Mapping the solid-state properties of crystalline lysozyme during pharmaceutical unit-operations

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Abstract

Bulk crystallisation of protein therapeutic molecules towards their controlled drug delivery is of interest to the biopharmaceutical industry. The complexity of biotherapeutic molecules is likely to lead to complex material properties of crystals in the solid state and to complex transitions. This complexity is explored using batch crystallised lysozyme as a model. The effects of drying and milling on the solid-state transformations of lysozyme crystals were monitored using differential scanning calorimetry (DSC), X-ray powder diffraction (XRPD), FT-Raman, and enzymatic assay. XRPD was used to characterise crystallinity and these data supported those of crystalline lysozyme which gave a distinctive DSC thermogram. The apparent denaturation temperature (T_m) of the amorphous lysozyme was ~201 °C, while the T_m of the crystalline form was ~187 °C. Raman spectra supported a more α-helix rich structure of crystalline lysozyme. This structure is consistent with reduced cooperative unit sizes compared to the amorphous lysozyme and is consistent with a reduction in the T_m of the crystalline form. Evidence was obtained that milling also induced denaturation in the solid-state, with the denatured lysozyme showing no thermal transition. The denaturation of the crystalline lysozyme occurred mainly through its amorphous form. Interestingly, the mechanical denaturation of lysozyme did not affect its biological activity on dissolution. Lysozyme crystals on drying did not become amorphous, while milling-time played a crucial role in the crystalline-amorphous-denatured transformations of lysozyme crystals. DSC is shown to be a key tool to monitor quantitatively these transformations.

KEYWORDS:

Crystalline-amorphous-denatured transformations; Differential scanning calorimetry; FT-Raman; Lysozyme crystals; Milling; X-ray powder diffraction.

1. Introduction

Lysozymes are a group of enzymes defined as 1,4-β-N-acetylmuramidases cleaving the glycosidic bond in the bacterial peptidoglycan. Hen egg white lysozyme (HEWL) is a single chain polypeptide of 129 amino acids cross-linked with four disulfide bridges resulting in a molecular weight of 14307 Da [1]. HEWL has the ability to lyse bacteria, and therefore it has particular interest for application in food and pharmaceutical products [2]. Previous researchers assured its potent antimicrobial efficiency [3] and its safety [4]. Also, other research has resulted in improved intranasal absorption and delivery [5] and lung delivery [6].

Zhou et al. [7] made lysozyme containing mats and they verified its excellent antibacterial activity against *Escherichia coli* and *Staphylococcus aureus*, and therefore, these mats have promising uses in antimicrobial packing, tissue engineering, and wound dressing. Sax and Winter [8] prepared sustained release lysozyme containing implants using hot melt extrusion. Schlocker et al. [9] used milling to prepare protein-loaded microparticles in industrial quantities. Milling has also been used to prepare protein particles suitable for pulmonary delivery [10]. However, milling and other pharmaceutical processes (e.g., drying, mixing) may produce uncontrollable variation of protein solid states (i.e., crystal structure and crystal habit) and also loss of protein activity [11]. Different lyophilized solid forms of proteins have been shown to produce different dissolution rates for reconstitution [12]. The stability of crystalline lysozyme has been shown to be greater than that of the amorphous form [13,14]. Therefore, it is essential to monitor the solid state transformations of lysozyme during pharmaceutical processes.

Differential scanning calorimetry (DSC) is a well-established and widely used technique to monitor solid state transformations. However, the thermal transitions of lysozyme, in common

with other proteins, are usually characterized in the solution state, and often using a high-sensitivity differential scanning calorimeter (HSDSC), which is capable of detecting the small changes in enthalpy that arise when proteins unfold within their solutions [15]. Modulated temperature differential scanning calorimetry [16] and thermally stimulated depolarized current [17] have been tested as alternatives. However, the thermal transitions in the solution state cannot differentiate the different solid forms. Therefore, researchers have studied the thermal transitions of lysozyme in solid state using conventional solid-state DSC. However, their results did not recognize the discrepancy between the thermal behaviours of the amorphous and crystalline lysozyme powders [13,14,18,19].

