

## **Changes in the structural and physicochemical characterization of pea starch modified by Bacillus-produced $\alpha$ -amylase**

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1 **ABSTRACT:** In this study, changes in structural and physicochemical properties of  
2 pea starch treated with Bacillus-produced  $\alpha$ -amylase were determined. The results  
3 showed that enzymatically modified pea starch had lower amylose content and granule  
4 size but higher branching degree and relative crystallinity. After enzyme hydrolysis, the  
5 distribution of A and B1 chains slightly decreased, while the distribution of B2 and B3  
6 chains increased lightly. Enzymatic hydrolysis preferentially occurred in the amorphous  
7 region and cannot change the crystalline structure of pea starch. Moreover, pea starch  
8 showed lower light transmittance, peak viscosity, breakdown viscosity, pasting  
9 temperature, shear viscosity, storage modulus and loss modulus, while the oil  
10 adsorption capacity and gelatinization enthalpy significantly increased with increasing  
11  $\alpha$ -amylase hydrolysis time. Correlation analysis indicated that  $\alpha$ -amylase hydrolysis  
12 had different effects on different pea varieties. This research could provide ideas for  
13 exploring new applications for enzymatically modified pea starch in food industry.

14 **Industrial relevance:** This study found that Bacillus-produced  $\alpha$ -amylase significantly  
15 changed the amylose content, granule size and viscosity of pea starch, which was  
16 helpful to further investigate the modified starch. This technology is expected to widen  
17 the applications of pea starch modified by Bacillus-produced  $\alpha$ -amylase in food industry,  
18 for example as thickener, stabilizer and beverage, to improve the texture, stability and  
19 shelf-life of various food products.

20 **Keywords:** Pea starch; Bacillus-produced  $\alpha$ -amylase; physicochemical properties;  
21 rheological properties

## 22 1. Introduction

23 Peas (*Pisum sativum* L.) are widely grown in temperate regions of the world and  
24 are the world's leading export crop, accounting for around 35-40% of the total trade in  
25 pulses (Ratnayake, Hoover, Shahidi, Perera, & Jane, 2001). Peas are now gaining more  
26 and more recognition due to their richness in starch, protein, resistant starch, dietary  
27 fiber and minerals (Zhou, Ma, Yin, Hu, & Boye, 2019). Traditionally, pea is consumed  
28 as dried seeds or as a fresh vegetable, the dried seeds are mainly applied in soups and  
29 are increasingly being processed into value-added food ingredients (Ren, Setia,  
30 Warkentin, & Ai, 2020). Pea flour has unique aromatic profiles and desirable functional  
31 properties and is often processed through milling, making it suitable for use in a variety  
32 of foods, including baked goods, noodles and meat products (Gu et al., 2021). Pea starch,  
33 accounting for about 40-50% of the seed, is the most abundant carbohydrate in pea  
34 seeds. The amylose content of pea starch is in the range of 30-60% with varying  
35 varieties and is considered to be an important factor determining the pea quality  
36 (Hoover et al. 2010). Compared to potato, wheat and maize starch, pea starch is  
37 considered as an inexpensive source of starch (Zhou, Ma, Yin, Hu, & Boye, 2019).  
38 Industrially, starches obtained from maize, potato, cassava and wheat are almost  
39 exclusively natural and modified. Nowadays, starches isolated from peas are widely  
40 used in industry due to their unique properties such as extent of digestion, high resistant  
41 starch content as well as high elasticity of gels (Sun, Sun, & Xiong, 2014), making them  
42 suitable substitutes to modified starches in a range of products (Raphaelides &  
43 Georgiadis, 2008).

