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Effect of Cosolvents (polyols) on Structural and Foaming Properties of Soy Protein Isolate

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Abstract

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Effect of polyols (mannitol, sorbitol, and xylitol) at three concentrations (5, 10, and 15% w/w) on the structure of soy protein isolates (SPI) was investigated. Changes in foaming properties of SPI were then examined with the addition of polyols at different concentrations. The interactions between SPI and polyols resulted in a substantial decrease in protein surface hydrophobicity and intrinsic tryptophan fluorescence intensity, along with the covering of tyrosine. Furthermore, circular dichroism (CD) spectroscopy of SPI suggested that a more ordered and compact conformation was induced by polyols. Consequently, these structural changes led to lower foamability of SPI. An increase in the viscosity of SPI suspension seemed to be advantageous for improving the foam stability of SPI.

Keywords: soy protein isolates (SPI); polyols; structural conformation; foam

Food demand of the growing world population has prompted the search for new protein sources. On this account, vegetable proteins are emerging as a promising alternative to partially take the place of animal proteins for human protein (Bolontrade & Scilingo 2013). Soy protein, with nutritionally balanced amino acids, is an important and relatively cheap source of vegetable proteins, so it has been widely used to formulate foods aiming to improve their nutritional and/or functional qualities (Yuan *et al*. 2013; Kim & Kim 2015). The ability of soy protein to provide desirable functional characteristics in particular food applications depends on its molecular structure and concentration, composition of the solution surrounding it, and its manufacturing procedure (Chanasattru *et al*. 2007). A better understanding of the effects of these factors on protein functionality may help rationally enhance the quality of protein-based food products.

Numerous foodstuffs contain not only proteins but also other ingredients, such as low-molecular-weight cosolvents, e.g., sugars and polyols (McClements 2002). These additives, such as mannitol, sorbitol, and xylitol, are bulk sweeteners which can be found in various food products, and which are especially investigated for their potential use as sucrose substitutes for foods more suitable for diabetics (Baier & McClements 2003). In addition to providing sweetness, the cosolvents could improve the conformation and functional performance of proteins in aqueous solutions (Chanasattru *et al*. 2008). For example, Kumar *et al*. (2011) investigated the effect of polyols on the solubility, stability, and conformation of bovine serum albumin (BSA) in the presence of polyethylene glycols (PEGs). They reported that polyols increased BSA solubility in the presence of PEGs, and stabilising polyols, such as sorbitol, induced subtle compaction of protein

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molecules. Moreover, the results showed there was a connection between the effect of polyols on the apparent solubility of protein and their effect on the conformational stability of protein. Additional studies indicated that sugar caused changes in the foaming of protein. The results showed that sugar addition decreased the foam capacity and increased the foam stability (Davis & Foegeding 2007; Lv *et al*. 2015).

However, the effect of polyols on the conformation and functional properties of soy proteins has not been studied yet. In this study, the protein solubility, surface properties, including hydrophobicity and exposures of tryptophan and tyrosine residues, and secondary structures were assessed in the presence of polyol (mannitol, sorbitol, and xylitol) solutions at different concentrations. Foaming properties of soy protein samples were subsequently investigated. Furthermore, the relation between foamability and altered protein structures was researched.

MATERIAL AND METHODS

Materials. All buffer reagents and chemicals used were of the highest purity grade available from commercial sources and were used without further purification. Mannitol, sorbitol, and xylitol were obtained from the Aladdin Industrial Corporation (China). 1-anilinonaphthalene-8-sulfonic acid (ANS) was purchased from the Sigma Aldrich Chemical Co. (USA). Deionised water was used for the preparation of all buffer solutions.

