Enzymatic hydrolysis is used to improve the functional characteristics of whey proteins. The type and specificity of the enzyme influence the properties of the resultant hydrolysate. In a recent invention, the whey protein hydrolysate (WPH) was utilized as a binder to facilitate the agglomeration of whey protein isolate (WPI). The first objective was to characterize the chemical properties of 3 lots of WPH obtained from a commercial manufacturer. The degree of hydrolysis (DH) of WPH was between 13.82 and 15.35% and not significantly (P > 0.05) different between the lots. From the MALDI-TOF, 10 to 13 and 2 different peptides were observed in the range of 2.5 – 5 and 5 – 8 kDa, respectively. It was also observed from the HPLC that the major whey proteins were completely hydrolyzed indicating a consistent hydrolysis. The second objective of the study was to evaluate the effectiveness of WPH as a binder in wet agglomeration of WPI. For this purpose, a 3 x 3 x 2 factorial design was conducted with pre-wet mass (60, 100, and 140 g), WPH concentration (15, 20, and 25%), and flow rate (11 and 16 rpm) as independent variables. Agglomeration of WPH was carried out in a top-spray fluid bed granulator (Midl-Glatt, Germany). All the experiments were performed in triplicates using 3 lots of WPH. Agglomerated WPH samples were stored at 25°C and analyzed for moisture, water activity, relative dissolution index (RDI), foaming, and emulsifying capacity. There was a significant (P < 0.05) difference in moisture content (range: 3 – 20%) and water activity (range: 0.08 – 0.80) among the agglomerated powders. High moisture content and water activity were observed for the treatments with higher pre-wet volume and higher flow rate and also resulted in clumping of the powders. The treatment that has 60 g of pre-wet, 20% WPH concentration and 16 rpm feeding speed combination had the highest RDI among all the samples. In conclusion, WPH can be used as a potential alternate to soy lecithin in wet agglomeration.

Key Words: agglomeration, whey, hydrolysate

Interaction of strawberry phenolic compounds with milk proteins. R. Singh* and R. Bajaj, NDRI, Karnal, Haryana India.

The bioactive properties of polyphenols have gained great importance due to the proven health benefits and incorporating it in milk system can serve as a basis for functional foods. But the question is what happens when they are present together because polyphenols have significant binding affinity to milk proteins, which can lead to the formation of protein-polyphenol complexes and significantly affect biological activities. Therefore, the present investigation is planned to study the interaction of strawberry polyphenols with milk proteins at different protein concentration (1–40 mg/mL), polyphenol concentration (0.5–2 mg/mL), processing temperature (73°C/ no hold and 90°C/15 min) and pH values (6.7 and 3.57). The reconstituted skim milk (8.5% SNF) was also prepared to have a combined effect of casein and whey proteins. The results (3 replicates) were analyzed using ANOVA and the Tukey test (P-values ≤0.05). Statistical analysis was performed using Prism software (version 5.01). It was found that binding of polyphenols was highest with casein (30mg/mL) and least with skim milk (8.5% SNF) and increased from 55 to 70% as casein concentration increased from 1 to 10 mg/mL. Antioxidant activity is measured by using DPPH assay. The DPPH activity of polyphenol remains unchanged with skim milk and decreased as protein concentration increased from 1 to 40 mg/mL. Effect of heating at different time-temperature combination had no effect on the binding of polyphenol and antioxidant activity. Increasing the pH of polyphenol from 3.57 to 6.7 resulted in increased antioxidant activity for casein, whey protein and milk-polyphenol system. Further, from spectrofluorimetric analysis of samples, it was observed that hydrophobic sites decreased from 400 to 20 at 8% SNF of milk, from 800 to 80 at 2.5% casein and from 700 to 80 at 2% whey protein from control to the samples blended with polyphenol extract. ANS (fluorescent dye 1-anilinonaphthalene-8-sulphonate) binding affinity decreased from 0.05 to 0.02 to 8% SNF, from 0.04 to 0.03 at 2.5% casein and from 0.06 to 0.05 at 2% whey protein from control to the samples blended with Polyphenol extract. These results will help in designing manufacturing processes of functional dairy products that improve yield and quality attributes.