44 Native starches are not entirely applied in the food industry due to their poor water  
45 solubility and heat stability, which cannot meet the requirements of specific applications  
46 (Cui et al., 2023). Therefore, native starches are often modified by chemical, physical  
47 or enzymatic methods to improve their industrial applications. Compared to chemical  
48 and physical methods, the enzymatic approach has the advantages of simple operation,  
49 high reaction efficiency and high yield, which is conducive to meeting the  
50 requirements and suitability of food products. It has also been reported that enzymatic  
51 modification can effectively improve the utilization of the native starch (Chen et al.,  
52 2021). Alpha-amylase is a commonly used enzyme that usually cleaves the  $\alpha$ -1, 4-  
53 glycosidic bond of amylose or amylopectin in the internal position to obtain a product  
54 with an  $\alpha$ -configuration (Lin et al., 2016). Previous studies have shown that the  
55 modification of starch with  $\alpha$ -amylase is effective in improving the structural and  
56 physicochemical properties of starch. Shariffa, Karim, Fazilah and Zaidul (2009) have  
57 reported that sweet potato starch was higher in amylose content, water solubility and  
58 swelling power after fungal-produced  $\alpha$ -amylase hydrolysis. Similarly, corn starch  
59 hydrolyzed by  $\alpha$ -amylase had higher amylose content, longer amylopectin chains along  
60 with smaller granules (Song et al., 2020). When treated with maltogenic  $\alpha$ -amylase, the  
61 molecular weight of rice starch was significantly reduced, while significant increase  
62 was observed in the short-chain levels (DP < 13) (Wang et al., 2022). Compared to  
63 fungal sources of  $\alpha$ -amylase, the Bacillus-produced  $\alpha$ -amylase has greater thermal  
64 stability and pH tolerance (Martínez et al., 1997), making it more suitable for certain  
65 industrial applications, such as starch liquefaction or baking. Additionally, Bacillus

66 strains are less susceptible to contamination and are highly capable of producing  
67 thermostable  $\alpha$ -amylase (Schwab et al., 2009). The modified cereal starches have  
68 unique physicochemical properties and specially applications. However, previous  
69 studies have mainly focused on the modification of potato and maize starch by  $\alpha$ -  
70 amylase, while few reports have been studied on the modification of pea starch by  
71 Bacillus-produced  $\alpha$ -amylase, especially regarding the changes in structural,  
72 physicochemical and rheological properties, which limits the application of modified  
73 pea starch in the food industry. Therefore, there is a need to explore potential  
74 applications of pea starch modification based on  $\alpha$ -amylase produced by Bacillus.

75 In this study, three pea varieties with different amylose content were used to  
76 investigate the effects of Bacillus-produced  $\alpha$ -amylase on the particle size distribution,  
77 amylopectin chain length distribution, branching degree, crystalline structure, short-  
78 ranged ordered structure, light transmittance, water and oil absorption capacity, pasting  
79 and thermal properties of the native pea starch. The changes in structural,  
80 physicochemical and rheological properties of the modified pea starch and its  
81 applications were then further explored by comparing with the native pea starch. The  
82 purpose of this research was to provide a theoretical basis for the development of the  
83 modified starch and widen the applications of pea starch modified by Bacillus-produced  
84  $\alpha$ -amylase in the food industry.

## 85 **2. Materials and methods**

### 86 *2.1 Materials*

87 Three pea varieties used in this study were Xiwan 1 (XW1), Xiwan 2 (XW2) and

88 Xiwan 3 (XW3) provided by the Minor Grains Laboratory of the Northwest A & F  
89 University. The XW1 and XW2 had wrinkled surfaces and were mainly used as grain  
90 varieties, while XW3 had smooth shape and was generally used for cooking. All  
91 varieties were planted in 2020 at the experimental farm in Guan village, Yangling,  
92 Shaanxi province. The thermostable Bacillus-produced alpha-amylase (Cas. No. 9000-  
93 90-2, 3700 U/g) was obtained from Beijing Solaibao Technology Co., LTD. All  
94 chemicals and reagents were of analytical grade.