Preparation of soy protein isolate (SPI). SPI was prepared according to the modified method of Jiang *et al*. (2009). SPI was prepared from Dongnong 42 soybeans (harvested in 2014). Soybeans were first milled. After removal of the hull, the flour was treated with n-hexane (5 : 1, v/v) to extract oil, and the extraction was repeated three times. The defatted meal was dispersed in deionised water (1 : 15, w/v) and the solution was adjusted to pH 8.0 with 2 M NaOH. The dispersion was stirred for 2 h to extract protein and then centrifuged at 12000 *g* for 30 min at 4°C using a GL-21M centrifuge (Cence Co., Ltd., China). The supernatant was adjusted to pH 4.5 with 2 M HCl and centrifuged at 6000 *g* for 30 minutes. The pellet was washed twice with deionised water, each done by suspension in 5-fold (w/w) deionised water followed by centrifugation at 12 000 *g* for 10 minutes. Thereafter, the protein pellet was resuspended in 5-fold (w/w) deionised water and neutralised to pH 7.0 with 2 M NaOH. The samples were freeze-dried and stored in a 4°C cooler. Protein content in the prepared SPI powder was 92% (w/w) which was determined according to AOAC 18th Ed. (2005), using a micro Kjeldahl digestion and distillation unit (KjelFlex K-360, BUCHI Corporation, Switzerland), with a nitrogen conversion factor of 6.25.

Protein solubility. Dilute protein solutions were prepared by dissolving 0.5 g of lyophilised SPI into 49.5 g of 10 mM phosphate buffer (pH 7.0) containing different polyol concentrations (0~15% w/w) and gently stirred for 2 h at room temperature (23 ± 1°C). The samples were centrifuged (Allegra 64R, Beckman Coulter Inc., USA) at 10 000 *g* for 10 min at room temperature. Protein content was determined by measuring the total nitrogen of supernatant using a micro Kjeldahl digestion and distillation unit (KjelFlex K-360; BUCHI Corp., Switzerland) and a 6.25 conversion factor. Protein solubility (%) was determined by dividing the total amount of protein within the supernatant by the original amount in the sample, multiplied by 100% (Chanasattru *et al*. 2008; Cheung *et al*. 2014).

Surface hydrophobicity. The protein surface hydrophobicity was measured spectrofluorometrically using 1-aniline-8-naphthalene sulphonate (ANS) (Kato & Nakai 1980), as modified by Yin *et al*. (2008). A stock solution of ANS (8 mM) was prepared in 10 mM phosphate buffer (pH 7.0) and stored in a screw-capped container wrapped with aluminium foil at room temperature. The samples were diluted with phosphate buffer (pH 7.0) to a final protein concentration in the range of 0.002 to 0.01%. Excitation and emission wavelengths were fixed at 390 and 470 nm, respectively, with 5-nm slit widths. To 4 ml of diluted sample, 20 µl of probe stock solution was added and mixed. The relative fluorescence intensity (FI) of the dilutions with and without ANS was measured with a spectrofluorophotometer (F-4500 Hitachi Ltd., Japan). The average of three observations of the net relative FI for each sample was then calculated by subtracting the relative FI attributed to protein in buffer without ANS probe. The initial slope of the net relative FI vs. protein concentration plot obtained by linear regression analysis was taken as a measure of protein hydrophobicity.

Intrinsic fluorescence emission spectra. Intrinsic fluorescence emission spectra of SPI samples were determined in an F-4500 spectrofluorometer (Hitachi Ltd., Japan). The SPI concentration in the absence and presence of different polyol solutions was di-

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luted to 0.1 mg/ml in a 10 mM phosphate buffer at pH 7.0. To minimise the contribution of tyrosine residues to the emission spectra, protein solutions were excited at 295 nm, and emission spectra were recorded from 305 nm to 400 nm at a constant slit width of 5 nm for both excitation and emission. The phosphate buffer used to dissolve SPI was used as a blank solution for all samples.

UV absorption spectra and second-derivative spectroscopy. Both zero-order and second-derivative ($dA^2/d\lambda^2$) UV spectra of SPI solutions in the absence and presence of different polyols, after dilution to the protein concentration of 0.1 mg/ml in a 10 mM phosphate buffer at pH 7.0, were obtained with a UV-6000PC spectrophotometer (Shanghai Metash Instruments Co., Ltd., China) with sodium phosphate buffer as the blank; the wavelength ranged from 200 nm to 400 nm at 1 nm increments.

