Sugar replacement with zwitterionic plasticizers like amino acids

R.G.M. van der Sman *, I.A.F. van den Hoek, S. Renzetti

Wageningen Food Biobased Research, Wageningen University & Research, Netherlands

A B S T R A C T

In this paper, we investigate the potential of zwitterions like amino acids as alternative (bulking) sugar replacers. Commonly, polyols or oligosaccharides are taken as sugar placers, but they are perceived as less attractive due to laxative problems. The choice of amino acids as alternative sugar replacers is inspired by their presence in Natural Deep Eutectic Solvents (NADES) and compatible solutes, next to carbohydrates. In these compounds, hydrogen bonding plays an essential role similar to sugar (replacers) in food. Because of the novelty of the topic, we first discuss at length NADES as a potential source of alternative plasticizers/sugar replacers. Subsequently, we perform a detailed analysis of their thermodynamic properties, to investigate whether amino acids and related zwitterions indeed have the appropriate properties for sugar replacement.

Our analysis shows that several zwitterions indeed have proper thermodynamic properties, which can make them good plasticizers and humectants. However, the use of several zwitterions can be restricted by their poor solubility, except for L-proline. Solubility problems can be circumvented by their use in mixtures of several sugar replacers, which enhances their solubility. The poor solubility makes it also difficult to characterize the glass transition temperatures of the pure solute $T_{g}$, Consequently, we have estimated them via extrapolation of the viscosity curves, which is shown to scale with $T_{g}/T$. We have taken $T_{g}$ of the plasticizer solution as a measure of the hydrogen bond density, $n_{OH,eff}$.

That measure is shown to explain the melting behaviour of biopolymers like egg white and starch in glycine and L-proline solutions, similar to sugar (replacers). However, our measurements of the biopolymer melting show indications of phase separation at high moisture contents for both amino acid solutions as for carbohydrate overall. The amino acids and other compatible zwitterions have very similar thermodynamic behaviour as sugars and their carbohydrate-based replacers. In proper combinations with alternative plasticizers, the zwitterionic compatible solutes can well be used in sugar replacement strategies for foods.

1. Introduction

In bakery products sugars provide a wide variety of functionalities, next to providing sweetness (Davis, 1995; Pareyt et al., 2009; Wilderjans, Luys, Brijs, & Delcour, 2013; van der Sman & Renzetti, 2019). For many of these other functionalities, sugar is acting as a plasticizer. Hence, in sugar reformulation studies one often replaces sugar by polyols to provide the plasticizer functionality (Struck, Jaros, Brennan, & Rohm, 2014). However, polyols are not viewed by the food industry as the ideal solution to sugar replacement due to their laxative problems (Ghosh & Sudha, 2012; Lenhart & Chey, 2017). Hence, there is a demand for another class of food-grade, natural plasticizers that can provide similar functionality as sugar, but with fewer calories.

The functionality of sugar and its replacers in bakery and confectionery products can largely be characterized by their behaviour as (1) plasticizer and (2) humectant (Wilderjans et al., 2013; van der Sman & Renzetti, 2019). As the plasticizer, the sugar determines the viscosity and glass transition of the food product (van der Sman, 2013a, 2013b; van der Sman & Mauer, 2019). The strength of the plasticizing function of carbohydrates and polyols can be characterized by the number of hydroxy groups available for intermolecular hydrogen bonding, $n_{OH,eff}$ (van der Sman, 2013b). Surprisingly, the volumetric density of hydrogen bonds (which is also related to $n_{OH,eff}$) determines the melting behaviour of biopolymers, which encompasses the gelatinization of starch, denaturation/thermosetting of gluten, soy, sunflower protein and the melting of gelatin (van der Sman, 2016; van der Sman & Renzetti, 2019; van der Sman & Mauer, 2019).

We view that alternative plasticizers to be used as sugar replacers can be found in the class of ingredients used in the field of Natural Deep Eutectic Solvents (NADES) (Liu et al., 2018). This field takes inspiration from nature, and in particular from the so-called compatible solutes, which are accumulated in micro-organisms in high quantities in case of severe environmental stress like freezing or drought (Yancey, 2005; Choi et al., 2011). Often, sugars and polyols act as compatible solutes, which protect cell membranes and proteins in stress conditions, which dehydrate the cell. The protective properties of compatible solutes are largely based on their plasticizer properties, i.e. their capability to replace water via providing hydrogen bonding. They are called compatible solutes because they do not interfere much with the cells’ metabolism (Chen & Murata, 2008). Next, to the neutral carbohydrates, micro-organisms are using also zwitterionic compounds as compatible solutes. They can be (1) amino acids like L-proline, glycine, L-alanine, and L-serine, or (2) amino acid derivatives like TMAO, betaine,

* Corresponding author.

E-mail address: ruud.vandersman@wur.nl (R.G.M. van der Sman).

https://doi.org/10.1016/j.foodhyd.2020.106113

Received 6 January 2020; Received in revised form 19 May 2020; Accepted 15 June 2020

Available online 17 June 2020

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choline, carnitine (having quaternary ammonium cation as a functional group), or (3) proline-like compounds like ectoine and hydroxyectoine (Yancey, Clark, Hand, Bowlsu, & Somero, 1982; Yancey, 2005).

For interested readers, we have written a short review on the use of NADES as alternative food plasticizers, which can be found as Supplementary Material to this paper.

In this manuscript below, we evaluate in particular the use of zwitterions like amino acids as alternative plasticizers, and in particular those having or modulating sweet taste. Amino acids having sweet taste are glycine, L-proline, L-alanine and L-serine (Schiffman, Sonnewald, & Gagnon, 1981; Nishimura & Kato, 1988).

The use of NADES ingredients, like amino acids and their derivatives, as plasticizers is not novel. In food science, the sweet amino acids (glycine, L-lysine and L-proline) have been studied occasionally as plasticizer for biopolymers (Stein & Greene, 1997; Taylor, Taylor, Belton, & Minnaar, 2009; Selmin, Franceschini, Cupone, Minghetti, & Cilurzo, 2015; Ahmad, Samuelsen, Garvik, & Oterhals, 2018). It is observed that mixtures of amino acids with starch can show browning due to Maillard reactions. Weak organic acids are also studied as plasticizers for biopolymers (Cao, Yang, & Fu, 2009; Yoon, 2013; Niazi, Zijlstra, & Broekhuis, 2015). Betain has been proposed as a plasticizer for soy (Kwoon, Slade, & Levine, 2017). NADES solvents have been considered as plasticizers for starch and cereal flour (Leroy et al., 2012; Abbott et al., 2014; Colomines, Decaen, Lourdin, & Leroy, 2016).