### 95 *2.2 Starch isolation*

96 Pea seeds were ground into flour using a universal crusher and pea starch was  
97 isolated following the method of Raghunathan, Hoover, Waduge, Liu and Warkentin  
98 (2017) with some modifications. Firstly, the pea flour was mixed with distilled water  
99 (1:3, w/v) and the solution was then passed through a 100-mesh sieve. Next, the crude  
100 extract was obtained and left at 25 °C for 24 h and centrifuged at 4000 g for 10 min.  
101 The sediment was then repeatedly washed with distilled water until it turned white.  
102 Finally, the starch samples were dried at 40 °C for 24 h, ground and passed through an  
103 80-mesh sieve. The main chemical composition of the native pea starch was  
104 summarized in Table S1.

### 105 *2.3 Preparation of $\alpha$ -amylase-modified starch*

106 Starch sample (30 g) was suspended in the 0.1 M sodium acetate buffer (pH = 6.0).  
107 Then,  $\alpha$ -amylase (0.59 g) was added to the starch suspension, pre-incubated at 50 °C  
108 for 30 min, gently stirred and shaken at 50 °C and 100 rpm for 4, 8 and 16 h, respectively  
109 (All samples were prepared under the same condition). Next, sodium hydroxide

110 solution (2 M) was added to make enzymes inactivated until each solution had a pH of  
111 10.8. The pH of each solution was then adjusted to 6.0 and the supernatant was removed  
112 and centrifuged at 4000 g for 10 min (repeated 3 times). Finally, the sediment was  
113 freeze-dried and the native and enzymatically modified starches were used for later  
114 analysis (Song et al., 2020).

#### 115 *2.4 Amylose content*

116 The amylose content of pea starch was determined using the iodine colorimetric  
117 determination following the method of Gao et al. (2016), and the content was calculated  
118 from the blue value and measured in 3 replicates with the results expressed as a  
119 percentage.

#### 120 *2.5 Structural characteristics of pea starch*

##### 121 *2.5.1 Granule size distribution*

122 The granule size distribution of pea starch was measured using a laser diffraction  
123 particle size analyzer (Master 2000, Malvern, England). Starch samples were measured  
124 from 0.1 to 2000  $\mu\text{m}$  with the shading factor of 1.3330 and the shading range of 12-  
125 17%. The measurements were reported in terms of the volume distribution.

##### 126 *2.5.2 Chain length distribution of amylopectin*

127 The amylopectin chain length distribution of pea starch was measured using high  
128 performance anion exchange chromatography equipped with pulsed amperometric  
129 detection (HPAEC-PAD) system (ICS 500+, Thermo Fisher Scientific, USA) according  
130 to the method of Yang et al. (2019). Pea starch (5 mg) was suspended in the ultrapure  
131 water (5 mL) and the solution was then heated in a boiling water bath for 60 min. Next,

132 the gelatinized sample (2.5 mL) was mixed with sodium acetate (125  $\mu$ L),  $\text{NaN}_3$  (5  $\mu$ L)  
133 and isoamylase (5  $\mu$ L) and left at 38  $^\circ\text{C}$  for 24 h to hydrolyze the  $\alpha$ -1, 6 glycosidic  
134 bonds. After centrifugation at 12000 g for 5 min, the samples were passed through a  
135 0.45  $\mu\text{m}$  membrane filter and the supernatant was taken for testing. The mobile phase  
136 A was 200 mM NaOH, phase B was 200 mM NaOH / 200 mM NaAC, and the column  
137 temperature was 30  $^\circ\text{C}$ . The chain length distribution was calculated based on the  
138 following formula: relative area = area / total area \* 100%.