Circular dichroism spectra. SPI solutions in the absence and presence of different polyols, which were used for circular dichroism (CD) analysis, were diluted to the protein concentration of 50 μg/ml in a 10 mM phosphate buffer at pH 7.0 (also as a blank solution). Aliquots of 100 μl each of SPI samples were placed in a 0.1 cm quartz CD cuvette (Hellma, Germany) and the CD spectra were collected in the range of 190~250 nm with a CD spectropolarimeter (J-715; Jasco Corp., Japan) at a scan rate of 100 nm per minutes. The other parameters of the instrument were a response of 0.25 s, band width of 1.0 nm, and step resolution of 0.2 nm. Five scans were averaged to obtain one spectrum. The CD data were shown on the basis of mean molar ellipticity, which was calculated as $[\theta]$ (deg cm^2/dmol) = $(100 \times X \times M)/(L \times C)$, where: X – signal (millidegrees) obtained by the CD spectrometer,; M –average molecule weight of amino acid residues in the protein (assumed to be 115); C – protein concentration (mg/ml) of the sample; L – cell path length (cm). The contents of different secondary structures were calculated with the CDPro software package (Jasco Corp., Japan), and CONTIN/LL was adopted as the algorithm (Jiang *et al*. 2009, 2015).

Foaming properties. Foaming properties (overrun and half-life of foam) were determined according to Yang and Foegeding (2010) and Liu *et al*. (2010) with some modifications. Lyophilised SPI (2 g) was dissolved in 198 g of deionised water containing different polyol concentrations (0~15% w/w) and stirred with a magnet bar for 2 h to a uniform dispersion at room temperature. The SPI solutions (50 ml) were poured into a 250-ml graduated cylinder and an Ultra-Turrax homogeniser (IKA T18 basic, IKA Werke GmbH & Co., Germany) was used at speed setting 5 for 2 minutes. The foam was gently scooped into a standard weigh boat (100 ml), levelled using a rubber spatula, and weighed. This process was completed within 2 min after whipping. The overrun was calculated by the following equation:

$$\text{FO (\%)} = \frac{m_s - m_f}{m_f} \times 100$$

where: m_s – weight (g) of the unwhipped protein solution; m_f – weight (g) of the whipped protein foam

Foam stability was measured by recording the length of the time required for half of the pre-foam mass to drain. The mass of the foam removed during the overrun measurements (less than 20%) was subtracted when calculating half of the pre-foam mass. The starting time for these measurements was taken immediately after foam formation. Each treatment was replicated three times at least to obtain the average drainage half-life (Yang & Foegeding 2010).

Statistical analysis. All experiments were carried out using at least two freshly prepared samples, and each sample was measured in triplicate. The data were analysed using one-way ANOVA. Means were compared by Duncan's multiple-range test at $P < 0.05$ (using the SPSS 20.0 software).

RESULTS AND DISCUSSION

Protein solubility. The solubility of SPI in the absence and presence of different concentrations of polyols is shown in Figure 1. With the addition of polyols, the solubility of SPI obviously increased ($P < 0.05$). For example, after the addition of 15% of mannitol, sorbitol, and xylitol, the solubility increased from 69% (control) to 76, 77, and 78%, respectively. This finding was similar to previous work, which indicated that the addition of sucrose increased 11S globulin solubility of legumin in an aqueous medium (Antipova & Semenova 1997). At all test concentrations, except SPI solutions added 10% (w/w) polyols, mannitol showed a similar effect to sorbitol on the solubility of SPI ($P > 0.05$). But the effect of mannitol is significantly different compared with that of xylitol on solubility ($P < 0.05$). Xylitol had the greatest effect on solubility, mannitol and sorbitol followed in that order. The reason why solubility was enhanced may be attributed to direct hydrogen bonding between polyols and proteins, which could lead to the forma-

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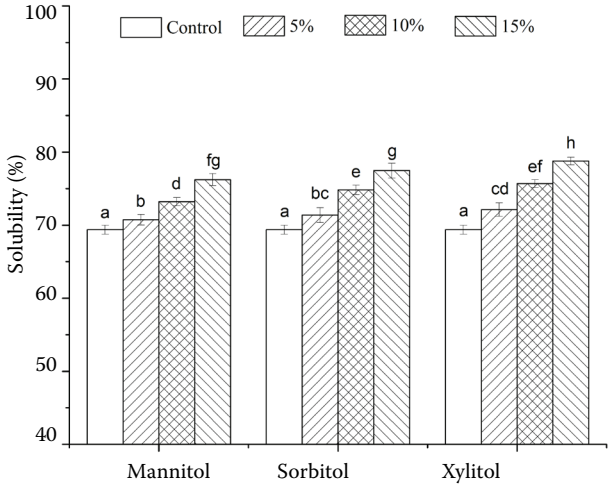

