trations that provide adequate viscosity, are needed to achieve stability while also maintaining solution overrun capabilities. This can inform the formulation of dairy-based gels set by acid or calcium such as whipped yogurts and mousses.

Key Words: acid-induced gelation, aeration, whey protein

0329 pH-triggered intragastric gelation of whey protein/alginate and its effect on sucrose release.

S. Zhang* and B. Vardhanabhuti, *University of Missouri, Columbia, MO.*

Protein digestion is highly influenced by gastric conditions, protein structures, and the presence of other food components in the gastrointestinal tract. Protein and dietary fibers are common food ingredients; however, the effect of dietary fiber on protein digestion is not fully understood. Our previous study showed that whey protein/pectin mixture formed intragastric gel under simulated gastric conditions, which slowed the degradation of protein and could potentially affect the digestion and release of other nutrients. The objective of this study was to investigate the in vitro gastric behavior of mixed whey protein and alginate, and its effect on the digestion pattern of protein and sucrose release. Mixed solutions of 5% whey protein isolate (WPI), alginate (0.01 to 0.05 alginate to WPI wt. ratio) and 10% sucrose were prepared by heating them together at 85°C for 30 min. Simulated gastric fluid (SGF) consisted of 0.034 M NaCl, 3.2 mg/g pepsin, and pH was adjusted to 1.2, 2, 3, and 4. The in vitro digestion was performed using reciprocating cylinder dissolution apparatus, with 10-g sample added to 78 g SGF (pepsin: protein = 1: 2). Rheological properties and electrophoresis were performed to evaluate the gastric behavior of the mixture, and HPLC was used to measure sucrose release during digestion. At low alginate to WPI ratios, alginate did not significantly affect the degradation of whey protein and the bioavailability of sucrose, as shown by SDS-PAGE and HPLC, respectively. Increasing biopolymer ratio to 0.05 led to extensive intragastric gelation immediately when samples were mixed with SGF at pH 1.2. The mechanism behind intragastric gelation is believed to be the cross-linking between oppositely charged protein and alginate molecules when pH was reduced to lower than the pI of protein. Sucrose was entrapped in the gel network since no sucrose was detected in the digestion media once the intragastric gel was formed. During dissolution, physical movement and proteolysis by pepsin led to slow degradation of the gel, which also resulted in the slow release of sucrose from the matrix in 20 min. Intragastric gelation was only observed in SGF at pH 1.2 and 2.0. This study indicated that at certain conditions whey protein and alginate mixtures could form intragastric gel, which delayed protein digestion and sucrose release from the matrix. These results can potentially lead to formulation of whey protein beverage having lowered postprandial glycemic response.

Key Words: intragastric gelation, digestion, sucrose

0330 Evaluation of an adsorbent for the removal of aflatoxin M1 from contaminated milk.

E. D. Womack*, D. L. Sparks, A. Brown, and S. H. Ward, *Mississippi State University, Mississippi State.*

Lactating cows that consume aflatoxin B_1 (AFB_1) contaminated feed containing approximately 20 parts per billion (ppb) may produce aflatoxin M_1 (AFM_1) contaminated milk that exceeds the FDA maximum allowable limit of 0.5 ppb. Current detoxification methods for the reduction of AFM_1 include the use of sequestering agents added to feed. The sequestering agents act as an enterosorbent to ameliorate the toxicity of AFB_1 by reducing intestinal absorption. However, not all AFB_1 is bound and the residual can be metabolized to AFM_1. Once this tolerance level of 0.5 ppb AFM_1 is surpassed, the milk must be discarded because it cannot be used for human consumption resulting in economic losses. The current study examines the proficiency of an adsorbent, powdered activated carbon (PAC) to bind AFM_1 in various milk types as PAC has excellent adsorption properties in an aqueous environment. A total of 24 samples ($r = 3$) contained artificially spiked AFM_1 (0.5 ppb) and 0.1%, 0.25%, and 0.4% PAC in whole, skim, and raw milk. Samples were shaken, extracted using Agilent QuEChERS extraction salts, and analyzed via liquid chromatography with mass spectrometry detection. A concentration of 0.5 ppb AFM_1 was spiked into 10 mL to yield a final concentration in whole (0.54 ± 0.07 ppb), skim (0.46 ± 0.01 ppb), and raw milks (0.56 ± 0.03 ppb). The highest concentration of PAC (0.4%) resulted in a significant decrease in AFM_1 contamination ($p < 0.05$) with a reduction of 65% (0.18 ± 0.08 ppb), 91% (0.05 ± 0.01 ppb), and 52% (0.24 ± 0.03 ppb) of AFM_1 from the whole, skim, and raw milks, respectively. No milk showed any significant difference in percent protein, lactose, or total fat relative to their milk blanks ($p > 0.05$) suggesting that PAC has no effect on milk constituents. Preliminary results show that the use of PAC can reduce the amount of AFM_1 below the FDA safety limit and, as a result, prevent the dumping of milk.