There is a renewed interest in lysozyme, and its solid state form can have a significant effect on dissolution and stability. We wished to explore how pre-treatment of lysozyme crystals affected thermal behaviour, in an attempt to use thermal profiles as a fingerprinting indicator of prior treatment. In this study, we prepare lysozyme crystals to be dried and/or milled, and appropriate mixtures of the treated forms were prepared. Our aim is to use DSC to monitor the potential solid state transformations of lysozyme during the treatment processes. We use Powder X-ray diffraction (PXRD), FT-Raman, and enzymatic assay for reference. To our knowledge this is the first application of DSC for the quantitative detection of crystalline, amorphous and denatured lysozyme forms.

2. Materials and methods

2.1. Materials

Hen egg-white lysozyme (HEWL) (purity; 95%) (Biozyme Laboratories, UK), *Micrococcus lysodeikticus* (Sigma-Aldrich), sodium chloride (NaCl) (99.5%) (Sigma-Aldrich) and sodium acetate anhydrous (purity; 98%) (BDH Chemicals Ltd., Poole, UK) were purchased as indicated. The purchased lysozyme sample was considered to be unprocessed lysozyme. Water was deionised and double distilled.

2.2. Sample Preparation

2.2.1. Preparation lysozyme crystals using batch crystallization method

One litre of a solution of lysozyme 4 % w/v in sodium acetate buffer (pH 4.6; 0.1 M) and one litre of a solution of sodium chloride 10 % w/v in the same buffer were separately passed through a 0.2 micron filter and then mixed in a glass container. The produced solution contained 2% w/v lysozyme and 5% w/v NaCl. This solution was then sealed and kept for ten days at 20 °C. Crystals formed were collected by filtration. Adsorbed water was removed by air drying (5 h). These procedures were used to prepare lysozyme crystals by a batch crystallisation method [13].

2.2.2. Preparation of dried lysozyme crystals

A glass column of dimensions 2m (three loops) × 6mm (outer diameter) × 4mm (inner diameter), was packed with lysozyme crystals. Anhydrous nitrogen gas was passed through the packed column at a flow rate of 10 ml/min, 30 °C and zero relative humidity for 10 days.

2.2.3. Preparation of milled dried lysozyme powders

Milling was achieved by rotating a marble pestle over the powder within a marble mortar at ~45 cycles per minute (cpm). Milling times of 3, 10, 20, 30, 45, and 60 min were used to produce different samples of milled dried crystals, named 3M, 10M, 20M, 30M, 45M, and 60M, respectively. Another two batches of 3M, 10M, 20M and 60M were also prepared for reference.

2.2.4. Preparation of amorphous lysozyme powders with different salt content

Precipitated samples were also prepared to explain the effect of NaCl on thermal behaviour of lysozyme particles. These amorphous samples were prepared using the same principle of batch crystallization method. Hence solutions containing 2 % w/v lysozyme plus different amount of NaCl (0, 0.096, 0.16, and 0.8 % w/v) in deionised water were dried under vacuum at a temperature 30 ºC for two days to produce lysozyme powders theoretically containing 0, 24, 40 and 200 NaCl molecules for each lysozyme molecule, respectively. These four lysozyme samples were named P0, P24, P40, and P200, respectively, and their amorphous nature was confirmed by XRPD.

2.2.5. Preparation of lysozyme mixtures from two different samples

Unprocessed lysozyme and the 3M sample were mixed at different ratios (w/w) of 3:7, 5:5, and 7:3 in 100 mg samples. The mixtures were lightly mixed in a mortar with a spatula for 10 min and then in a small plastic bag for 10 min to ensure their homogeneity.

2.3. Microscopy

A Zeiss Axioplan2 polarizing microscope (Carl Zeiss Vision GmbH; Hallbergmoos, Germany) was used to visualize the samples. The accompanying software (Axio Vision 4.2) was then used to determine the projected area diameters of the powders.

2.4. Thermogravimetric analysis (TGA)

The water content of each sample was estimated using Thermo Gravimetric Analysis (TGA 7 Perkin Elmer Ltd., Beaconsfield, UK). Samples of 3-10 mg were heated from 30 °C to 210 °C at a scan rate of 10 °C/min in aluminium pan under nitrogen flow at 20 ml/min. Each sample was analysed in triplicate. The decrease in the weight before decomposition was calculated and was considered as water content. TGA results were validated by re-analyzing the water content of some samples using Karl Fischer Titration (KFT) (701 KF Titrino with 703 Ti stand, Metrohm, Switzerland). Using TGA instead of KFT is that only a few mg is enough for TGA.