Figure 1. Solubility of soy protein isolates in the absence (control) and presence of different polyol concentrations (5~15% w/w); different letters at the top of the column indicate significant differences ($P < 0.05$)

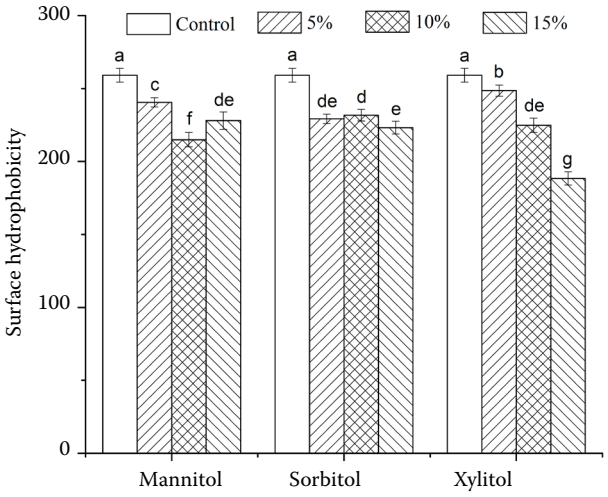

Figure 2. Surface hydrophobicity of soy protein isolates in the absence (control) and presence of different polyol concentrations (5~15% w/w); different letters at the top of the column indicate significant differences ($P < 0.05$)

tion of an extra hydrophilic layer around the protein surface that, in turn, could bring about increasing protein hydration and consequently solubility in an aqueous solution (Semenova *et al*. 2002).

Surface hydrophobicity. Determined by using the ANS fluorescent probe, surface hydrophobicity of SPI with the addition of polyols was found to be substantially lower than that of SPI (Figure 2). For example, after the addition of 15% mannitol, sorbitol, and xylitol, the hydrophobicity decreased from 259 (control) to 228, 223, and 188, respectively. The hydrophobicity decreased ($P < 0.05$) with the increasing concentration of xylitol. With mannitol addition, the surface hydrophobicity of SPI fluctuated. No difference in surface hydrophobicity between SPI solutions added 5 and 10% sorbitol was observed ($P > 0.05$). However, the lower surface hydrophobicity was observed in SPI solutions added 15% sorbitol, compared with that of the sample added 10% sorbitol ($P < 0.05$). The decrease in hydrophobicity could be interpreted from two aspects: First, probably because of hydrogen bonding between polyols and proteins in an aqueous solution, a firmly bound layer of polyol molecules may be formed around the protein molecule which would decrease the hydrophobicity of the protein surface and subsequently increase the thermodynamic affinity of protein in aqueous media (Guzey *et al*. 2003). Second, polyols may induce the rearrangement of hydrophobic surface regions into the protein interior, and consequently inhibit the binding of hydrophobic probes to soy proteins (Vagenende *et al*. 2009). These results were a strong evidence of protein compaction, which must have resulted from the enclosure of hydrophobic side-chain groups that were originally exposed to the exterior of protein molecules, and they were also an indication of a change of the tertiary structure.

Intrinsic fluorescence spectroscopy. The fluorescence spectrum is determined chiefly by the polarity of the environment of tryptophan and tyrosine residues and by their specific interactions and provides a sensitive means of characterising proteins and their conformation (Pallarès *et al*. 2004). Figure 3 shows the intrinsic fluorescence emission spectra of SPI in the absence and presence of different polyols. When the excitation wavelength is 295 nm,

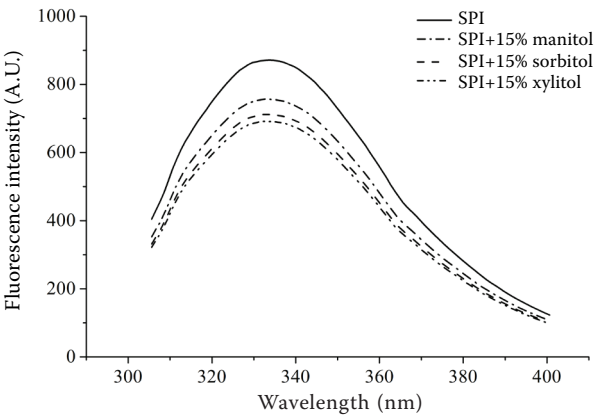

Figure 3. Fluorescence emission spectra of soy protein isolates in the absence and presence of 15% (w/w) polyols