Key Words: AFM_1, activated carbon, milk

0331 Application of FT-IR and flow cytometry to evaluate the effect of sodium chloride on probiotic bacteria.

N. Shah and A. Gandhi*, *The University of Hong Kong, Hong Kong.*

The aim of the study was to investigate the effect of varying sodium chloride concentrations on cell membrane, viability and proteolytic activity of probiotic bacteria. Reconstituted skim milk was inoculated with *Lactobacillus acidophilus* at varying salt concentrations (0-10% NaCl) and pH levels (4.0, 5.0 and 6.0) and ACE-inhibitory activity and proteolytic activity were determined. Additionally, the effects of NaCl reduction and its substitution with KCl on cell membrane of certain probiotic bacteria (*Lb. acidophilus*, *Lb. casei* and *B. longum*) and

a pathogenic bacterium, *Escherichia coli* were investigated using Fourier transform infrared spectroscopy (FT-IR). A critical NaCl concentration that inhibited the growth of *E. coli* without significantly affecting the growth of probiotic bacteria was determined by monitoring cell growth and FT-IR spectra. To evaluate the effect of substitution of NaCl with KCl, substitution was performed at critical total salt concentration at varying concentrations (0%, 25%, 50%, 75% and 100% KCl). Furthermore, the effects of varying NaCl concentrations on viability, membrane integrity and metabolic activity of these probiotic bacteria were studied using conventional technique and flow cytometry. The findings revealed that in *Lb. acidophilus* degree of proteolysis increased with higher salt concentration at pH 5.0 and 6.0 and ACE-inhibitory activity was highest at pH 5.0 at all salt concentrations. Fourier transform infrared spectroscopy results demonstrated significant shifts occurring in amide-I and amide-III regions when *Lb. acidophilus* was subjected to varying salt concentrations. Further, the conventional technique revealed that 2.5% was the critical level of NaCl to inhibit the growth of *E. coli* without significantly affecting the growth of most probiotic bacteria. The FT-IR analysis also highlighted the changes that occurred mainly in amide regions on increasing NaCl concentration from 2.5 to 3% in most bacteria. The findings suggest that 50% substitution of NaCl with KCl at 2.5% total salt could inhibit *E. coli*, without affecting the probiotic bacteria. Lastly, the observations from conventional culture technique were compared with the findings from flow cytometric analysis on metabolic activities of the cells and it was revealed that there was a correlation between culturability and dye extrusion ability of *Lb. casei* and *B. longum*. However, a certain population of *Lb. acidophilus* was viable as per the plate count method but the efflux activity was compromised. The metabolic activity of *Lb. casei* was found to be highest among the three probiotic bacteria.

Key Words: FTIR, flow cytometry, probiotic bacteria

0332 Genomic insights into high exopolysaccharide-producing dairy starter bacterium *Streptococcus thermophilus* ASCC 1275. N. Shah, Q. Wu* and H. M. Tun, *The University of Hong Kong, Hong Kong.*

Streptococcus thermophilus ASCC 1275 (ST 1275) is a typical dairy starter bacterium and produces the highest known amount (~1,000 mg/L) of exopolysaccharide (EPS) in milk within this species. This organism produces both capsular and ropy EPS and possesses textural modifying properties for yogurt and cheese. In this study, de novo shotgun paired-end pyrosequencing was applied to complete the whole genome of ST 1275. The genome size of ST 1275, a plasmid-free bacterium, was ~ 1.85 Mbp with an average GC content of 39.1%. A novel *eps* gene cluster for EPS assembly containing two-pair genes of *eps*C-*eps*D for determining the chain length of EPS was found in ST 1275 genome, which confirms that ST 1275 produces two types of EPSs as found in our previous studies. Compared with other sequenced *S. thermophilus* strains, ST 1275 possessed the lowest numbers of 5 rRNA operons and 55 tRNAs suggesting that this organism may have a more effective protein synthesis machinery. The highest number of four separate CRISPR (clustered regularly interspaced short palindromic repeats)-Cas (CRISPR-associated) loci was found in ST 1275 genome indicating that this organism may have a better adaptive immunity against various bacteriophage infections. Further analysis including carbohydrate utilization, effective proteolytic system, sophisticated stress response systems and defense systems in ST 1275 was performed to provide genomic insights into its adaptation to milk and as a cell factory for EPS production during milk fermentation. The elucidation of ST 1275 genome makes this organism as a model dairy starter bacterium for the research of high EPS yield and capsular/ropy EPS producer from the species of *S. thermophilus*.

Key Words: genome sequencing; EPS biosynthesis; *Streptococcus thermophilus*

0333 Effectiveness of pulsed light treatment on the inactivation of pathogenic and spoilage bacteria on cheese surface. J. Proulx*[1], L. Hsu[1], B. Miller[1], G. Sullivan[1], K. Paradis[2], and C. I. Moraru[1], [1]*Cornell University, Ithaca, NY,* [2]*McGill University, Montreal, QC, Canada.*

Cheese products are susceptible to post-processing cross-contamination that can lead to both food safety issues and significant losses due to spoilage. Pulsed Light (PL) treatment, consisting of short, high-energy light pulses, could represent a solution to address this issue since it is a nondestructive technology that can effectively inactivate microorganisms on surfaces. This study examined the effectiveness of PL on the inactivation of the spoilage microorganism *P. fluorescens* and the pathogen surrogates *E. coli* ATCC 25922 and *L. innocua*. The effect of inoculum level, cheese surface topography, and the presence of clear polyethylene packaging were evaluated in a full factorial experimental design. The challenge microorganisms were grown to stationary phase: *P. fluorescens* 1150 was grown at 30°C in tryptic soy broth (TSB) while *E. coli* ATCC 25922 and *L. innocua* FSL C2–008 were grown at 37°C in TSB and brain heart infusion (BHI), respectively. White cheddar and processed cheese, chosen for their different surface topography, were cut into 2.5 cm × 5 cm slices. The samples were then spot inoculated using ten droplets of 10 μL per slice, resulting in an initial concentration of either 5 or 7 log CFU/slice. Inoculated samples were dried overnight at 4°C. For treatments through packaging, sterile UV-transparent low-density polyethylene packaging was placed on top of the inoculated cheese samples immediately before the PL treatment. Cheese samples were then exposed to PL doses of 1.1 to 13.2 J/cm^2. PL-treated samples were stomached for 2 min in Butterfield Phosphate Buffer, the extract then plated on selective media and survivors enumerated by standard plate