### 139 *2.5.3 Branching degree analysis*

140 The branching degree of pea starch was measured by nuclear magnetic resonance  
141 (NMR) spectroscopy following the method of Bai and Shi (2016). The sample (10 mg)  
142 and D6-DMSO (1 mL) were added into the EP tube, then heated at 80  $^\circ\text{C}$  and left for  
143 12 h. After centrifugation at 12000 g for 10 min, the supernatant was added into the  
144 NMR tube for detection. The frequency was 500.23 MHz for  $^1\text{H}$ , and the  $^1\text{H}$  spectra  
145 were collected in 32 individual scans. The peak position of  $\alpha$ -1, 4 bond was around 5.05  
146 ppm, while  $\alpha$ -1, 6 bond was near 4.71 ppm. The degree of branching (DB) was  
147 calculated as follows:  $\text{DB} = \alpha\text{-1, 6} / (\alpha\text{-1, 6} + \alpha\text{-1, 4})$ .

### 148 *2.5.4 X-ray diffraction (XRD)*

149 The crystalline structure of pea starch was determined using an X-ray  
150 diffractometer (D/Max 2550 VB +/-PC, Rigaku, Japan) through the method of Zhang et  
151 al. (2019). The samples were measured by the diffractometer at 40 kV and 100 mA in  
152 the diffraction angle ( $2\theta$ ) from 5 $^\circ$  to 40 $^\circ$  at a constant speed of 10  $^\circ$ /min. The relative  
153 crystallinity (%) was calculated from the ratio of crystallinity area to total diffraction

154 area.

### 155 *2.5.5 Fourier transformed infrared spectrometry (FTIR) analysis*

156 The short-range ordered structure of pea starch was performed using a FTIR  
157 spectrometer (7000, Varian, USA) equipped with an ATR single-reflectance cell  
158 containing a germanium crystal (45° incidence angle) following the method of Zhu et  
159 al. (2017).

## 160 *2.6 Physicochemical properties of pea starch*

### 161 *2.6.1 Light transmittance*

162 The light transmittance of pea starch was measured as described by Chao et al.  
163 (2015). The starch paste (1 g/mL) was heated in boiling water for 30 min. After  
164 gelatinization, the starch samples were cooled and placed at room temperature (25 °C)  
165 for 24 h. Then, a visible-light spectrophotometer (Lab Tech Ltd., Beijing, China) was  
166 used to determine the light transmittance at 650 nm with distilled water as a reference.

### 167 *2.6.2 Absorption capacity of water and oil*

168 The water absorption capacity and oil absorption capacity of pea starch was  
169 measured through the method of Song et al. (2020). The oil used in this study was edible  
170 peanut oil with room temperature. Absorption capacity (g/g) was calculated by dividing  
171 the weight of wet precipitate by the dry weight of the sample. The analysis was  
172 performed in triplicate.

### 173 *2.6.3 Pasting properties*

174 The pasting properties of pea starch were carried out using a Rapid Visco Analyzer  
175 (Perten, Stockholm, Sweden) according to the method of Gao et al. (2016). Briefly, the  
176 starch slurries were held at 50 °C for 1 min before heating from 50 to 95 °C at 12 °C/min.

177 Then, the samples were maintained at 95 °C for 2.5 min, cooled to 50 °C at a constant  
178 rate of 12 °C/min and finally held at 50 °C for 2 min. The peak viscosity (PV), trough  
179 viscosity (TV), breakdown viscosity (BD), final viscosity (FV) and setback viscosity  
180 (SB) were observed from the pasting curve.

#### 181 *2.6.4 Thermal properties*

182 The differential scanning calorimetry (DSC; Q2000, USA) was used to measure  
183 the thermal behavior of pea starch through our previous method reported by Gao et al.  
184 (2020). Briefly, starch sample and deionized water were mixed at a ratio of 1:3, and the  
185 solution was then added to the aluminum pan. Next, the pan was sealed hermetically  
186 and kept at 4 °C for 24 h before analysis. The samples were heated from 30 to 100 °C  
187 at a constant rate of 10 °C/min. An empty sealed aluminum pan was used as a reference.