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only Trp produces a fluorescent emission (Shang *et al*. 2007; Li *et al*. 2008). Without the addition of polyols, SPI samples showed an emission maximum at around 333 nm. The interaction with polyols led to a slightly blue-shifted wavelength of tryptophan maximum fluorescence emission spectrum (both from 333 to 332 nm). Moreover, with the addition of 15% mannitol, sorbitol and xylitol, the fluorescence intensity of SPI decreased from 872 to 757, 712, and 692, respectively. Previous studies indicated that the fluorescence emission maximum shifted to a shorter wavelength and the fluorescence intensity decreased as the environmental hydrophobicity of fluorophore decreased (Kwaambwa & Maikokera 2007; Wu *et al*. 2009). Although the blue shift of the fluorescence emission maximum of SPI added 15% (w/w) polyols is not significant, the simultaneous decrease in fluorescence intensity in our study is an indicative of conformational changes of SPI. A blue shift of the fluorescence emission maximum suggests a change in Trp residues to a more hydrophobic environment, while the decrease in fluorescence intensity indicates a possible increase of the intramolecular quenching of Trp residues, and potentially reversible structural changes (Liang *et al*. 2008; Stănciuc *et al*. 2012). Furthermore, a reduction of fluorescence intensity may occur as a result of the proximity between Trp and quenchers, such as hydrogen bonds and disulphide (Stănciuc *et al*. 2015).

UV-vis spectra. Since UV spectroscopy could not resolve overlapping bands in the normal spectrum into the individual contributions of aromatic side chains, second-derivative spectroscopy was used to detect the conformational changes concerning the microenvironments of aromatic amino acids (Zhao & Yang 2008). As shown in Figure 4, the second-derivative spectrum of SPI in the absence and presence of different polyols showed two maxima at 289 and 296 nm and two minima at 285 and 291 nm. The peak at 296 nm can be assigned to tryptophan alone (Jiang *et al*. 2009). Compared with the peaks of SPI, second-derivative peaks of SPI with the addition of polyols at 296 nm slightly shifted to a longer wavelength. Furthermore, there were changes in amplitude, determined by calculating the ratio (r = a/b) of the two peaks to trough values marked in Figure 4. With added mannitol, the value of a and b decreased. While with the addition of sorbitol and xylitol, the value of *a* decreased and the value of b did not change significantly. The ratio of a/b declined substantially in all SPI with the addition of polyol samples; for example, after the addition of 15% mannitol, sorbitol, and xylitol, the value of r decreased from 0.90 to 0.82, 0.79, 0.79, respectively. Ragone *et al*. (1984) confirmed that for tyrosine, the value of r decreases as the solvent polarity decreases, while it is almost independent of the solvent polarity for tryptophan. Thus, in the second derivative spectrum of protein, the value of r and the positions of the peaks and troughs are a function of relative amounts of the two aromatic amino acids and of the average polarity of the environments of tyrosines and tryptophans (Lange & Balny 2002). In this study, the value of r for all the SPI with the addition of polyol samples was lower than in control samples, which indicated the change in three-dimensional positions and the movement of Tyr residues of SPI to a hydrophobic region during the interaction with polyols (Lange & Balny 2002). The second-derivative UV results were in accordance with those from the ANS and tryptophan fluorescence analyses, which all showed structure folding when SPI had interactions with polyols in an aqueous solution.