In pharmacy amino acid are also used as plasticizers for stabilization of mixtures with proteins (Mattern, Winter, Kohnert, & Lee, 1999; Al Husban, Perrie, & Mohammed, 2011; Iztzu, Yoshida, Shibata, & Goda, 2016). Traditionally pharmaceutical formulations contain a hydrophilic biopolymer like gelatin, dextran or maltodextrin with sugars or polysols. However, due to restrictions on sugar levels for obese or diabetes patients, amino acids are investigated as sugar replacers. Their application is challenged by the occurrence of phase separation and subsequent crystallization. In a way, it is quite comparable to phenomena observed in mixtures of starch and polysols (van der Sman, 2019a), which are plasticizers of comparable size as amino acids.

Small amino acids like glycine and L-alanine have a strong plasticizing effect, but they also crystallize easily, if compared to carbohydrates (Al Husban et al., 2011). Because of their solubility problems, amino acids are always used in a mixture of plasticizers (Mattern et al., 1999). It is shown, that amino acids in combination with sugars can produce a glassy system without crystals (Lueckel, Bodmer, Helk, & Leuenberger, 1998; Kasraian, Spitznagel, Juneau, & Yim, 1998; Forney-Stevens, Bogner, & Pikal, 2015). If the amount of amino acids exceeds the sugar, the amino acid will crystallize. A partial phase diagram is constructed for glycine/sucrose (Suzuki & Franks, 1993). Furthermore, in mixtures of plasticizers of different sizes, one can expect some synergy. One has observed that the stability of lyophilized sucrose-protein systems is enhanced by adding amino acids (Forney-Stevens et al., 2015), which is attributed to the hole-filling mechanisms, similar to glycerol in trehalose or gelatin matrices (Bellavia, Paccou, Guinet, & Hédoux, 2014; Ubink, 2016).

The above short overview of the literature shows there is a potential for zwitterions like amino acids for use as novel sugar replacers. However, one must use them in mixtures of different plasticizers to avoid solubility problems. Furthermore, in these mixtures, one must be aware of undesired taste effects, Maillard reactions or crosslinking reactions. The effectiveness of the use of these zwitterions as sugar replacers, in their role of plasticizer and humectant, largely depends on their thermodynamic behaviour. For the remainder of this paper, we investigate this behaviour of the sweet amino acids, glycine, L-alanine, and L-proline, and also in combination with other plasticizers like sugars. For their behaviour as plasticizer and humectant, we are interested in (a) the water activity, (b) the solubility, (c) the glass transition temperature, and (d) their influence on the melting of biopolymers.

The latter two properties are governed by the density of hydrogen bonds (van der Sman, 2013b, 2016; van der Sman & Renzetti, 2019).

To estimate the density of hydrogen bonds of the pure plasticizer, one must know about the glass transition of the dry ingredient — which is often difficult to measure. However, recently we have shown that the viscosity of semi-dilute solutions of the plasticizer can be used as an alternative means to determine that (van der Sman & Mauer, 2019). Hence, we will investigate also the viscosity of amino acid solutions and other solutions with zwitterions having a molecular structure similar to glycine. For our investigations, we have largely used data already available in the literature. Some novel data from our lab is used, which is explained in forthcoming papers (Renzetti, van den Hoek, & van der Sman, 2020).

The remainder of the paper is organized as follows. First, we describe the theories used in describing the thermodynamic behaviour of (sweet) amino acids. We have chosen for the Flory–Huggins theory for the thermodynamic description of amino-acids, because it is the framework we have used previously for the thermodynamic behaviour of carbohydrates (Van der Sman, 2017). Moreover, we intend to use this framework in the future to investigate the behaviour of complex mixtures of biopolymers, carbohydrates, amino-acids and water. In particular, we are interested in how amino acids as co-plasticizer influence the melting of biopolymers, like egg white or starch — for which the Flory–Huggins theory is a suitable theory (Van der Sman & Meinders, 2011). We are aware of the fact that in literature other theories from molecular thermodynamics are developed for describing amino acids, like UNIFAC (Gupta & Heidemann, 1990) and PC-SAFT (Held, Cameretti, & Sadowski, 2011). We conclude with a critical comparison of the Flory–Huggins theory with UNIFAC and PC-SAFT, indicating its limitations and advantages for describing food systems with predominantly hydrophilic ingredients.

2. Thermodynamic properties of sweet amino acids

Due to the poor solubility of amino acids in water, we have also analysed their properties in ternary mixtures with carbohydrates and water. Hence, the Flory–Huggins theories for ternary mixtures will be given. Note that, the binary case of a amino-acid solution is a special case, via setting the concentration of the carbohydrate to zero.

2.1. Flory–Huggins theory for ternary mixtures

Like ternary systems comprising two carbohydrates, we describe the thermodynamics of amino acid/carbohydrate/water systems using Flory–Huggins theory (Van der Sman, 2017). We will test the theory via the water activity of the amino acid solutions at room temperature. The glass transition of the pure amino acids is found to be lower than room temperature. Hence, the free-volume extension of the theory is not required in this study.