2.5. Powder X-ray diffraction (PXRD)

X-ray powder diffraction patterns of the powders were obtained using a Siemens D5000 diffractometer (Siemens, Karlsruhe, Germany), using CuKα radiation (λ = 1.5418A°). The generator was set to 40 kV and 30 mA. Samples were placed into plastic sample holder with zero background and levelled using a glass cover slide. Samples were scanned over an angular range of

2-10° (2θ), with a step size of 0.001° and a count time of 3 s per step. The sample stage was spun at 30 rpm. The instrument was calibrated prior to use, using a silicon standard.

2.6. Differential scanning calorimetry (DSC)

Differential scanning calorimetry (DSC) thermograms were obtained using a Perkin-Elmer Series 7 DSC (Perkin-Elmer Ltd., Beaconsfield, UK). Samples (4-7 mg) were sealed in aluminium pans. The escape of water was facilitated by placing a pinhole in the lid prior to sealing. The samples were equilibrated at 30 °C and heated to 210 °C at a scan rate of 10 °C/min under a flow of anhydrous nitrogen (20 ml/min). Each sample was analysed in triplicate. The temperature axis and cell constant of the DSC cell were calibrated with indium (10 mg, 99.999 % pure, melting point 156.60 °C, and heat of fusion 28.40 J/g).

2.6.1. Evaluation of microcalorimetric data

T_m and calorimetric transition enthalpies (ΔH_{Cal}) were measured by DSC, and then the cooperative unit size (n') was calculated after baseline correction using Eq. (1):

$$n' = \Delta H_{vH}/\Delta H_{Cal} \quad (1)$$

where ΔH_{vH} is the corresponding van't Hoff enthalpy of the unfolding. Bammel et al. [20] indicated that ΔH_{vH} can be obtained from:

$$\Delta H_{vH} = 4RT_m^2 \Delta C_p(\max)/\Delta H_{Cal} \quad (2)$$

where *R* is the universal gas constant (8.314×10^{-3} kJ K^{-1} mol^{-1}), $\Delta C_p(\max)$ is the maximum heat capacity and it is calculated from:

206 $\Delta C_p(\max)$ = peak height / (scan rate × sample weight) (3).

207

208 *2.7. FT-Raman spectroscopy*

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210 FT-Raman spectra of samples were recorded with a Bruker IFS66 optics system using a
211 Bruker FRA 106 Raman module. The excitation source was an Nd: YAG laser operating at 1064
212 nm and a laser power of 50 mW was used. The FT-Raman module is equipped with a liquid
213 nitrogen cooled germanium diode detector with an extended spectrum band width covering the
214 wave number range 1800-450 cm^{-1}. Samples were placed in stainless steel sample cups and
215 scanned 200 times with the resolution set at 8 cm^{-1}. The observed band wave numbers were
216 calibrated against the internal laser frequency and are correct to better than ±1 cm^{-1}. The spectra
217 were corrected for instrument response. The experiments were run at a controlled room
218 temperature of 20 ±1°C.

219

220 *2.8. Enzymatic assay*

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222 Lysozyme catalyzes the hydrolysis of β-1,4-glycosidic linkages of cell-wall
223 mucopolysaccharides [18]. This principle was used to measure the activity of lysozyme as follows.
224 30 µl of lysozyme solution 0.05 % in phosphate buffer (pH = 5.2; 10 mM) was added to 2.97 ml
225 substrate bacterial suspension 0.025 % of *Micrococcus lysodeikticus* in phosphate buffer (pH =
226 6.24; 66mM). The decrease in the absorption at 450 nm was monitored by using a UV-Vis
227 spectrophotometer (Pu 8700, Philips, UK). The activity was determined by measuring the decrease
228 in the substrate bacterial suspension concentration with time. Hence the slope of the reduction in

229 the light absorption at 450 nm against the time of 3 min, starting when the protein solutions were
230 mixed with the substrate bacterial suspension, was considered to be the indicator of the activity
231 [21]. The measurements were performed in controlled temperature room at 20 °C to avoid
232 fluctuation of lysozyme activity. The concentrations of the protein solutions had been determined
233 prior to the activity tests using Eq. (4).