#### 188 *2.6.5 Rheological properties*

189 The TA instrument rheometer (DHR-1, USA), employed with a stainless parallel  
190 plate geometry (40 mm diameter) and a gap size of 1000 µm, was used to determine  
191 the rheological behaviors of pea starch. The starch suspension (8%, w/v) was  
192 gelatinized completely and then cooled to room temperature (25°C). Next, the starch  
193 sample was transferred to the parallel plate of rotary rheometer and covered by a circle  
194 of silicone oil to prevent moisture to evaporate. All the experiments were conducted at  
195 25°C.

#### 196 *2.7 Statistical analysis*

197 All experiments were conducted in triplicate. The results were analyzed using one-  
198 way ANOVA through the SPSS 17.0 software. The significant difference level among

199 the means was conducted using the Duncan's multiple range test ( $P < 0.05$ ). All figures  
200 were drawn using Origin Pro software (version 2021, USA).

### 201 **3. Results and discussion**

#### 202 *3.1 Amylose content*

203 The amylose contents of the native and enzymatically modified pea starch were  
204 summarized in Table 1. It was clearly shown that the amylose content of pea starch  
205 ranged from 26.20 to 39.38%, and that was significantly reduced with increasing  $\alpha$ -  
206 amylase incubation time. It has been reported that the amylose content of legume starch  
207 was between 27.35 and 35.21% (Zhou, Hoover, & Liu, 2004), which was slightly lower  
208 than our findings. In addition, significant differences in amylose content were obtained  
209 among the three pea varieties, with XW1 having the highest value, followed by XW2  
210 and XW3, respectively. Compared to the corresponding native starch, the amylose  
211 content of XW1, XW2 and XW3 after 16 h of enzymatic hydrolysis decreased by 12%,  
212 14% and 14%, respectively. Song et al. (2020) have found that the amylose content of  
213 corn starch was significantly reduced when treated with Bacillus-produced  $\alpha$ -amylase,  
214 which was consistent with the results of this study. It has been reported that the value  
215 of amylose content is not only related to the amylose molecules, but also to the long  
216 branches of amylopectin when enzymatic hydrolysis of starch (Shariffa, Karim, Fazilah,  
217 & Zaidul, 2009). In addition,  $\alpha$ -amylase has been shown to preferentially hydrolyze  
218 amylose chains, which indicated that  $\alpha$ -amylase preferentially acted on amylose of pea  
219 starch, leading to the decrease of amylose content.

#### 220 *3.2 Granule size distribution*

221 As can be seen from Fig. 1, there were significant differences in granule size  
222 distribution of the native and enzymatically modified pea starch among different pea  
223 varieties. It was clearly shown that all starch samples showed a unimodal curve of  
224 granule size distribution, but the corresponding particle size was different when the  
225 volume distribution reached the maximum value (Fig. 1 A-C). Normally, the particle  
226 size distribution is divided into A-granule ( $> 15 \mu\text{m}$ ), B-granule (5-15  $\mu\text{m}$ ) and C-  
227 granule ( $< 5 \mu\text{m}$ ) according to the finding of Bechtel, Zayas, Dempster, & Wilson  
228 (1993). In this study, the granule size distribution of pea starch was mainly A and B  
229 granules, ranging from 92.54 to 99.60% (A-granule) and from 0.40 to 7.46 (B-granule),  
230 respectively (Table 1). With the extension of  $\alpha$ -amylase hydrolysis time, the distribution  
231 of A-granule significantly decreased while obvious increase was obtained in B-granule,  
232 meaning that prolonged enzyme hydrolysis could lead to the breakage of large starch  
233 granule, thus reducing the volume distribution of pea starch. Additionally, both the D  
234 [3,2] and D [4,3] significantly decreased with the increase of  $\alpha$ -amylase hydrolysis time,  
235 ranging from 24.83 to 28.64  $\mu\text{m}$  (D [3,2]) and from 27.11 to 31.08  $\mu\text{m}$  (D [4,3]),  
236 respectively. These results of this study confirmed that  $\alpha$ -amylase hydrolysis was  
237 effective in reducing granule size and probably be related to the rupture and damage of  
238 native starch granules due to hydrolysis (Zhao et al., 2018), which was consistent with  
239 the previous report by Jiang et al. (2017). In addition, the volume distribution of the  
240 native pea starch had different reaction to  $\alpha$ -amylase hydrolysis. With the increase of  
241  $\alpha$ -amylase hydrolysis time, the volume distribution of all starch samples significantly  
242 increased, while the granule size of the corresponding pea starch was different when