The chemical potentials of the two plasticizers \(i = \{s, g\}\) and water \(i = w\) are as follows (Van der Sman, 2017):

\[
\mu_i = \frac{\ln \phi_i}{N_i RT} - \frac{1}{N_i} \phi_i \left(1 - \frac{1}{N_i}\right) \mu_w + \frac{1}{N_i} \phi_i \left(1 - \frac{1}{N_i}\right) \mu_s + (\chi_{si} \phi_s + \chi_{gi} \phi_g)(1 - \phi_i) - \chi_{si} \phi_s \phi_w
\]

\[
\mu_i = \frac{\ln \phi_i}{N_i RT} - \frac{1}{N_i} \phi_i \left(1 - \frac{1}{N_i}\right) \mu_w + \frac{1}{N_i} \phi_i \left(1 - \frac{1}{N_i}\right) \mu_s + (\chi_{si} \phi_s + \chi_{gi} \phi_g)(1 - \phi_i) - \chi_{si} \phi_s \phi_w
\]

\[
\mu_w = \frac{\ln(\phi_w)}{RT} + (1 - \frac{1}{N_w}\phi_s \phi_g) + (\chi_{si} \phi_s + \chi_{gi} \phi_g)(1 - \phi_i) - \chi_{si} \phi_s \phi_w
\]

\[
\phi_i = \text{the volume fraction of compound } i, N_i = \text{the molar volume of compound } i, \text{relative to that of water, and } \chi_{ij} \text{ is the Flory–Huggins interaction parameter between compound } i \text{ and } j. \text{ Recall the relation between chemical potential of water and water activity:}
\]

\[
\mu_w = RT \log(a_w)
\]
The chemical potentials of the plasticizers $\mu_i$ and $\mu_w$ will be used to describe their solubility. In saturated solutions, the chemical potential of the dissolved plasticizers is equal to the chemical potential of the crystalline phase $\mu_X$. This is also used to describe the solubility, which is the concentration/volume fraction where

$$\mu_k = \mu_X$$ (3)

The chemical potential of the crystalline phase of the solute is expressed as follows (Van der Sman, 2017):

$$\mu_X(T) = -\Delta H_f (1 - \frac{T}{T_f}) - \Delta c_p,\text{mix}(T - T_f) - \frac{1}{2} \Delta c_p,\text{mix}(T^2 - T_f^2) - T (\Delta c_p,\text{mix} - T \Delta c_p,\text{mix}) \ln(T_f/T)$$ (4)

$T_f$ is the melting temperature of the pure amino acid, $\Delta H_f$ is the melting enthalpy at $T = T_f$, $\Delta c_p$,mix is the change in specific heat between crystalline and liquid phase of the pure amino acid at $T = T_f$, and $\Delta c_p,\text{mix}$ is the derivative of $\Delta c_p,\text{mix}$ with temperature. Often, the melting temperature is difficult to measure independently, and the chemical potential is often approximated by the following expression:

$$\mu_X(T)/RT = A + B/T + C\ln(T_f/T).$$

We will also investigate the freezing behaviour of ternary systems. The freezing line will be computed using the condition for equilibrium:

$$\mu_k = \mu_{ice},$$

or

$$\Delta \mu(T) = \mu(T) - \mu(T)_{ice} = 0.$$ (5)

$\Delta \mu(T)$ is the chemical potential difference between ice and the maximally freeze-concentrated solution. The glass transition of the maximally freeze-concentrated solution, and the glass transition temperature of water, $T_g,w$, is the latent heat of fusion for ice. Given the ratio of the two plasticizers present in the unfrozen phase, we can compute the freezing temperature of the ternary mixture $T = T_f$, as a function of the volume fraction of water $\phi_w$. Due to freeze-concentration $\phi_w$ will continuously decrease from its initial value while lowering the freezing point $T_f$, which is obtained via setting $T = T_f$ in the expression of $\mu_{ice}$.  

2.2. Glass transition

Frozen ternary mixtures of amino acids and carbohydrates are characterized by $T_g$, the glass transition of the maximally freeze-concentrated solution. Its value can be obtained from the intersection of the freezing line and glass transition line. Above, we have indicated how the freezing line can be computed using the condition $\mu_k = \mu_{ice}$. The glass transition line will be computed using the Couchman–Karasz relation:

$$T_g = \frac{y_x T_g,\text{mix} \Delta c_p,\text{mix} + y_i T_g,\text{mix} \Delta c_p,\text{mix} + y_w T_g,\text{mix} \Delta c_p,\text{mix}}{y_x \Delta c_p,\text{mix} + y_i \Delta c_p,\text{mix} + y_w \Delta c_p,\text{mix}}$$ (6)

$T_g$ is the glass transition of the pure component $i$, $y_i$ is the mass fraction, and $\Delta c_p,\text{mix}$ is the change in specific heat at the glass transition of the pure component, measured in $J/kgK$. The indices indicate the various compounds in the ternary mixture $w$ for water, $s$ for sugars, and $g$ for polysaccharides or amino acids. For water and sugars the parameter values are known. For many sugars and polysaccharides the apparently universal value of $\Delta c_p,\text{mix} = 0.42$ $kJ/kgK$ K (Van der Sman & Meinders, 2011). However, for the smaller polysaccharides holds a different universal value: $\Delta c_p,\text{mix} = 0.85$ $kJ/kgK$ (van der Sman, 2013b). Possibly, for amino acids there is also a universal value. Due to their small size, we expect this value to be similar to that of polysaccharides.

2.3. Hydrogen bonding and viscosity

As shown recently, the melting behaviour of biopolymers is modulated by plasticizers, which can be quantified by $n_{OH,eff}$, which is a measure for the volumetric density of intermolecular hydrogen bonds (van der Sman, 2016; van der Sman & Renzetti, 2019; van der Sman & Mauer, 2019). $n_{OH,eff}$ is computed based on all plasticizers present, including water:

$$n_{OH,eff} = \frac{N_{OH,w}}{\nu_w} + \frac{N_{OH,i}}{\nu_i} + \frac{N_{OH,g}}{\nu_g}.$$ (7)

with $v_i$ is the molar volume of compound $i$, and $N_{OH,i}$ is the effective number of hydroxyl groups per molecule available for hydrogen bonding. Originally, we have proposed to compute these numbers via the glass transition of the pure compound $T_g,i$ (van der Sman, 2013b):

$$1 + \frac{1}{2} \frac{N_{OH,i}}{\nu_i} = \frac{1}{2} \frac{T_{g,i} - T_{g,w}}{T_{g,w}}.$$ (8)

$T_{g,w}$=139 K is the glass transition temperature of water, and $T_{g,w}$=475 K is the glass transition temperature of an infinitely long carbohydrate, i.e. polysaccharides including starch and dextrins (van der Sman, 2013b). Note, that for water follows $N_{OH,w} = 2$, which has effectively two hydroxyl groups.

