the new process produced cheeses containing about 52 and 58% moisture, while they both had a fat on a dry basis of > 45% and a protein on dry basis of about 43 to 44%. Cheeses produced by the new process are in a particulate form directly from the cheese making and do not require stretching, brining, or shredding. The objective was to determine the free oil release, expressible serum, meltability, apparent viscosity, and pizza baking characteristics of cheese produced by this new process. Free-oil release of full-fat Mozzarella during pizza baking can often be excessive. Cheeses produced by the new process released 4 to 7% of their oil, while commercial low-moisture Mozzarellas released 25% of their fat. Cheeses from the new process had lower (almost zero) expressible serum release after 4 days of refrigerated storage while the commercial low-moisture Mozzarellas released more than 20% of their moisture after 4 days of refrigerated storage. The cheeses from the new process held their moisture much better when baked on a pizza. Cheese produced by the new process had a tube meltability that was nearly twice that of the commercial cheese of the same age and this difference was clearly visible when the cheeses were baked on pizza. The melted cheese consistency, measured as apparent viscosity by helical viscometry, was much softer and more stretchable than the commercial products. Addition of CO_2 to milk prior to rennet coagulation changed the calcium-protein equilibria in the cheese and increased partitioning of caseins into the water phase of the cheese. Higher casein solubility in the water phase of the cheese increased water and fat holding capacity and this provided excellent baking properties of the high moisture cheese without any added non-dairy ingredients.

Key Words: Mozzarella, CO_2, functionality

429 Caseins as molecular chaperones: Functional analysis and structural considerations. Y. H. Yong* and E. A. Foegeding, *Department of Food, Bioprocessing and Nutrition Sciences, North Carolina State University, Raleigh*.

Denaturation and aggregation of proteins are reactions that are relevant to functional applications of proteins in foods. Depending on concentration, aggregation can result in turbidity, precipitation or gelation. One of the approaches to improve the thermal stability of globular proteins is through addition of other compounds to alter the aggregation process. Numerous studies have shown the ability of molecular chaperones to assist proper folding/unfolding and assembly/disassembly of proteins, especially during stressed conditions. In 1999, a mixture of α_{s1} - and α_{s2} -casein was reported for the first time to possess molecular chaperone-like properties to prevent a variety of proteins and enzymes from different types of stress-induced aggregation. In the intervening 10 years, around a dozen journal papers have reported the molecular chaperone properties of caseins, including α-, β-, κ-caseins, whole casein and sodium caseinate. We have summarized and compared the results of these studies to see if they could be explained by a common mechanism. Also, as caseins were reported to be acting in a manner similar to the small heat shock proteins (sHSP) family, we evaluated the similarities and differences of caseins and α-crystallin (first sHSP as a molecular chaperone) from the viewpoints of their structural information (primary to quaternary) and their functional assistance on select substrate proteins. Caseins were compared to another natively unfolded protein, namely α-synuclein, that also has been reported to act like a molecular chaperone. Through all these details, we provide an insight of the role of caseins as a distinct group of molecular chaperones.

Key Words: caseins, molecular chaperones

430 Development and functionalities of milk protein-based paper glue. X. Chen[2,1], Y. L. Gao[2,1], L. H. Zhou[1], and M. R. Guo*[1], [1]*University of Vermont, Burlington*, [2]*Inner Mongolia Agriculture University, Huhhot, Inner Mongolia, China*.

Commercial paper glue products on the market may contain toxic compounds harmful to the people and the environment. Prototype of environmentally safe paper glues containing polymerized whey protein (PWP) and sodium caseinate were developed and optimized under a full factorial experiment design with factors of protein content, denature temperature, time and other ingredients. The prototypes were analyzed for physicochemical properties including pH value, ash contents, total solids and viscosity, and functional properties including bonding strength, water resistance, temperature and moisture resistance. When compared with the commercial product, the prototypes had higher pH value (6.6/4.7), higher ash content (0.3%/0.1%), lower total solids (15.8%/31.2%) and higher viscosity (5975/2472 mPa), respectively. Bonding strength is considered as the main index because it is the most important property for glues. The bonding strength of the prototypes was up to 161.4 N while commercial sample was 154.6 N. According to the ASTM standards, the water resistance and temperature-and-moisture resistance of the prototypes were better than those of commercial samples. The statistic analyses indicated that the denaturation time had significant effects ($P<0.05$) on bonding strength, while both WPI/PVA ratio and denaturation temperature had very significant effects ($P<0.01$).

Key Words: milk protein, paper glue, bonding strength

Dairy Foods: Dairy Foods/Cheese

431 ADSA Pioneer: A century of predictive cheese yield formulas. D. B. Emmons*, *Food Research Laboratory, Research Branch, Agriculture and Agri-Food Canada,, Guelph, ON, Canada*.

Predictive cheese yield formulas have evolved over more than 100 years from one based only on casein and fat. A major change in 1910 included moisture and a constant for salt and whey solids. Refinements have included salt and whey solids as separate factors, exclusion of whey solids from moisture associated with cheese protein, and use of paracasein instead of casein. Various parts or all of formulas are used in monitoring or controlling experiments and cheese making. The General formula is based on the sum of cheese components: fat, protein, moisture, salt, whey solids free of fat and protein, as well as milk salts associated