243 the volume distribution peaked. This finding showed that the volume distribution of  
244 different pea varieties responded differently to  $\alpha$ -amylase hydrolysis, indicating that  $\alpha$ -  
245 amylase hydrolysis can change the volume distribution of pea starch, thereby resulting  
246 in variations in the physicochemical properties of starch granules. Differences in the  
247 response of different pea varieties to  $\alpha$ -amylase may be related to the genotype.

### 248 *3.3 Chain length distribution*

249 Generally, the branch chains of amylopectin are classified into A-chains (DP 6-12),  
250 B1-chains (DP 13-24), B2-chains (25-36) and B3-chains (DP > 37) based on the degree  
251 of polymerization (DP) (Hanashiro, Abe, & Hizukuri, 1996). In this study, the highest  
252 content of B1-chains (52.78%, mean of the three varieties, below) were noticed of the  
253 native pea starch, followed by A-chains (19.20%) and B2-chains (15.45%), and a small  
254 amount of very long chains (12.56%) was also observed (Fig. 1 D-F). These results  
255 indicated that the B1-chains may play a major role in the relative properties of the native  
256 pea starch. In addition, the chain length distribution of the native pea starch firstly  
257 increased and then reduced with increasing DP values, with all starch samples having  
258 the highest peak at DP 13. After enzymatic hydrolysis, the chain length distribution of  
259 all samples still had a maximum value at DP 13, with the average branched chain length  
260 of enzymatically modified starch ranging from 21.86 to 21.96% (XW1), from 21.69 to  
261 22.02% (XW2) and from 21.97 to 22.08% (XW3), respectively. The distribution of A-  
262 chains and B1-chains on pea starch significantly decreased with the prolongation of  
263 enzyme hydrolysis time, while slight increases were observed in the distribution of B2-  
264 chains and B3-chains (Table 1). These results may be related to the fact that the stearic

265 acid in the pea starch structure blocked the hydrolysis of the amylopectin chains (B2-  
266 chain and B3-chain). Moreover, the difference values among three pea varieties  
267 significantly differed at different hydrolysis time, with XW1 and XW2 showing the  
268 most significant effect after 4 h enzymatic modification while XW3 showed the most  
269 significant effect after 8 h enzymatic modification (Fig. 1 G-I). This result indicated  
270 that the *Bacillus*-produced  $\alpha$ -amylase had different impacts on the pea varieties, which  
271 may be related to the variations in amylose content.

### 272 *3.4 Branching degree analysis*

273 The branching degree of pea starch was summarized in Table 2, and the peak  
274 intensities of  $^1\text{H}$  NMR spectra were shown in Fig. S 1. All samples produced resonance  
275 signals from 4.2 to 5.6 ppm (Fig. S 1 A-C). For the  $^1\text{H}$  NMR spectrum of pea starch,  
276 the signals at 5.05 and 4.71 ppm were assigned to  $\alpha$ -1, 4 and  $\alpha$ -1, 6-linked heterodimeric  
277 protons, respectively. These results showed that the DB of the native pea starch ranged  
278 from 0.76 to 1.05%, and that of the wrinkled pea was slightly higher than that of the  
279 smooth pea (Table 2). After enzyme hydrolysis, the signals of the enzymatically  
280 modified starch slightly changed at different chemical shift positions. In addition, the  
281 value of the DB was in the range of 1.83-3.66% with increasing  $\alpha$ -amylase incubation  
282 time from 4 h to 16 h. Compared with the native pea starch, the DB of the enzymatically  
283 modified pea starch was much higher and was increased by 146.32% (XW1), 218.10%  
284 (XW2) and 342.11% (XW3), respectively. These results confirmed that the new  
285 branched chain was hydrolyzed from the  $\alpha$ -1,4-glycosidic linkage in the native pea  
286 starch chain, and transformed into a new  $\alpha$ -1,6-glycosidic linkage on other chains as