234 $$[\text{Protein}] = Abs_{280nm} / E_{280nm} \quad (4)$$

235 where [protein] is the concentration of protein in the tested solution w/v%, Abs_{280nm} is the
236 absorption of the tested protein solution at 280nm, E_{280nm} is the absorption of protein standard
237 solution with concentration 0.05 w/v%. The concentrations of the solutions were diluted to be
238 about 0.05 % w/v so as to give absorption of less than 0.8. The activities of all samples were
239 measured relative to that of a corresponding fresh sample, which was considered as the standard
240 solution.
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243 **3. Results and discussion**
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245 *3.1. Microscopy*
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247 Fig. S1 shows the photomicrograph of a lysozyme crystal. The anisotropic crystals
248 exhibited a birefringence phenomenon when viewed under a polarizing microscope. The elongated
249 prism-like crystals were in general of a projected area diameter of ~1200 μm (Fig. S1). Their shape

was consistent with their preparation temperature, which was 20 °C. The crystal shape of lysozyme is known to be affected by temperature, and a temperature of ~20 °C usually results in elongated prism-like crystals [22]. Samples 3M, 10M, 20M, and 30M had diameters of ~80 µm (Fig. S2), ~7 µm (Fig. S3), ~2.5 µm (Fig. S4), and less than 1 µm (Fig. S5), respectively.

3.2. Thermogravimetric analysis (TGA)

The results of TGA analysis were used to estimate the water content of the crystal forms. The thermograms (Fig. 1) indicate that on drying using the conditions described above, the water content decreased from 17.3±1.0 % w/w to 2.6±0.3 % w/w. The obtained values of water content in protein powders using TGA were previously shown to be consistent with Karl Fischer titration data [13].

3.3. X-ray powder diffraction (XRPD)

The diffractogram presented in Fig. 2A shows an absence of diffraction peaks for the unprocessed lysozyme powder indicating that it was amorphous. However, in Fig. 2B diffraction peaks for the lysozyme crystals at 2θ angles less than 8° are present. Proteins are large molecules and are crystallized typically in unit cells having high d values, and so according to Bragg's law, lysozyme crystals are expected to diffract x-ray at low 2θ angles.

Because lysozyme crystals exist in different forms, the CMPR program (Version 1.32) [23] was employed for phase identification. The observed PXRD peaks of the crystals at 2.82°, 3.56°, 4.47°, 5.21°, 6.09°, and 6.97° (Fig. 2B) fitted the faces (H,K,L) {(1,1,1), (3,1,0), (4,0,0), (4,1,1),

(4,3,1), (5,3,1)} of the tetragonal form of lysozyme with parameters A=78.54, B=78.54 and C=37.77, $\alpha = \beta = \gamma = 90°$ taken from protein data bank reference number 193L [24].

Dried lysozyme crystals were also characterised using PXRD and data indicated that the degree of crystallinity was predominantly maintained. The fact that the intensity of the XRPD peaks, which did not notably change (Fig. 2C), was evidence to this effect. Minor up shifting in the diffracted peaks after drying was noticed. This can be due to shrinkage of the unit cell to lower d values upon dehydration. The cell volume of tetragonal lysozyme crystals shrunk under the effect of pressure without a loss in its diffraction property [25]. Our XRPD finding agrees with previous results. For example, both monoclinic and triclinic crystals of HEWL have been shown to maintain their ability to diffract X-rays after dehydration [26] and [27], respectively. However, it contradicts some previous low frequency Raman spectra results, which showed that tetragonal lysozyme crystals resulted in crystallinity loss and conversion into an isotropic material (amorphous) after drying from ~33.5 % w/w to ~9 % w/w water content by equilibrating at ~30% r.h. [28,29]. In general, although dehydration firstly transfers a protein crystal to a metastable state, which then collapses and loses its packing structure, some crystals survive their crystallinity upon dehydration [26]. The findings of the present study would suggest that the conditions of the drying process would play an important part as to whether crystallinity is maintained. Thus if protein crystals are to be used as a drug delivery vehicle after bulk crystallisation then the subsequent milling and drying conditions will require close control and monitoring to obtain consistent results.

Milling of the dried crystals did produce a loss in crystallinity. XRPD was able to follow the loss of crystallinity of dried lysozyme crystals with comminution time. In case of 3M, the three minutes of milling did not induce crystallinity loss (Fig. 2D) as indicated by PXRD. However, the intensity of the diffracted peaks of sample 10M decreased (Fig. 2E). This indicates that lysozyme

crystals became partially disordered after only 10 minutes of milling. Fig. 2F shows that 20 minutes of milling was sufficient to produce a diffractogram with no clear peaks for the 20M sample, and so its XRPD spectrum became similar to that of the amorphous lysozyme (unprocessed) (Fig. 2A) which is consistent with transformation to the amorphous state.

