M1  The role of sweeteners and protein source on high-protein low-carbohydrate bar shelf life. H. Keefer*, S. Nishku, and M. A. Drake, North Carolina State University, Raleigh NC.

A desirable protein bar has a favorable flavor and texture to consumers and a shelf life of at least 6 mo. There are several available protein sources and sweeteners, so it is important to investigate implications on bar sensory properties and shelf stability. A previous study evaluated the impact of protein source and sweetener on bar flavors and sweetness profiles. The objective of this study was to characterize the impact of sweetener and protein source on the texture and shelf life of high protein low carbohydrate bars. The protein bars (15 formulas, replicated twice) consisted of a protein source (whey, milk, or pea) and a sweetener (sucrose, fructose, monk fruit, stevia, or sucralose) with fiber and vegetable shortening. Bars (15 g protein per serving) were placed in moisture barrier pouches and stored 35 d at 35°C for accelerated shelf life testing. Instrumental hardiness (g) and color measurements (L a b*) were taken and descriptive analysis (DA) of texture was conducted at d 1, 7, 14, 21, 28, and 35. Linear mixed model analyses were conducted for each time point with sugar and protein source and their interaction as fixed effects. Protein source and sweetener had a significant interaction for instrumental and sensory properties (P < 0.05). Bars with whey protein and fructose were harder than other bars until d 21. Whey protein bars, regardless of sweetener, were denser at all time points than pea or milk protein bars. Bars made with pea protein were the driest, least cohesive, and had the fastest rate of breakdown across shelf life (P < 0.05). Whey protein bars had the greatest change in color compared with pea or milk protein, but all protein bar formulas visibly darkened and increased in yellow/red color over time (P < 0.05). Both sweetener and protein source affect protein bar characteristics and should be chosen carefully. These results are important to understand and predict how sugar reduction and/or sweetener replacement affects the sensory and textural properties of protein bars with different protein types.

Key Words: protein bar, texture, hardening

M2  Developing a blood glucose meter-based method for the rapid measurement of lactose in dairy ingredients. C. Wagner*, J. Amamcharla1, A. Rao2, and L. Metzger3, 1 Kansas State University, Manhattan, KS, 2 Agropur Ingredients, La Crosse, WI, 3 South Dakota State University, Brookings, SD.

Commonly used lactose assays (enzymatic absorbance [EZ] and HPLC) for dairy ingredients are relatively expensive and time-consuming. A blood glucose meter (BGM)-based method has been used successfully as a rapid lactose assay in milk. The BGM method involves diluting the sample to an appropriate level with water or buffer, adding lactase enzyme, incubating at 40°C for ~15 min, and measuring the resulting glucose content with the BGM. A standard curve developed between glucose content with the BGM. A standard curve developed between the sample to an appropriate level with water or buffer, adding lactase enzyme, incubating at 40°C for ~15 min, and measuring the resulting glucose content with the BGM. A standard curve developed between the known lactose concentration and BGM reading is used to quantify lactose in unknown samples. The objective of this study was to evaluate the BGM-based lactose analysis method in whey- and skim milk-derived (WD and SMD, respectively) ingredients and was done in 4 phases. In phase 1, the effect of pH and lactose concentration on the BGM reading was investigated using a factorial design with 2 factors (pH: 6.03–6.89 and lactose: 0.2% or 0.4%) and found that BGM readings were significantly (P < 0.05) affected by pH at both lactose levels. In phase 2, the effect of total solids and ingredient type on the BGM reading was investigated using a factorial design with 2 factors (ingredient type: WD or SMD and total solids: 0–8%). It was observed that the BGM reading was significantly (P < 0.05) affected by both ingredient type and total solids. Phase 3 involved developing a linear relationship between the BGM reading and an EZ reference method to ascertain the accuracy of the proposed BGM method. Different ingredient type (WD or SMD) and total solids (0.5–27%) model solutions were measured using the BGM and EZ methods. The percent bias (BGM method − EZ method) was found to be between 2.2 and 6.8%. In phase 4, 15 samples procured from commercial sources were evaluated using the BGM method and EZ method as the reference method. High lactose (>47%) and low lactose (<13%) samples yielded absolute biases between −5.3 and 1.4% and 0.3 and 0.8%, respectively. Overall, the BGM method is a promising tool for rapid, low-cost analysis of lactose in both high-lactose and low-lactose dairy ingredients.