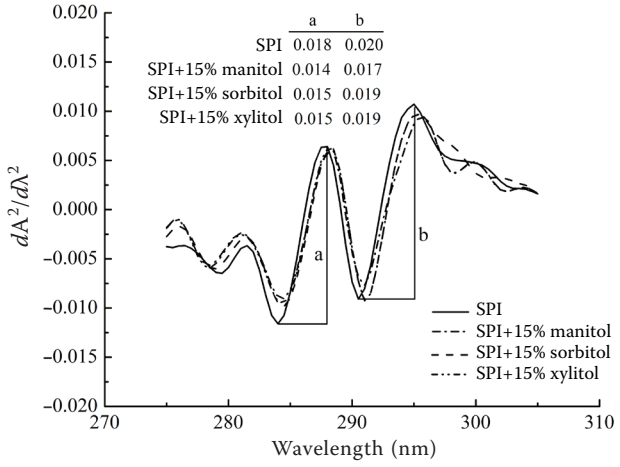

Figure 4. Second-derivative UV spectra of soy protein isolates in the absence and presence of 15% (w/w) polyols

Circular dichroism spectra. CD spectroscopy is an established technique for doing research on protein structure, dynamics, and folding because of its sensitivity to detect very small changes in protein secondary and tertiary structures (Zhang *et al*. 2012). The far-UV CD spectra of SPI in the absence and presence of different polyols are presented in Figure 5. The CD spectra of SPI presented a positive band near 194 nm with a zero crossing around 200 nm, and a negative band near 209 nm. These features most probably implied α/β type structure (Galazka *et al*. 2000). The positive peak at

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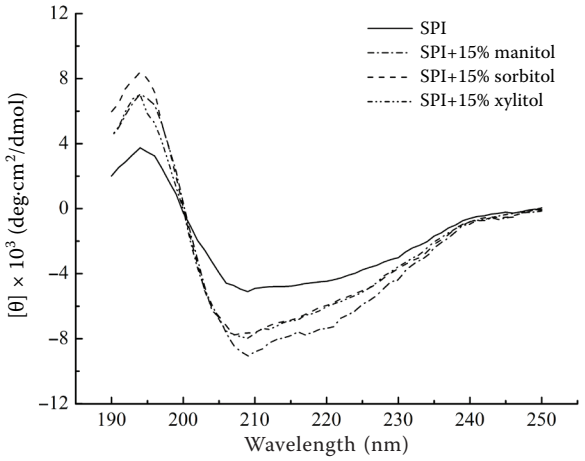

Figure 5. Circular dichroism spectra in the far-UV region of soy protein isolates in the absence and presence of 15% (w/w) polyols

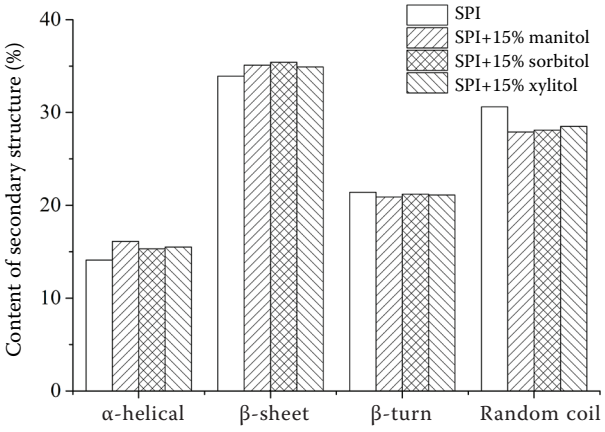

Figure 6. The content of each secondary structure (%) of soy protein isolates in the absence and presence of 15% (w/w) polyols

194 nm indicated the existence of β-sheet structure and the negative peak at 209 nm was characteristic of α-helical structure (Choi & Ma 2007; Zhao *et al*. 2015). As polyols were added, the positive and negative molar residue ellipticity peaks of SPI samples increased, which showed that the amounts of α-helix and β-sheet had risen (Tong *et al*. 2012). This result was proved by the changes of secondary structure contents of SPI with and without the addition of polyols calculated by JASCO secondary structure software (Figure 6). With the addition of polyols, the ordered structure content (α-helical + β-sheet) of SPI increased, mainly at the expense of the unordered structure content (β-turn + random coil), indicating that the secondary conformation was changed after SPI interacted with polyols in an aqueous solution (Zhang *et al*. 2014). In general, α-helix and β-sheet of proteins lie in the interior part of polypeptide chains. Now when the ordered structure content increased, polyols might lead to more compact protein molecules (Xue *et al*. 2013). This finding was similar to previous work, which indicated that the cosolvents (glycerol, sucrose, and trehalose) induced a slight partial formation of the secondary structure of proteins (McClements 2002; Chen *et al*. 2013). The structural changes of proteins may be attributed to formed hydrogen bonds with polyols, which could alter the original intramolecular interactions in the interior of the protein molecules and lead to their folding (Semenova *et al*. 2002).