If a plasticizer, like amino acids, has poor solubility in water, it is difficult to determine the glass transition of the pure compound. If the amino acid solution is cooled in the DSC, it will crystallize quite easily, because the mobility of water is still high if the solution gets supersaturated. Sugars have a high solubility, and the mobility of water in supersaturated conditions is sufficiently low, that the solution can remain supersaturated — as crystallization is kinetically hindered (Shalaev & Kanev, 1994).

Recently, we have shown for carbohydrates that viscosity can be an alternative means to determine $N_{OH,i}$ (van der Sman & Mauer, 2019). For (semi)-dilute solutions the viscosity at constant temperature is shown to be linear with $n_{OH,eff}$. We will investigate the viscosity of binary amino acid solutions, and ternary amino acid/carbohydrate solutions, and compare it with the master curve obtained for carbohydrates (van der Sman & Mauer, 2019).

Already very early, the viscosity of dilute aqueous solutions of plasticizers like sugars and amino acids has been compared to the Einstein correction for spheres suspended in the solution (Daniel & Cohn, 1936):

$$\eta = \eta_0 (1 + K \phi)$$ (9)

$\eta_0$ is the solvent solution and $\phi$ is the volume fraction of the suspended spheres. For hard spheres it holds that $K = 2.5$. The volume fraction can be computed from $\phi = v_i c$, with $v_i = M_i/\rho_i$ the molar volume, and $c$ the molar concentration. It is claimed if the viscosity of plasticizer solutions is plotted against $K \phi$, also for higher concentrations, a master curve is obtained (Daniel & Cohn, 1936). It literature the above relation is often formulated in terms of the molarity of the solute, $m$, and it is extended as a quadratic relation:

$$\eta = \frac{\eta_0}{1 + B m + D m^2}.$$ (10)

Already early the hypothesis is formed that $K$ or the B-coefficient depends on the type and number of functional groups of the solute (Daniel & Cohn, 1936).

2.4. Hydrogen bonding and biopolymer melting

In previous papers we have shown that the melting behaviour of starch, gluten, egg white, gelatin and soy in presence of a variety of sugar (replacers) can be mapped to a single master curve (van der Sman, 2016; van der Sman & Renzetti, 2019; van der Sman & Mauer, 2019), if plotted against the effective volume fraction of plasticizers $\phi_{w,eff}$, which is defined as:

$$\phi_{w,eff} = \frac{\nu_w n_{OH,eff}}{N_{OH,w}}.$$ (11)

For pure water, it holds that $\phi_{w,eff} = \phi_w$, and the master curve coincides with that of the binary biopolymer/water system. For the binary system the curve can be described by the Flory theory of biopolymer melting (Van der Sman & Meinders, 2011; van der Sman, 2016):

$$\frac{1}{T_m} - \frac{1}{T_m,0} = \frac{\nu_w R}{\nu_w \Delta H_m} (\phi_w + \chi_{eff} \phi_w^2)$$ (12)
of glycine and L-alanine. This is achieved via the use of small aerosol data from Ref. Marsh et al. (2017) extend beyond the solubility range 2011; Van der Sman, 2017). Furthermore, we like to remark that the temperature independent over a wider temperature range, i.e. 273–373 K, similar to the case of carbohydrates (Van der Sman & Meinders, 2011). We assume that the crystalline phase does not interact with water. Hence, a certain fraction of the biopolymer to the amorphous phase of the semi-crystalline polymer (Van der Sman, 2012). We have made use of the material properties as listed in Table 1, which also shows the backbone is another important determinant of the Flory–Huggins interaction parameter (van der Sman, 2019b). For the investigated amino acids, this ratio is particularly high for glycine and L-alanine, both showing even negative values — indicating high hydrophilicity.

### 3. Results

#### 3.1. Thermodynamic characterization

##### 3.1.1. Water activity

In Fig. 1 we show the sorption isotherms for several amino acids. The used data sources are listed in Table 2. We have fitted the Flory–Huggins theory to their sorption isotherms, using Eq. (2) to relate the chemical potential of water \( \mu_w \) to water activity \( a_w \). We have made use of the material properties as listed in Table 1, which also shows the fitted interaction parameters \( \chi_{xw} \). The sorption isotherms in Fig. 1 are at different temperatures, which are listed in Table 2. Within the temperature range 288–303 K the moisture sorption is independent of temperature. It is likely that moisture sorption of amino acids is temperature independent over a wider temperature range, i.e. 273–373 K, similar to the case of carbohydrates (Van der Sman & Meinders, 2011; Van der Sman, 2017). Furthermore, we like to remark that the data from Ref. Marsh et al. (2017) extend beyond the solubility range of glycine and L-alanine. This is achieved via the use of small aerosol droplets, with radii in the range of 4-30 μm, where crystallization is inhibited, but droplet curvature effects on water activity are negligible. This means a considerable extension of the data range for fitting the Flory–Huggins theory to the moisture sorption of glycine and L-alanine, which adds to the accuracy of the fitted interaction parameter \( \chi \).

The values of the interaction parameters are surprisingly compared to what we have found earlier for polyols and sugars (Van der Sman, 2017). A first explanation is the magnitude of the interaction parameter is quite dependent on the molecular size (van der Sman, 2019b). Furthermore, for small-sized molecules, amino acids have several functional groups, that can participate in hydrogen bonding: the amide group, and the carboxyl group. The latter can even be decomposed in a carbonyl and hydroxyl group, each capable of hydrogen bonding. The ratio of hydrogen bonding groups and the number of carbon atoms in the backbone is another important determinant of the Flory–Huggins interaction parameter (van der Sman, 2019b). For the investigated amino acids this ratio is particularly high for glycine and L-alanine, both showing even negative values — indicating high hydrophilicity.

##### 3.1.2. Solubility

Solubility data are presented in Fig. 2. Data is obtained from Fasman et al. (1977), Amend and Helgeson (1997), Held, Neuhaus, and Sadowski (2010). The solid lines are obtained via predictions using Flory–Huggins theory, i.e. Eq. (3). Performing fitting with four parameters \((T_s, \Delta H_w, 4\chi_{p, w}, 4\chi_w)\) shows there is no unique set of parameters.
describing the solubility lines. Also, in literature one finds a wide variety of parameter sets, describing the solubility curve (Kuramochi, Noritomi, Hoshino, & Nagahama, 1996; Figueiredo, Da Silva, & Silva, 2013; Xu, Pinho, & Macedo, 2004). Consequently, we have performed fittings using fixed values for \( T_g, \Delta H_g \), using recent literature data from Held et al. (2011), Chua, Do, Schick, Zaitsau, and Held (2018). The fitted parameters are listed in Table 3.