Key Words: lactose analysis, biosensor, protein ingredients

M3  Characterization of milk and soy phospholipid liposomes and their effects on inflammation using an adipocyte model. E. Kosmeri*, D. Rocha-Mendoza, I. García-Cano, O. Ziouzenkova, and R. Jiménez-Flores, The Ohio State University, Columbus, OH.

Milk phospholipids (PLs) are valuable dairy components and appear to impart human health benefits, including improved cognitive function in infants and adults. Furthermore, PLs have been shown to lower LDL cholesterol and improve intestinal barrier function. The commercial food industry uses other dietary sources of PLs, such as soy lecithin. However, it remains unclear whether dissimilar composition of PLs from different dietary sources convey the same benefits. The hypothesis of this work was that milk and soy PLs (MPLs and SPLs, respectively) will produce different physiological responses in cell culture. Our objective was to develop a cell-based method to compare the potential health benefits of milk and soy PLs to ultimately focus on inflammation. To improve stability of PLs in cell culture media, liposome structures made from milk and soy PLs were prepared, optimized, and fully characterized. Large and stable unilamellar vesicles (LUVs) were attained with particle sizes of 232.1 ± 7.5 and 221.8 ± 10.0 nm in diameter and zeta potentials of −16.41 ± 2.49 and −28.01 ± 2.81 mV for MPL- and SPL-LUVs, respectively. Subsequently, 3T3-L1 adipocytes were treated with 0.05, 0.25, 0.5, and 1.5 mg/mL MPL- or SPL-LUVs and analyzed for changes in cell viability and cytotoxicity. The optimized conditions showed that the non-toxic, physiological range for cell culture was between 0.05 and 0.5 mg/mL. There was also a significant difference (P < 0.05) between cell viability of MPL- and SPL-LUVs treated cells at 0.25 and 0.5 mg/mL, suggesting that MPL-LUVs may have greater bioavailability compared with SPL-LUVs. These findings lead to our prediction that MPL-LUVs will have a greater anti-inflammatory effect than SPL-LUVs because of differences in PL composition, specifically sphingomyelin. To test this, adipocytes will be stimulated with bacterial endotoxins and characterized for NF-kB-mediated inflammation after treatment with LUVs. We propose that PL compositional differences may be the basis for differences in physiological response.

Key Words: phospholipids, liposomes, inflammation

M4  Forward osmosis concentration of skim and whole milk at different temperatures: effect on flux and milk powder quality. A. Beldie* and C. I. Moraru, Cornell University, Ithaca, NY.

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Milk concentration is typically achieved either by thermal evaporation or reverse osmosis (RO). Thermal evaporation leads to cooked flavor and color changes, and it is energy intensive. Additionally, thermal evaporators are prone to fouling and biofilm formation. On the other hand, RO is affected by fouling, which limits the achievable concentration level. The main objective of this work was to evaluate forward osmosis (FO) as an alternative method for concentrating milk, at different temperatures. Another objective was to assess the quality of milk powders obtained by spray drying the FO concentrates. Pasteurized skim and whole milk (Cornell Dairy, Ithaca, NY) were concentrated at 4°C, 15°C and 25°C, in triplicate, using a laboratory scale FO unit (Ederna, France), equipped with a polymeric membrane. Concentrates were dried using a lab-scale spray drier (Armfield, UK). Data were analyzed statistically by one-way ANOVA. For skim milk, water flux at the beginning of the process (15–20 min) was 2.21 ± 1.64 L/(m²h) at 25°C, 2.98 ± 0.62 L/(m²h) at 15°C, and 2.52 ± 0.39 L/(m²h) at 4°C. These values were not statistically different (P > 0.05). Comparable initial fluxes were obtained for whole milk: 2.29 ± 0.94 L/(m²h) at 25°C, 2.67 ± 0.26 L/(m²h) at 15°C and 2.59 ± 0.23 L/(m²h) at 4°C. Flux decreased with time under all processing conditions. Flux drop was less pronounced at higher temperatures for both skim and whole milk: for whole milk, the flux after 8h reached 52% of the initial flux at 25°C, 30% at 15°C and 24% at 4°C. Higher temperatures also allowed faster FO concentration. For skim milk, 40°Bx was reached after 7h at 25°C, after 8.5h at 15°C and after ~10h at 4°C. Whole milk concentration was slower, with 30°Bx achieved after ~7h at 25°C, 8h at 15°C and ~9h at 4°C. No differences in reconstitution behavior were observed for skim powders obtained from FO concentrates vs thermal concentrates. Slight differences in color were observed, but they were not significant (P > 0.1). These results demonstrate that FO is a viable method for nonthermal concentration of milk, able to achieve concentration factors higher than RO, comparable to thermal evaporation.