3.4. Differential scanning calorimetry (DSC)

Lysozyme DSC thermograms, in the solid state, typically show two endothermic peaks. The broad peak ranging from ~30 to ~140 °C is due to water removal, and its area depends on the water residue in the samples. The second peak at ~200 °C, and its peak maximum was considered to reflect the apparent denaturation temperature (T_m) [13,14,18,19,30]. Fig. 3A shows a typical lysozyme thermogram demonstrating the presence of peaks at similar positions to those mentioned above. Thermograms for all other samples show a consistent water removal peak. However, the position and magnitude of T_m peak was found to depend on the solid state form of the lysozyme powder. The differences observed from DSC analysis align with the differences between the states previously observed by XRPD (Fig. 2). Amorphous lysozyme obtained as received (unprocessed lysozyme) thermally peaked at a T_m of about ~201 °C (Fig. 3A), while samples of crystalline lysozyme (crystals, dried crystals, or the minimally milled 3M sample) gave a lower T_m of about ~187 °C (Figs 4B, 4C and 4D). Evidence that the 10M sample was transformed partially to an amorphous form was apparent from inspection of the DSC thermal scan since it contained two distinct T_m's consistent with amorphous and crystalline lysozyme forms respectively at separate T_m of ~187 and ~201 °C (Fig. 3E). Similar to the XPRD evidence above, DSC data suggested that

318 further milling completed the amorphous transformation, with the 20M sample being amorphous,
319 and hence it only had the T_m of an amorphous state at ~201°C (Fig. 3F).

320 Close scrutiny of the thermograms showed that for sample 20M (amorphous lysozyme),
321 T_m was slightly decreased by only ~1 °C compared to that of the other amorphous lysozyme
322 (unprocessed sample). However, this small difference was significant (t-Test: $P < 0.05$) (Table 1).
323 This minor reduction is likely to be due to the presence of NaCl content in the former sample. The
324 amount of NaCl in the lysozyme crystal is approximated to be ~10 NaCl molecules for each
325 lysozyme molecule. At the preparation pH, each molecule of lysozyme needed ~10 Cl^- ions of
326 NaCl to shield its positive charges, which induce the repulsion between lysozyme molecules. This
327 shielding by counter ions of the precipitant (NaCl) is necessary to start nucleation and form crystals
328 in which these ions are trapped [31]. The precipitated samples which were precipitated with
329 different salt contents (P0, P24, P40, and P200) revealed a strong inverse relationship between salt
330 content and T_m (correlation coefficient r = -0.92). The values of T_m were 202.2±0.3, 200.3±0.5,
331 198.2±0.5, and 195.8±0.2, respectively, and their DSC profiles and amorphous PXRD patterns are
332 provided in supplementary data (Fig. S6 and Fig. S7). Therefore, according to this correlation, the
333 presence of around 10 NaCl molecules for each lysozyme molecule reduces T_m by ~ 1 °C.

334 The T_m of a protein does not necessarily represent a solid-liquid transformation. Proteins
335 do not melt, but they change their molecular conformation from a native to denatured state at the
336 T_m which overcomes the attractive intra-molecular forces, which preserve their native state. In
337 solution state where lysozyme molecules are well separated from each other by water molecules,
338 the T_m of lysozyme is ~76 °C [32]. The cooperative unit (n') is typically thought to estimate the
339 lowest number of molecules which form an independently melting cluster of molecules within a
340 sample [33] and is used as an indicator of the degree of unfolding cooperativity of lysozyme [15].

In solution state, n' of lysozyme solutions ranges from 1 to 2 (i.e., ~1.5) [34] Compared with the solution state, n' of lysozyme in the dried amorphous form (e.g. unprocessed or 20M sample) was estimated to increase from ~1.5 to ~10.5, and this is associated with the increase in T_m from ~76 to ~201°C (Table 1).

We can postulate that when the cooperative unit increases, a higher temperature is needed to unfold the lysozyme molecular aggregates, and that the larger the cooperative unit, the higher the T_m. The n' of the crystalline form (e.g. crystals, dried crystals, 3M) was lower than those of the amorphous form by ~2.5 unit (t-Test: $P < 0.05$) (Table 1). This explains the reduction in T_m of the crystalline form by ~14 °C compared to the amorphous form. Although the unfolding of proteins is an intra-molecular phenomenon rather than an inter-molecular phenomenon, the unfolding of a molecule within a molecular aggregate is resisted by the steric hindrance and repulsion of the other molecules in the unit.