### Table 3

<table>
<thead>
<tr>
<th>Compound</th>
<th>( T_g ) (K)</th>
<th>( \Delta H_g ) (kJ/mol)</th>
<th>( \Delta C_{p,x} ) (J/mol/K)</th>
<th>( \Delta C_{p,g} ) (J/mol/K)</th>
</tr>
</thead>
<tbody>
<tr>
<td>L-alanine</td>
<td>608</td>
<td>22.0</td>
<td>92</td>
<td>-0.038</td>
</tr>
<tr>
<td>Glycine</td>
<td>569</td>
<td>21.0</td>
<td>35</td>
<td>-0.0005</td>
</tr>
<tr>
<td>L-proline</td>
<td>562</td>
<td>13.3</td>
<td>17</td>
<td>-0.0002</td>
</tr>
</tbody>
</table>

### 3.2. Viscosity

Unfortunately, there is no data available on glass transitions of other ternary amino acid/carbohydrate solutions. Hence, we will investigate whether \( T_g \) of pure amino acids can be estimated from viscosity data, which is more widely available in the literature. In our previous study, we have shown that the viscosity of carbohydrate solutions is related to the ratio of \( T/T_g \) which \( T \) the temperature of the solution (van der Sman & Mauer, 2019). In food science, it is common to use the WLF-theory to describe viscosity near the glassy state. However, the WLF theory with universal constants cannot explain all viscosity data of carbohydrates (Recondo, Elizalde, & Buera, 2006; Sillick & Gregson, 2009; Dupas-Langlet, Meunier, Pouzot, & Ubbink, 2019). Yet, the scaling of viscosity with \( T/T_g \) can produce master curves for carbohydrates, over a wide range from pure liquid water to the glassy state \( 0.4 < T/T_g < 1.0 \). Hence, we investigate whether the viscosity data of amino acid solutions also adheres to a master-curve if plotted against \( T/T_g \).

For estimation of the glass transition of the solution, we will use the Couchman–Karasz relation, using \( \Delta C_{p,x} \approx 0.85 \text{ kJ/kg K} \) of the dry amino acid will be estimated via collapsing the available viscosity data onto the master curve of polyls, as determined in our previous study (van der Sman & Mauer, 2019). As \( \Delta C_{p,x} \approx 0.85 \text{ kJ/kg K} \) of amino acids is similar to that of polyols, we will collapse the amino acid data to the master curve of polyls, rendering an estimate of \( T_g \) of the dry amino acid. The expression of the viscosity master curve is:

\[
\log(\eta) = a_1 q + a_2 q^2 + a_3 q^3
\]

with \( q = T/T_g - 0.35 \), \( \eta_0 = 0.231 \text{ mPa.s} \), \( a_1 = 3.9 \), \( a_2 = 7.9 \), and \( a_3 = 16.0 \).

Data sources for the viscosity of amino acid solutions are listed in Table 4, which also includes some data from our lab. In Fig. 5 we show
how these experimental data are fitted to the master curve. The fitting
is performed via minimizing the sum of least squares to $T_{\text{g,}\,\text{eff}}$. The error
in the estimation is computed using the covariance and Jacobian.

Compared to the literature data, the data from our lab show larger
deviations from the master curve at low and high values of $T_{\text{g,}\,\text{eff}}$. The literature data is often obtained via the Ubbelohde viscometer, while
we have used a general-purpose rheometer from TA Instruments (Renzetti et al., 2020). Hence, we have used only the literature data to fit
$T_{\text{g,}\,\text{eff}}$ of the amino acids.

The resulting $T_{\text{g,}\,\text{eff}}$ are also listed in Table 4. Note that the fitted $T_{\text{g,}\,\text{eff}}$
of glycine (225 ± 20 K) is considerably lower than estimated from the
freezing behaviour of glycerine/sucrose solutions (280 ± 5 K), albeit
that the error in the estimation of $T_{\text{g,}\,\text{eff}}$ from the viscosity data is rather large.
Below, when investigating the melting point depression of biopolymers,
we will use both values for $T_{\text{g,}\,\text{eff}}$ and observe which value provides the
best prediction.

The viscosity of other zwitterions (as listed in Table 5), with structures
typical to glycine, has been investigated. Only the B and D-
coefficients from fitting Eq. (10) to the viscosity data have been reported.
We compare these data with the above master curve for amino
acids and estimate their $T_{\text{g,}\,\text{eff}}$. The experimental data of these zwitterions
compared to the master curve is shown in Fig. 6.

The investigated zwitterions are very similar, and they differ only
in the presence or absence of some functional group. Hence, from
the analysis of these viscosity data, we can learn how $T_{\text{g,}\,\text{eff}}$ depends on
the type and number of functional groups.

In Table 5 we have reported the fitted $T_{\text{g,}\,\text{eff}}$ values and the estimation
error. Despite large estimation errors in $T_{\text{g,}\,\text{eff}}$ we do observe that additional
methyl-groups hardly increase the $T_{\text{g,}\,\text{eff}}$, while additional hydroxyl
groups or peptide linkages will increase $T_{\text{g,}\,\text{eff}}$. This can be explained by
the fact that methyl groups do not contribute to hydrogen bonding,
contrary to the hydroxyl groups and the peptide bond (van der Sman,
2019b).

3.3. Effects on biopolymer melting

Glycine and L-proline are investigated on their effect on protein
denaturation and starch gelatinization. We compute $\phi_{\text{w,eff}}$ based on
the $T_{\text{g,}\,\text{eff}}$ found in the previous sections. $T_{\text{g,}\,\text{eff}}$ is converted in to $N_{\text{OH,}\,\text{eff}}$
using Eq. (8), and $n_{\text{OH,}\,\text{eff}}$ of the amino acid/plasticizer solutions is computed using Eq. (7). We note, that in these computations we take
the $T_{\text{g,}\,\text{eff}}$ values as obtained from the viscosity data, as listed in Table 5.
This is also done for glycine, as the value $T_{\text{g,}\,\text{eff}}=280$ K renders less
agreement with other experimental data.