**Key Words:** forward osmosis, milk concentration, nonthermal processing

M5 Utilization of acid whey as a fermentation aid to develop an enriched feed ingredient. A. Mayta-Apaza*, I. García-Can, D. Rocha-Mendoza, and R. Jiménez-Flores, The Ohio State University, Columbus, OH.

The processing of strained yogurts, and fresh cheeses, such as ricotta or cottage, generates large amounts of waste streams known as acid whey (AW) that require significant capital investments for proper disposal. Similarly, the fishery industry produces about 45% of the whole fish as waste at the end of its production chain. To valorize these by-products, this study is based on the hypothesis that fermentation of the mixture of AW and fish waste (FW) would break down complex nutrients, increasing its nutritional value for aquaculture. The objective of this study was to optimize fermentation parameters using lactic acid bacteria (LAB) and a mixture of AW and FW. The first step was screening of the LAB in the OSU “Parker Chair” LAB Collection to identify the strain with the highest proteolytic activity. Then, 3 fermentation systems (FS) were inoculated with Lactobacillus rhamnosus and set up as follows: 1) FS1: 36% FW, 12% fish muscle, 48% AW, and 4% molasses; 2) FS2: 38% FW, 12% fish muscle, and 50% AW; 3) FS3: 48% FW, 48% AW, and 4% molasses. The fermentation lasted 14 d at room temperature, and samples were collected every 48 h. The soluble protein concentration and peptide concentration of the samples were evaluated with colorimetric assays (Bradford and cadmium-ninhydrin), SDS-PAGE, pH, and microbial count of LAB was monitored simultaneously. The results showed a significant increase (P < 0.05) of peptides over time in the 3 fermentation systems. However, FS2 had 3.6 times more peptides than that of day zero’s, and the values of Bradford and SDS-PAGE images were consistent with the results presented in the peptide assay. The pH dropped significantly (P < 0.05) from 5.88 to 4.09 for FS1 and FS3 on the first 6 d due to the content of molasses and lactic acid production. Conversely, FS2 had a significant increase from 5.96 to 7.07. The LAB count fluctuated within each fermentation system and over the 14 d. In conclusion, this study presents an alternative to the current handling of acid whey and fish waste, exploiting their residual nutrients for delivery of higher quality protein to animal diets with minimal treatment.

**Key Words:** acid whey, lactic acid bacteria, protein hydrolysis

M6 A natural antimicrobial from Bacillus subtilis, a predominant constituent of membrane biofilms. P. Verma*1,2 and S. Anand1,2, 1Midwest Dairy Foods Research Center, Brookings, SD, 2Dairy and Food Science Department, South Dakota State University, Brookings, SD.

Current cleaning and sanitation protocols may be ineffective in cleaning separation membranes and result in the formation of resilient multispecies biofilms. These old biofilms may show bacterial predominance on prolonged use of the membranes. In our previous study, we isolated organisms such as Bacillus subtilis, Bacillus licheniformis, Exiguobacterium auranticum, and Acinetobacter radioresistens from an 18-mo-old reverse osmosis membrane. Competitive exclusion studies revealed the predominance of B. subtilis within the membrane biofilm microflora. This study investigates the antimicrobial activity of B. subtilis as a cause of its predominance. The culture was incubated in tryptic soy broth (TSB) at 37°C, and microfiltered to prepare cell-free extracts (CFEs) at 8-, 10-, 12-, 14-, 16- and 18-h intervals. The CFEs were freeze-dried and re-suspended in minimum quantities of HPLC grade water to create concentrated solutions. The antimicrobial activities of CFEs were tested using agar-well assay against the biofilm constitutive microflora and some common food pathogens. The experiments were conducted in triplicates and means were compared for significant differences using a general linear mixed model procedure of SAS. The results indicated the highest antimicrobial activity of 12 h CFE of B. subtilis against other Exiguobacterium sp., E. auranticum, A. radioresistens, Listeria monocytogenes, and Bacillus cereus, with average inhibition zone sizes of 16.5, 16.25, 20.6, 18.0, and 13.8 mm, respectively. On treating with proteinase K, the CFE completely lost its antimicrobial activity, establishing it to be a proteinaceous compound. The amino acid profiling revealed the total crude protein in CFE to be 51% (wt/wt) having its major constituent to be glutamic acid (13% wt/wt). The CFE was thermally stable on exposure to the common temperature used for sanitizer applications (23.8°C for 5 and 10 min). Based on this study, the proteinaceous antimicrobial compound produced by B. subtilis may result in its predominance.