287 shown in Fig. S1. It has been reported that the DB of corn starch was increased with  
288 increasing time of 1,4- $\alpha$ -glucan branching enzyme action (Li et al., 2016), which was  
289 consistent with the finding of our study.

### 290 *3.5 Crystalline structure*

291 The XRD patterns of the native and enzymatically modified pea starch were  
292 presented in Fig. 2 A and the relative crystallinities were summarized in Table 2.  
293 Generally, cereal starches are divided into three main types based on their XRD spectra,  
294 including A-type, B-type and C-type (Cheetham & Tao, 1998). In this study, all starch  
295 samples exhibited a typical C-type diffraction pattern with strong peaks at around 15°,  
296 17° and 23° ( $2\theta$ ) and a small peak at about 6° ( $2\theta$ ), indicating that the X-ray diffraction  
297 pattern of the native pea starch was not changed when treated with  $\alpha$ -amylase. Similar  
298 phenomenon was observed on corn starch with A-type patterns treated with  $\alpha$ -amylase  
299 (Song et al., 2020). In addition, the peak position of pea starch was also not affected  
300 after enzyme hydrolysis, which might be that the double-helical crystalline structure  
301 was not changed by Bacillus-produced  $\alpha$ -amylase. For enzymatically modified pea  
302 starch, the peaks appeared to be sharper and higher than those of the native starch (Fig.  
303 3 A), indicating that the enzyme hydrolysis of Bacillus-produced  $\alpha$ -amylase mainly  
304 occurred in the amorphous region of the starch granules (Shariffa, Karim, Fazilah, &  
305 Zaidul, 2009). With the increase of  $\alpha$ -amylase hydrolysis time, the relative crystallinity  
306 of pea starch significantly increased, and the relative crystallinity of enzymatically  
307 modified pea starch was significantly higher than that of the native pea starch, ranging  
308 from 28.36 to 32.14% (XW1), from 28.67 to 30.14% (XW2) and from 27.83 to 31.08%

309 (XW3), respectively (Table 2). Similar change trend was observed on corn starch  
310 treated with Bacillus-produced  $\alpha$ -amylase (Song et al., 2020; Zhao et al., 2018),  
311 indicating that the crystalline structure of the C-type starch granule was more resistant  
312 to enzyme hydrolysis of bacillus-produced  $\alpha$ -amylase than the amorphous structure.  
313 However, enzyme hydrolysis resulted in lower value of the relative crystallinity on  
314 wheat starch (Li, Li, & Guo, 2020), while no significant changes were founded in  
315 relative crystallinity on waxy maize starch and normal potato starch (Teng, Torsten,  
316 Wang, Li, & Jovin, 2016), meaning that the relative crystallinity of various starch  
317 sources responded differently to  $\alpha$ -amylase hydrolysis. Amylopectin is the main  
318 crystalline component of starch granules, while amylose can weaken the crystalline  
319 structure of amylopectin (Zhang et al., 2019). The low relative crystallinity of starch  
320 may be attributed to a poorly organized crystalline structure (Zhou, Hoover, & Liu,  
321 2004). In this study, the increased relative crystallinity indicated that the crystalline  
322 structure of pea starch became better when treated with  $\alpha$ -amylase. Starch granules with  
323 higher amylose content have stronger resistance to enzyme hydrolysis. This explanation  
324 seemed reasonable, since the amylose content of pea starch was lower as the enzyme  
325 hydrolysis time increased in this study (Table 1), which can be used to explain the  
326 higher relative crystallinity degree of pea starch after  $\alpha$ -amylase hydrolysis.