Mind that $n_{\text{OH,}\,\text{eff}}$ does not constitute the density of hydroxyl groups, but it must be regarded as the density of (intermolecular)
hydrogen bonds, weighed against the strength of the hydrogen bond as
imparted by the different functional groups (hydroxyl, carboxyl, amine,
and peptide linkage). We investigate whether $n_{\text{OH,}\,\text{eff}}$ or rather $\phi_{\text{w,eff}}$
still explains the change in biopolymer melting. Below, we discuss
the effect of different plasticizer solutions with amino acids on the
denaturation of egg white proteins and gelatinization of wheat starch.
Details on experimental methods are out of the scope of this paper,
but they are discussed in detail in a forthcoming paper (Renzetti et al.,
2020).

3.3.1. Egg white denaturation

In the same round of experiments, we have investigated egg white
denaturation for the binary protein/water system for different moisture
contents, and for ternary protein/plasticizer/water systems. The latter
data set is extended with literature data. The first data set renders
the desired master curve of the denaturation temperature, $T_{\text{d}}$, versus
$\phi_{\text{w,eff}}$. The second data set allows us to compare the effect of amino
acids and carbohydrates as modulators of biopolymers melting point.
Results are shown in Fig. 7. We have listed the references of the used
literature data sources in Table 6, together with the symbols used in
Fig. 7 to indicate the various mixtures. For the labelling of symbols,
we use the Matlab codes for plotting symbols.

The master curve for the denaturation of egg white is obtained from
the Flory–Huggins theory of melting point depression using $T_{\text{m}}=400$ K,
$\chi_1=0.8$, $\Delta H_{\text{m}}=52$ kJ/mol, and assuming that 60% of the protein is
crystalline. These parameter values are estimated via fitting the theory
to the experimental data for water.

In Fig. 7 we observe that the data for ternary mixtures largely
follows the master curve for the binary protein/water system, confirming
the hypothesis that egg white denaturation is also governed

Table 4

<table>
<thead>
<tr>
<th>Compound</th>
<th>Temperature (°C)</th>
<th>Reference</th>
<th>Symbol</th>
<th>$T_{\text{g,},\text{eff}}$ (K)</th>
</tr>
</thead>
<tbody>
<tr>
<td>L-Proline</td>
<td>25</td>
<td>Belibâgli and Ayranci (1990), Schobert and Tschesche (1978), Samuel, Kumar, Jayaraman, Yang, and Yu (1997)</td>
<td>cx</td>
<td>250 ± 3</td>
</tr>
<tr>
<td>Serine</td>
<td>5–35</td>
<td>Belibâgli and Ayranci (1990), Yan et al. (1999)</td>
<td>y</td>
<td>245 ± 20</td>
</tr>
</tbody>
</table>

Fig. 5. Viscosity of amino acids as function of $T_{\text{g,}\,\text{eff}}$, using our lab data (Renzetti et al., 2020) and literature data, as listed in Table 4.

Fig. 6. Viscosity of zwitterions, similar to glycine, as function of $T_{\text{g,}\,\text{eff}}$, using literature data as listed in Table 5.
by hydrogen bond density as computed via $\phi_{OH,eff}$. At high moisture contents, we observe for both carbohydrates and amino acids deviations from the master curve, which we attribute to phase separation effects (Renzetti et al., 2020). This will be investigated in more detail in a future publication.

3.3.2. Starch gelatinization

Similarly, we have investigated the effect of glycine and L-proline of the melting temperature of starch, which is compared to data of some other carbohydrates and the binary starch/water system. The results are shown in Fig. 8. The solid line is the prediction by Flory theory of melting point depression, as obtained in our previous studies (Van der Sman & Meinders, 2011). The concentration of carbohydrates and L-proline in the solutions added to the starch are 30%, while glycine has a concentration of 15%, due to its limited solubility.

We observe that the experimental data collapse to a single curve, which follows the Flory–Huggins theory with $T_m=500$ K, $z_1 = 0.8$, $\Delta H_m=24$ kJ/mol, and assuming that 45% of the starch is crystalline.

Again at high values of $\phi_{OH,eff}$ there are some indications of phase separation between the biopolymer (starch) and the solute (either amino acid or carbohydrate). From the above results for both egg white and starch, we conclude that (sweet) amino acids can be treated on the same footing as carbohydrates: they influence biopolymer melting via their effect on the hydrogen bond density.

4. Critical discussion on Flory–Huggins theory

As suggested by the reviewers we add a critical discussion of the Flory–Huggins theory in comparison to alternative molecular thermodynamic theories applied to amino-acids. These alternative theories fall within the field of chemical engineering called molecular thermodynamics, which has been pioneered by Prausnitz (Prausnitz & Tavares, 2004). We discuss two of these alternative theories, UNIFAC (Fredenslund, Jones, & Prausnitz, 1975) and PC-SAFT (Held, Sadowski, Carneiro, Rodríguez, & Macedo, 2013), which are exponents of two different classes of theories: (a) theories describing the excess free energy, and (b) theories describing equation of state, respectively. While UNIFAC describes only the activity coefficients of solutes and solvents, PC-SAFT can also describe other thermodynamic properties like density, boiling point, vapour pressures, and specific heat. These molecular thermodynamical theories are developed as an engineering tool to estimate the thermodynamic properties of chemical mixtures in the absence of experimental data.

UNIFAC theory describes interaction on the level of functional groups, thereby using the concept of local composition, as devised by Wilson (1964). This account for the non-random mixing of mixtures of compounds having different functional groups, leading to the clustering of similar groups at the molecular level as occurs in alcohol solutions. UNIFAC requires a lot of parameter values, which need to be fitted to a large amount of experimental data (Held et al., 2013). Parameters in UNIFAC are the Bondi areas and volumes of the various functional groups, entering the combinatorial part of the free energy, and two interaction parameters for each pair of functional groups. The main thesis of the UNIFAC theory is that these parameters are independent of the molecules containing these functional groups. If a reliable database of parameters is constructed the UNIFAC theory can be predictive for activity coefficients of a multitude of solutes and solvents, requiring no experimental input of mixture data. But, it is said to be limited if compounds have polar groups near to each other, such as polyhydroxy compounds as polyols and sugars (Prausnitz & Tavares, 2004).