Table 1 and Fig. 3 show that milling decreased the ΔH_{Cal} of the unfolding peak of the crystalline form (ΔH_{Cal}^{Cr}) with a corresponding increase in the ΔH_{Cal} of the unfolding peak of the amorphous form (ΔH_{Cal}^{Am}). When ΔH_{Cal}^{Cr} vanished, ΔH_{Cal}^{Am} reached a maximum of 105.9 kJ.mol^{-1} (as in the case of 20M sample), which is lower than those of both the crystalline form (dried crystals) and the amorphous form (unprocessed sample). Therefore, the complete crystalline-amorphous transformation associated with slightly mechanical denaturation (~17%). The further milling denatured gradually the amorphous form, as ΔH_{Cal}^{Am} decreased gradually by milling (i.e., 30M and 45M samples). Prolonged milling of dried crystals produced thermal evidence of a loss of unfolding due to the absence of a T_m as in the case of 60M (Fig. 3I). Fig. 4 summarizes the correlation between the milling time and the calorimetric unfolding enthalpies of the crystalline and amorphous peaks. This observation coupled with the milling data discussed above is

suggestive that milling initially induced a partial crystalline-amorphous transformation, followed by a complete amorphization transformation, and then on subsequent prolonged milling produced complete mechanical denaturation. Although a small part of lysozyme molecules denatured during the crystalline-amorphous transformation, the mechanical denaturation of crystalline lysozyme mainly goes through amorphous state. Similarly, the other two batches of 3M, 10M, 20M and 60M verified the crystalline-amorphous-denatured transformations of lysozyme powders during milling and the distinctive thermal behaviours of each form (Table 2).

3.4.1. Quantitative analysis of lysozyme solid states by DSC

Conventional DSC has been used to estimate the different solid phases in lactose powders. The estimation depended on knowing the enthalpy of solid phase transformation for each form. This DSC approach has been previously verified [35].

Applying the same approach to monitor the processing of the lysozyme powders, crystalline lysozyme (i.e. crystals) and amorphous lysozyme (i.e. unprocessed powder) produced similar enthalpies (t-Test: $P > 0.05$), with an average of 125 and 134 kJ.mol^{-1}, respectively. Therefore, these values were considered as the enthalpy of the native solid lysozyme. We assume that milled solid lysozyme powders would consist of mixtures of crystalline, amorphous and/or denatured lysozyme. The percentages of crystalline form (Cr%), amorphous form (Am%), and denatured form (De%) in the lysozyme powders can be determined from:

$$\text{Cr\%} = (\Delta H_{Cal}^{\sim 187}/125) \times 100 \quad (5)$$

$$\text{Am\%} = (\Delta H_{Cal}^{\sim 201}/134) \times 100 \quad (6)$$

$$\text{De\%} = 100 - (\text{Cr\%} + \text{Am\%}) \quad (7)$$

where $\Delta H_{Cal}^{\sim 187}$ and $\Delta H_{Cal}^{\sim 201}$ are the measured enthalpy (kJ.mol^{-1}) of the unfolding peaks at T_m of ~187 and ~201 °C, respectively.

To test the quantitative hypothesis amorphous lysozyme (unprocessed sample) and crystalline lysozyme (3M sample) were mixed at different ratios of 3:7, 5:5, and 7:3 and then they analysed by DSC (same procedures). According to Eq. (5), (6) and (7), the amorphous sample contains 100% native lysozyme, but the crystalline sample, which had $\Delta H_{Cal}^{\sim 187}$ = 114.4 kJ.mol^{-1}, contains 91.5% native and 8.5% denature lysozyme. Therefore, the three mixtures of unprocessed:3M (3:7, 5:5 and 7:3) should contain (27.4%, 70.0%, 2.6%), (45.7%, 50.0%, 4.3%) and (64.0%, 30.0%, 6.0%) of (Cr%, Am%, and De%), respectively. These calculated crystalline, amorphous and denatured percentages using the above equations were similar to the actual percentages in the mixtures listed in Table 3. Fig. 5 shows the distinctive unfolding peaks of the crystalline and amorphous forms of the mixtures.