Key Words: polyphenol, protein, interaction


The industrial production of “lactose-free” dairy products is typically achieved through the use of β-galactosidases to hydrolyze the lactose naturally present. This process not only generates glucose and galactose but also a range of lactose analogs and galacto-oligosaccharides (GOS) that are produced through concomitant transglycosylation reactions. As a result, “lactose-free” dairy products often contain a range of lactose analogs and GOS at concentrations comparable to or higher than the residual lactose content. The most prominent by-product in “lactose-free” samples is α-lactolactose (1,6–β-D-galactosyl-glucose) which can often reach total concentrations of ~0.05 g/L when final concentration of lactose can in some cases be < 0.01 g/L. Traditional enzymatic lactose determination procedures involve the use of a β-galactosidase to hydrolyse the residual lactose in “lactose-free” products coupled with measurement of the glucose or galactose released. With these sample types, the selectivity of the β-galactosidase employed is of paramount importance since the non-selective enzymatic hydrolysis of the lactose analogs such as allolactose present in the sample also leads to additional glucose/galactose formation and results in the overestimation of lactose content. Briefly, this novel enzymatic procedure comprises a sample pre-treatment to enzymatically remove glucose, a selective β-galactosidase hydrolysis step, and a creep calculation to account for unselective hydrolysis. This method was fully characterized in terms of its linear range (2.3–113 mg lactose/100 g), limit of detection (LOD) (0.13 mg lactose/100 g), limit of quantification (LOQ) (0.44 mg lactose/100 g) and reproducibility (<3.2% CV). A range of commercially available lactose-free samples was analyzed. The lactose values obtained compared favorably with those obtained using quantitative high-performance anion exchange chromatography – pulsed amperometric detection (HPAEC-PAD) analysis. This method achieved Official Method First Action Status at the AOAC annual meeting in September 2019.

Key Words: analytical method, lactose-free, enzymatic assay


Recent advances in filtration have led to an increased interest in micellar casein products. These microfiltered milk products are mostly depleted of whey proteins and differ from caseinates as they are believed to retain much of the original micellar structure found in milk. While much is known about the impact of ionic strength on milk gels generally, research on whey-depleted micellar casein gels is limited. We found that the ionic environment of casein dispersions had a significant impact on gel properties. Micellar casein dispersions prepared in water at 4% protein exhibited low conductivity (0.9 mS cm⁻¹), indicative of low ionic strength, compared with reconstituted skim milk (4.9 mS cm⁻¹). When acidified with thermostable starter cultures at 40°C, micellar casein dispersions made in NaCl or milk permeate gelled at lower pH and formed firmer gels (at pH 4.6) compared with samples prepared in water. 4% casein dispersions did
not form a gel at pH 4.6 if prepared in NaCl at 150 mmol kg$^{-1}$ and above. Dispersions were also prepared at 4 and 8% protein with increasing concentrations of NaCl and cold-acidified at 2°C to pH 4.6 using 0.5 M HCl. Cold-acidified dispersions were then warmed to 30°C at a rate of 0.5°C/min in a rheometer to measure gel development without gelation pH and time as confounding factors. Cold-acidified dispersions formed a gel around 25°C as long as ionic strength was below a certain threshold level, which was dependent on protein level. Storage modulus of cold-acidified casein gels increased, and loss tangent decreased, with increasing ionic strength and protein content. This research shows that weaker casein gels may be formed by lowering the ionic strength of the dispersion and the mechanisms for the weaker gel can be partially explained by the higher gelation pH but is also likely due to electrostatic and hydrophobic interactions resulting from the lower ionic strength. Very low ionic strength may encourage more hydrophobic interactions between caseins allowing for gelation at higher pH values. Control of the ionic environment of micellar casein dispersions greatly impacts its acid gelation behavior.

**Key Words:** casein, acid, gel

368  **Modeling the effect of temperature and water activity on thermal resistance of *Salmonella* in dairy powders.** X. Wei$^1$, B. Chaves$^1$, M.-G. Danao$^1$, S. Agarwal$^3$, and J. Subbiah$^2$, $^1$University of Nebraska, Lincoln, NE, $^2$University of Arkansas, Fayetteville, AR, $^3$Mars Wrigley, Chicago, IL.

*Salmonella* persistence in dairy powders has caused several foodborne outbreaks. The selection of pasteurization processing conditions requires determination of the thermal inactivation kinetics of *Salmonella* in dairy powders. The objectives of this study were to 1) determine the thermal inactivation kinetics of dairy powders at different fat content and water activity ($a_w$); 2) evaluate multiple models for describing the effect of temperature, $a_w$, and fat content on inactivation of *Salmonella* in dairy powders. Two types of dairy powders, nonfat dry milk (0.62% fat content, wt/wt) and whole milk powder (29.46% fat content) were inoculated with a 5-strain *Salmonella* cocktail and equilibrated to 3 $a_w$ levels (0.10, 0.20 and 0.30) for the isothermal treatment at 75, 80 and 85°C to obtain the D- and z-values. Response surface and modified Bigelow models were used to fit the collected data. The thermal resistance of *Salmonella* significantly increased ($P < 0.05$) as $a_w$ decreased, which suggested that a higher temperature or longer processing time would be required to achieve the desired inactivation of *Salmonella* at lower $a_w$. Fat content did not have a significant impact on thermal inactivation kinetics and therefore, data from both dairy powders were pooled to develop a combined model. Response surface model was compared with modified Bigelow model. Modified Bigelow model performed well to predict D-values (root-mean-square error (RMSE) = 1.47 min) and log reductions (RMSE = 0.47 log cfu/g), when compared with the response surface model (RMSE = 1.61 min and 0.48 log cfu/g). This study provides guidance to the dairy industry to understand the influence of temperature and $a_w$ on the thermal inactivation of *Salmonella* in dairy powders and identify the proper temperature and time combinations for the development and implementation of the pasteurization process to ensure food safety.

**Key Words:** modified Bigelow model, response surface model, D and z values