PC-SAFT can account for chain-like molecules, which can have associative functional groups performing hydrogen bonding. The theory uses 6 pure-component parameters: (1) the (temperature-dependent) segment diameter, (2) the number of segments per molecule, (3) the
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Debye–Huckel ternary mixtures involving salts can be described (Held, dependent (Grosse Daldrup et al., 2010). Extending the theory with 𝑘 acids and water, or one amino-acid and two solvents (Fuchs et al., 2006; be made for the solubility of ternary mixtures involving two amino-acids are predicted (Fuchs et al., 2006; Lee & Kim, 2010). In UNIFAC the that can describe solubility data, as observed throughout literature. dependent specific heat, solute activity coefficients are near unity. If one assumes temperature-
equation must be determined via fitting to experimental data. However, holds for all three considered theories. The parameters within this equation, for the chemical potential of the crystalline phase, Eq. (4), the solid phase does not follow from the thermodynamics theories describ-
number of association sites is assumed equal to twice the number of interaction parameter between solutes. UNIFAC can be fully predictive for ternary mixtures comprising two solutes, but only for the case of zero interaction parameter between solutes. UNIFAC can be fully predictive for ternary or even more complex mixtures but requires thoughtful determination of the functional groups and their interaction parameters.

UNIFAC is applied to variety of amino-acids and small peptides (Ku-
ramochi et al., 1996; Ninni & Meirelles, 2001; Figueiredo et al., 2013), and carbohydrates (Ninni, Camargo, & Meirelles, 2000; Ferreira, Brig-
nole, & Macedo, 2003). UNIFAC interaction parameters between polar groups often have to be readjusted if solutes contain multiple strongly polar groups, like OH or COOH groups. These hydrogen bonding groups show strong cooperative effects (Maffia & Meirelles, 2001).

PC-SAFT has been applied to amino-acids, and dipeptides (Cameretti
Sadowski, 2010; Held et al., 2011). Amino-acids are assumed to have 2 interaction sites for each hydroxyl, amino- and carboxylic group. A large variety of amino-acids different amino-acids and dipeptides have been characterized (Lee & Kim, 2010; Held et al., 2011). It is shown that the number of segments is linear with the molar weight, and association parameters can be assumed constant for all amino-acids. PC-SAFT is also applied to small carbohydrate solutions (Held et al., 2013). The number of association sites is assumed equal to twice the number of OH-groups, all having the same association energy and volume. 𝑘, between carbohydrate and water, is linear dependent on temperature. 𝑘, between carbohydrates is assumed zero.

UNIFAC and PC-SAFT is often used for describing solid–liquid equi-
lum for amino-acids or carbohydrates (Fuchs, Fischer, Tumakaka, & Sadowski, 2010; Grosse Daldrup, Held, Ruether, Schembecker, & Sadowski, 2010; Held et al., 2011) Amino-acids are assumed to have association sites. The parameters required for the chemical potential of the crystalline/ solid phase does not follow from the thermodynamics theories describing the activities of solutes and solvent in the liquid phase. The above equation, for the chemical potential of the crystalline phase, Eq. (4), holds for all three considered theories. The parameters within this equation must be determined via fitting to experimental data. However, it is said that solubility is largely determined by the temperature dependency of the parameters characterizing the crystalline phase, as solute activity coefficients are near unity. If one assumes temperature-
dependent specific heat, 𝛿𝐶, there are often multiple parameter sets, that can describe solubility data, as observed throughout literature.

Combined with dissociation equilibrium and Debye–Huckel the solu-
ibility of amino-acids at different pH and temperature of amino-acids are predicted (Fuchs et al., 2006; Lee & Kim, 2010). In UNIFAC the charged groups are defined as separate functional groups, with newly estimated interaction parameters (Figueiredo et al., 2013).

Using parameters established from binary solutions, predictions can be made for the solubility of ternary mixtures involving two amino-
acids and water, or one amino-acid and two solvents (Fuchs et al., 2006; Held et al., 2013). For PC-SAFT the interaction parameter between two amino-acids, 𝑘, is often found to be non-zero and temperature-
dependent (Grosse Daldrup et al., 2010). Extending the theory with Debye–Huckel ternary mixtures involving salts can be described (Held, dispersion energy (for vanderWaals interaction), (4) the number of association sites, (5) the association energy, and (6) the association volume. For water these parameters are well known, assuming 4 asso-
ciation sites. PC-SAFT has common mixtures rules for computing pa-
rameters for mixtures for pure-component data, but also requiring the binary interaction parameter 𝑘, which can be temperature-dependent.

Flory–Huggins (FH) theory is also regarded by Prausnitz as a mole-
cular thermodynamic theory, which he applied to swelling of polymeric gels (Hino & Prausnitz, 1998). FH theory is more simple than other molecular thermodynamic theories like UNIFAC and PC-SAFT. Flory–
Huggins theory only assumes random mixing. Furthermore, the descrip-
tion of activity coefficients of solutes and solvents requires only the estimation of a single parameter, 𝜇.

Nevertheless, FH theory is successfully applied to hydrogen bond-
ing materials like biopolymer solutions (Hancock & Zografi, 1993; Shamblin, Hancock, & Zografi, 1998; Zhang & Zografi, 2001; Ub-
bink, Giardiello, & Limbach, 2007; Van der Sman & Meinders, 2011) and gels (Van der Sman, 2015; Li, Zhao, Chen, & Mercadé-Prieto, 2016), solutions of carbohydrates (He, Fowler, & Toner, 2006; Van der Sman, 2017), and aqueous mixtures of both biopolymers and carbo-
hydrates (Zhang & Zografi, 2001; van der Sman, 2013a), and even more complex mixtures involving salts (via extension with Debye–Huckel or even Pitzer theory) (van der Sman, 2012; van der Sman, Houlder, Cornet, & Janssen, 2020). FH theory is also applied to describe solubility of carbohydrates in water, and also in ternary systems of two carbohydrates in water is well-described (Van der Sman, 2017). Often, a small-valued interaction parameter between the two carbohydrates was required.