**Key Words:** biofilms, antimicrobial activity, predominance

M7 Manufacturing low-spore-count skim milk powders by combining optimized raw milk holding conditions and hydrodynamic cavitation. N. Awasti*, P. Chaudhary, and S. Anand, Department of Dairy and Food Science, South Dakota State University, Brookings, SD.

The presence of high numbers of Bacillus spores in skim milk powder limits its application for creating UHT products. The dairy industry has been emphasizing on developing strategies for reducing sporeformers and spores in skim milk powder. Previous studies conducted in our
lab showed that it is possible to produce lower spore count skim milk powder, either by optimizing raw milk holding conditions or by using hydrodynamic cavitation as a process intervention. It was hypothesized that by combining the 2 processes it may be possible to further lower the sporeformers and spore counts in the final product. Pilot-scale challenge studies were conducted by spiking raw skim milk with approx. 4.0 log cfu/mL sporeformers and 2.0 log cfu/mL spores of *Bacillus licheniformis*. The inoculated raw skim milk was divided into 3 parts and exposed to 3 treatment (T1, T2 and control) for keeping the spore and sporeformer populations low in raw milk, before manufacturing skim milk powder. Powder prepared using treatment 1 (T1) includes raw milk holding at 4°C for 24 h, treatment 2 (T2) includes holding at 4°C for 24 h combined with 2 pass hydrodynamic cavitation, whereas, control includes holding raw spiked skim milk at 10°C for 4 h and then at 7°C for up to 72 h (PMO based conditions). Spiked raw milk samples from all 3 treatments were HTST pasteurized (73°C for 15 s), evaporated, and dried (outlet and inlet temperature of 200 and 95°C) to obtain skim milk powders. Spore and sporeformer counts of samples from 3 treatments were statistically compared after initial treatments (T1, T2, and control), pasteurization, evaporation, and drying steps. Final spore and sporeformer counts from powder prepared using T1 (0.58 ± 0.04, 1.82 ± 0.05 log cfu/g), T2 (0.33 ± 0.27, 1.49 ± 0.07 log cfu/g) and control (2.74 ± 0.30 log cfu/g) were significantly different (*P* < 0.05) with respect to each other. Our results demonstrate that combining cavitation with optimized raw milk holding conditions (treatment T2) produces skim milk powder with least sporeformers and spore counts.

**Key Words:** cavitation, spore, powder

Deproteinized whey (DPW) is obtained as a permeate fraction during ultrafiltration of whey and generally contains a minimum of 76% (db) lactose. It is further processed into a non-hygroscopic and free-flowing DPW powder by crystallization and spray drying. The DPW may undergo changes such as caking and Maillard browning during storage. The aim of this study was to investigate the effect of different levels of lactic acid (LA) and galactose (GA) on the physical, chemical, and thermal properties of DPW powders. Two lots of concentrated permeate with total solids of ~77% were procured from a commercial manufacturer. The total solids were adjusted to 45% TS and was divided into 9 subsamples with treatment combinations of high, medium, low levels of lactic acid by adjusting the pH to 5.0 by adding 0.2% lactic acid, pH 5.55 with no addition and pH 6.10 by adding 2% NaOH and galactose (0, 0.15, and 0.30%) as per the experimental design. The DPW powders were spray dried in a lab-scale spray dryer with inlet temperature 180°C and the outlet air temperature 83–88°C. The water activity (aw) and L* values of the powders immediately after spray drying were not significantly different (*P* > 0.05) and was in the range 0.074 to 0.098 and 91.89 to 92.81, respectively. It was observed that the pH of the powders decreased with increase in lactic acid contents. The pH of low LA and high LA powder were found to be 6.60 and 5.78, respectively. The titratable acidity also increased with increasing lactic acid content and ranged from 0.03 to 0.08% LA. The hygroscopicity values were not significantly different (*P* > 0.05) for the powders and were determined to be in the range 7.8 to 11.3% and the caking tendency of the powders ranged from 97.73 to 98.55%. The thermal properties of the stored DPW powders were determined with differential scanning calorimetry and a dehydration endothermic peak at around 142°C was observed which represented loss of crystalline water. Overall, the DPW powders did not show any significant difference for all the treatment combinations immediately after production.

**Key Words:** deproteinized whey powder, lactic acid, galactose