3.5. FT-Raman study

Raman spectroscopy was used to compare the molecular conformation of crystalline (3M sample), amorphous lysozyme (20M sample) and extensively milled (denatured) lysozyme (60M sample) with dried lysozyme crystals. The band at 1447 cm^{-1} indicates the CH bending vibrations of aliphatic side chains, and its intensity and position are unaffected by changes induced in protein structure after dehydration or applying different stresses [36]. Therefore, it was used as internal intensity standard to normalize Raman spectra before comparison (Fig. 6A).

Compared to the amorphous form of lysozyme (20M sample), the crystalline form (dried crystals and 3M sample) showed greater intensity of the ν Ca-C–N mode at 930 cm^{-1} (Fig. 6B),

and produced a higher vibration mode of amide III (N-H in-plane bend + C-N stretch) at ~1265 cm^{-1} (Fig. 6C) and a lower and sharper vibration mode of amide I (C=O stretch) at ~1660 cm^{-1} (Fig. 6D). The intensity of ν Ca-C–N mode at 930 cm^{-1} [37], upshifting of amide III (N-H in-plane bend + C-N stretch) [38], and downshifting and sharpening of the line of amide I (C=O stretch) at ~1660 cm^{-1} [39] indicates a higher α-helix content. This means that the crystalline form maintained the α-helix structure of native lysozyme more than the amorphous form. The native secondary structure of lysozyme consists of three alpha helix regions extending 5-15, 24-34 and 88-96 amino acid residues [24].

Rich α-helix structures have a low tendency to aggregate compared to rich β-sheet structures [15]. This possibly explains why the crystalline form had less tendency to thermally unfold in lower n' compared to the amorphous form. Therefore, according to our above postulation, the spectroscopic observation that the crystalline form contains more alpha helix may explain why the crystalline lysozyme unfolded at lower T_m.

Comparison of the spectrum of the denatured lysozyme (sample 60M) with that of the amorphous form shows that mechanical denaturation induced further reduction in the intensity of ν Ca-C–N mode at 930 cm^{-1} (Fig. 6B), which in turn implies a further reduction in α-helix content.

3.6. Enzymatic assay

Interestingly, milled samples did not show a reduction in biological activity (ANOVA: $P > 0.05$) (Table 4). The ability of lysozyme to re-nature on dissolution is a possible explanation for this finding. Indeed, previous research has shown the strong refolding ability of lysozyme upon dissolution in aqueous media [40]. Likewise, despite significant loss of the Raman vibrations of

lysozyme upon denaturation by γ-irradiation, the denatured lysozyme samples almost fully recovered their biological activity on dissolution [39].

4. Conclusions

Bulk crystallisation of protein therapeutic molecules for controlled drug delivery studies is of interest to the biopharmaceutical industry. The complexity of biotherapeutic molecules is likely to lead to complex material properties of crystals in the solid state. Here we exemplify, using the model drug lysozyme, the effects of processing lysozyme crystals and are able to show distinct differences in the properties of the materials after processing which could be used in optimising and controlling processes for the purposes of quality by design.

By drying lysozyme crystals using a controlled method we were able to evidence the removal of water and maintain crystallinity. However, the size reduction of dried lysozyme crystals by milling was shown to promote formation of an amorphous solid-state form. Raman spectroscopy provided evidence that the amorphous form was then denatured in the solid state by further milling. The milling time was the critical attribute determining the extent of the transformations. DSC was successfully employed in monitoring the three different states of lysozyme (namely crystalline, amorphous, and denatured) in the solid state. The DSC thermogram of the crystalline lysozyme exhibited T_m at ~187 °C which was lower than that of amorphous lysozyme by ~14 °C. The mechanically denatured lysozyme did not provide a thermal unfolding transition. The calorimetric enthalpies of the crystalline and amorphous peaks were used to analyze quantitatively the three different states of lysozyme. XRPD data were consistent with the crystallinity of lysozyme identified by DSC. Interpretation of the Raman data from the same

samples is consistent with a crystalline form having a lower tendency to aggregate due to its greater α-helix rich structure compared to the amorphous form. Significantly, although the molecular arrangement and molecular conformation of lysozyme changed during milling, its biological activity did not decrease. Clearly, subtle changes in solid-state processing conditions of crystalline lysozyme can bring about major changes in its solid-state properties. The effects of a wider range of milling variables, including different mill types, on lysozyme solid-state transformations and behaviour will be the subject of a future study.

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