Foaming properties. Foams are biphasic colloidal systems with a continuous liquid or aqueous phase and a dispersed gas or air phase. Food foams are generally caused by whipping, shaking, or sparging, and the method used affects the characteristics of the foam. The two common characteristics of foams are foamability (that measures the volume of the foam produced, and is normally expressed as % overrun) and foam stability (which is the volume of the liquid drained from the foam at half of the total time) (Panyam & Kilara 1996). The foaming properties of SPI in the absence and presence of different concentrations of polyols were investigated and expressed as overrun and half-life of foam (Figure 7). The foam overrun (FO) of SPI with the addition of polyols was significantly lower ($P < 0.05$) than that of SPI (Figure 7). This result indicated that polyols had a negative effect on the foamability of SPI. With the addition of 15% (w/w) mannitol, sorbitol, and xylitol, the FO of SPI solution decreased from 1099% (control) to 712, 810, and 755%, respectively. The finding was similar to that reported by Davis and Foegeding (2007), who noted that the foamability of whey protein isolate (WPI) and egg white protein (EWP) could be impaired by sucrose. With the addition of mannitol and xylitol, the FO of SPI samples gradually decreased ($P < 0.05$) with increasing concentration (Figure 7). With increased concentration of sorbitol from 5 to 10%, the FO of SPI did not significantly decline ($P > 0.05$). With the addition of 15% sorbitol, the value of FO decreased ($P < 0.05$).

The foaming ability of proteins is related with their film-forming ability at the air-water interface. Proteins which quickly adsorb at the newly formed air-liquid interface during foaming and undergo unfolding and molecular rearrangement at the interface show

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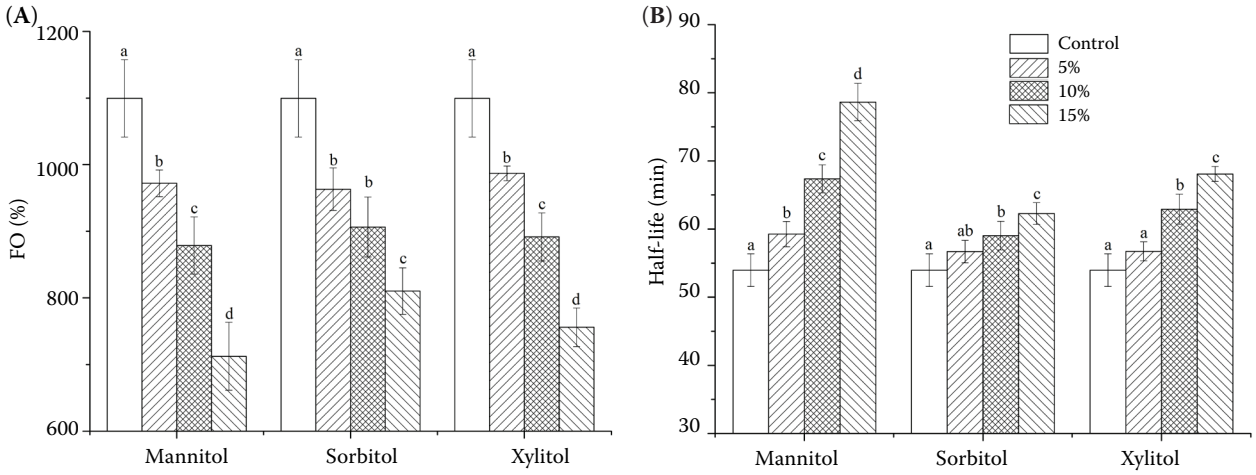

Figure 7. Overrun (A) and half-life (B) of foam prepared from 1% (w/w) soy protein isolates solutions containing different polyol concentrations (0~15% w/w)

FO – foam overrun; control – soy protein isolates solution without polyols; different letters at the top of the column indicate significant differences ($P < 0.05$)

better foaming ability than proteins which slowly adsorb and resist unfolding at the interface (Aewsiri *et al*. 2011). The protein molecules may form hydrogen bonds with polyols, which led to increased hydrophilicity and decreased surface activity, while the adsorption of protein declines in the presence of polyols. Thereby the protein molecules which participate in the hydrogen bond formation with polyols preferentially remain in bulk rather than to adsorb to the interface. Consequently, polyols have a disadvantageous effect on the foaming ability of SPI (Raikos *et al*. 2007).