FH is extended towards the glassy state by Vrentas and Vrentas (1991), which is shown to hold for biopolymers (Hancock & Zografi, 1993), and numerous food systems (Van der Sman & Meinders, 2011; van der Sman, 2012). Often, other molecular thermodynamics theories hold only in the liquid state (Fredenslund et al., 1975). For the class of carbohydrates and polysaccharides, the interaction parameter is shown to be a function of the molecular weight (Van der Sman & Meinders, 2011; Van der Sman, 2017). Expanding this class to more general non-food polyols shows that the interaction parameter is a function of chain length (expressed as the number of carbons), and the ratio of the number of OH groups and carbon atoms (van der Sman, 2019b). The latter shows that it is probable that the FH interaction parameter can be related to the functional group theory. The same study shows that FH fails if the polyol has a strong non-uniform (non-random) distribution of OH-groups — like polyols with amphiphilic character. For these compounds, we expect clustering at the molecular scale, as in alcohols.

We conclude that FH theory is well able to describe the thermody-
namic properties of aqueous solutions of small solutes, which interact mainly via hydrogen bonding, such as carbohydrates and amino acids. In that, it is comparable to UNIFAC and PC-SAFT. Furthermore, all three theories can describe solid–liquid equilibria for the solutes.

The predictive power of PC-SAFT and FH theories is shown for ternary mixtures comprising two solutes, but only for the case of zero interaction parameter between solutes. UNIFAC can be fully predictive for ternary or even more complex mixtures but requires thoughtful determination of the functional groups and their interaction parameters.

Table 6

Data sources used for denaturation of (dried) egg white and ovalbumin.

<table>
<thead>
<tr>
<th>Reference</th>
<th>Solvent</th>
<th>Symbol</th>
</tr>
</thead>
<tbody>
<tr>
<td>Van der Plancken, van Loey, and Hendrickx (2006)</td>
<td>Water</td>
<td>k+</td>
</tr>
<tr>
<td>Bäck, Oakenfull, and Smith (1979)</td>
<td>Sugar/polyol solutions</td>
<td>m</td>
</tr>
<tr>
<td>Nafchi, Tabatabaee, Panhani, Rahji, and Karim (2013)</td>
<td>Monosaccharide solutions</td>
<td>m+</td>
</tr>
<tr>
<td>Renzetti et al. (2020)</td>
<td>Water</td>
<td>ko</td>
</tr>
<tr>
<td></td>
<td>L-proline solution</td>
<td>bo</td>
</tr>
<tr>
<td></td>
<td>Glycine solution</td>
<td>go</td>
</tr>
<tr>
<td></td>
<td>Sucrose solution</td>
<td>mo</td>
</tr>
<tr>
<td></td>
<td>Glucose solution</td>
<td>rs</td>
</tr>
<tr>
<td></td>
<td>Xylitol solution</td>
<td>yd</td>
</tr>
</tbody>
</table>
PC-SAFT and UNIFAC can also predict activity coefficients for solutes in solvent mixtures like water/alcohol — while there is no FH model available for that. We think the latter is due to the restricted degrees of freedom of the FH theory: there is only a single interaction.

For aqueous mixtures with small food-borne solutes, we think FH theory is only suitable to strongly hydrophilic solutes — having a uniform/random distribution of hydrogen bonding functional groups. The sweet amino-acids investigated in this paper are an example of that. FH theory will have more difficulty with amino-acids with relatively large aliphatic chains, fatty acids, or dicarboxylic acids. The value of FH theory is even stronger in complex mixtures of small hydrophilic solutes with biopolymers or oligomers, as found in a wide variety of foods, like bakery, dairy, and confectionery products — making it a good vehicle for investigating questions like sugar replacement in foods.

5. Conclusions

Taking inspiration from the novel field of NADES we have investigated whether zwitterions like amino acids and some quaternary ammonium compounds can be used as alternative sugar replacers. As sugar replacers, they should have good water sorption properties and good plasticization of biopolymers. These properties have been investigated using literature data, and data from our lab. The acquired data have been analysed with theories that have been used primarily for the analysis of polysols as sugar replacers.

Our results show that the investigated zwitterions are good plasticizers and humectants, albeit with poor solubility, with L-proline being an exception showing good solubility up to 60%–70%. Their thermodynamics can indeed be described with the same theories as previously used for common sugar replacers, namely Flory–Huggins (FH) theory and Couchman–Karasz for the glass transition. Comparing FH theory with other molecular thermodynamics theory like PC-SAFT and UNIFAC, we conclude that FH will be more suitable for strongly hydrophilic zwitterions, but it will probably fail for zwitterions with large aliphatic segments.

The poor solubility of many of the zwitterions makes it difficult to measure the glass transition. We have shown the glass transition can either be determined via a) the glass transitions of frozen solutions, which also contain better soluble carbohydrates like sucrose, or b) via extrapolating the viscosity. The viscosity of zwitterion solutions is shown to be a function of $T_g/T$, following the master curve earlier formulated for polysols.

Due to the poor solubility, the viscosity can only be measured for a limited range, leading to large confidence intervals for the estimated glass transition of the pure solute $T_{g,s}$. We think it is worthwhile to further investigate how $T_{g,s}$ depends on the number and type of functional groups to provide a better estimate of $T_{g,s}$ of particular amino acid-like plasticizer.

Finally, we have tested the influence of glycine and L-proline on the melting of biopolymers, namely the denaturation of egg white and gelatinization of starch. As found for carbohydrates these amino acids also depress the melting point of biopolymers, as a function of the hydrogen bond density. The effective hydrogen bond density can be computed from the glass transition of the applied solution, similar to other sugar replacers. Interestingly, we have observed indications of phase separations at quite high moisture contents, for both amino acids as common carbohydrates.

Summarizing, (sweet) amino acids and related quaternary ammonium zwitterions have good potential as sugar replacers, showing very similar behaviour as carbohydrates regarding plasticizing and humectant behaviour. Many of the amino acids have poor solubility, but that can be circumvented by using a mixture of plasticizers, which have improved solubility.

CRediT authorship contribution statement

R.G.M. van der Sman: Conceptualization, Supervision, Writing.
I.A.F. van den Hoek: Investigation, Data curation. S. Renzetti: Methodology.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

This research was performed with additional funding from the Top Consortia for Knowledge and Innovation Agri & Food of the Dutch Ministry of Economic Affairs.

Appendix A. Supplementary data

Supplementary material related to this article can be found online at https://doi.org/10.1016/j.foodhyd.2020.106113.

References