As is known to all, adsorption of protein in an adequate amount within the time scale of foam production is a condition for efficient foam formation, closely related to the rate at which the surface tension can be lowered. Therefore, one of the most important factors for foam formation is the protein adsorption rate, which counts on protein concentration, protein molecular weight, protein structure, and solution conditions (Martin *et al*. 2002). Some previous researches have suggested that disordered, smaller, and more flexible proteins were better surface agents than ordered, larger, and more rigid ones, causing a greater affinity of the protein for the interface, allowing it to overcome the barrier against adsorption, which is developed at the interface while proteins were compactly arranged. This fact contributes to a rapid decrease in the surface tension, as a result, the foaming ability of protein increases (Moro *et al*. 2011; Báez *et al*. 2013). Therefore, the shift of soy protein to more compact and less flexible conformations in polyol/water mixtures, which is proved by fluorescence, UV absorption, and CD measurements, may result in the decreased foamability of SPI (Báez *et al*. 2013).

The foaming ability is improved by an increase in protein surface hydrophobicity. The higher surface hydrophobicity promotes a rapid decrease in the surface tension, a favourable factor for foam formation (Moro *et al*. 2011; Báez *et al*. 2013). When polyols were added into SPI solution, a decrease in the surface hydrophobicity of resulting SPI was obtained (Figure 2). The decrease in a hydrophobic region on the surface of SPI restrained SPI molecules from localising at the air-water interface and reducing the surface tension more effectively. This resulted in the decreased foaming ability of SPI after addition of polyols.

It was also noted that the increased viscosity of SPI solutions added polyols could reduce the mobility of protein molecules, hence the transport processes involved in the movement of the protein molecule from the aqueous phase to the subsurface and the surface may be slowed down, which led to a decrease in the foaming ability of SPI (Guzey *et al*. 2003; Foegeding *et al*. 2006; Lv *et al*. 2015). Furthermore, the higher viscosity of SPI solutions with addition of polyols allowed less air to be incorporated during whipping, which became a factor of hindering the foam formation (Raikos *et al*. 2007; Yang & Foegeding 2010).

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Figure 7 illustrates the effect of polyols on the foam stability of SPI. It can be observed that the foam of SPI with the addition of polyols is more stable compared to SPI (control). With the addition of mannitol, the foam stability of SPI samples gradually increased ($P < 0.05$) because of increasing concentration (Figure 7). The addition of 5% (w/w) sorbitol and xylitol has not improved the foam stability of SPI ($P > 0.05$). With higher concentration, the foam stability was apparently enhanced ($P < 0.05$). For samples with the addition of 15% (w/w) mannitol, sorbitol, and xylitol, the half-life of foam increased from 54 min (control) to 79, 62, and 68 min, respectively. A similar result was obtained by Lv *et al*. (2015), who reported that the foam stability of chestnut protein increased with the addition of sucrose. The increase in foam stability may attribute to the ability polyol to raise the viscosity of the bulk phase (McClements 2002; Lau & Dickinson 2005). A high viscosity should inhibit the movement of a liquid through the network of thin films and plateau borders, which slowed the drainage rate, and consequently increased the foam stability (Yang & Foegeding 2010).

CONCLUSIONS

Overall, structural and surface property analyses led to a general conclusion that the interaction of SPI with polyols induced an increased structural order and a compaction of protein molecules. The structure of SPI which primarily involved second structure and tertiary structure has changed to some extent. Whereas the foaming ability was impaired after SPI interacted with polyols at all concentrations tested in an aqueous solution, the addition of polyols produced structures that were clearly more rigid, and more obviously adverse to the foam formation than SPI controls (without polyols). Furthermore, the increase in the viscosity of SPI suspension may be favourable for improving the foam stability of SPI.

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