### 327 *3.6 ATR-FTIR analysis*

328 The ATR-FTIR method was used to measure the short-ranged ordered structure of  
329 the native and enzymatically modified pea starch, and the spectra of the starch samples  
330 were presented in Fig. 2 B. It was clear that the position of the characteristic absorption

331 peak of pea starch cannot be changed after  $\alpha$ -amylase hydrolysis, indicating that the  
332 Bacillus-produced  $\alpha$ -amylase hydrolysis neither changed the type of chemical group in  
333 the starch molecules nor produced a new one (Zhao et al., 2018). Normally, the  
334 absorbance intensity of starch at 1045, 1022 and 995  $\text{cm}^{-1}$  varies with the change of its  
335 conformation, and these values can reflect the crystalline characteristics of the starch  
336 granules (Lopez-Baron et al., 2018). The ratio of 1045/1022  $\text{cm}^{-1}$  ( $R_1$ ) is used to  
337 determine the ordered degree, while the ratio of 1022/995  $\text{cm}^{-1}$  ( $R_2$ ) can be used as an  
338 indicator of the proportion of amorphous to ordered carbohydrate structure (Jiang et al.,  
339 2020). In this research, the  $R_1$  ratio of pea starch ranged from 0.71 to 0.83 (XW1), from  
340 0.79 to 0.96 (XW2) and from 0.80 to 0.93 (XW3), respectively (Table 2). With  
341 increasing  $\alpha$ -amylase hydrolysis time, the  $R_1$  ratio obviously increased and the  $R_1$  ratio  
342 of enzymatically modified pea starch was much higher than that of the native starch.  
343 The higher crystalline fraction presented after enzymatic hydrolysis suggested that the  
344 mechanical damage caused by Bacillus-produced  $\alpha$ -amylase mainly affected the  
345 amorphous region of pea starch granules rather than the crystalline region, and the  
346 amorphous region was more easily digested by Bacillus  $\alpha$ -amylase during the  
347 incubation process (Chen & Zhang, 2012), which was similar to the findings for corn  
348 starch reported by Zhao et al., (2018). However, the  $R_2$  ratio significantly decreased,  
349 and after 16 h of enzymatic modification, the ratio of  $R_2$  decreased by 0.70% (XW1),  
350 5.79% (XW2) and 2.40% (XW3), respectively, compared with the native starch (Table  
351 2), which suggested that the helical alignment of pea starch can be changed by Bacillus-  
352 produced  $\alpha$ -amylase hydrolysis. These results suggested that Bacillus-produced  $\alpha$ -

353 amylase hydrolysis played a main role in increasing crystalline regions of pea starch,  
354 which could be explained by the increase of the relative crystallinity degree as shown  
355 in Table 2. In addition, significant differences in  $R_1$  ratio were obtained among three  
356 pea varieties, with XW1 having a lower  $R_1$  ratio than XW2 and XW3, but a higher  $R_2$   
357 ratio, indicating that XW1 was less ordered but had a higher helical alignment than  
358 other varieties and the differences among three pea starches might be attributed to the  
359 biological origin, the molecular structure of amylopectin, and the contents of amylose  
360 and amylopectin (Li & Zhu, 2017).

### 361 *3.7 Light transmittance*

362 The light transmittance of the native and enzymatically modified pea starch was  
363 presented in Table 2. Significant difference was observed between the wrinkled and  
364 smooth pea, and the native starch was in the order of XW1 (92.53%) > XW2 (91.74%) >  
365 XW3 (90.01%). After incubation with  $\alpha$ -amylase, the light transmittance of all samples  
366 significantly decreased and ranged from 39.92 to 83.50%. Compared to the native  
367 starch, the light transmittance of pea starch after 16 h enzymatic hydrolysis was reduced  
368 by 50.74% for XW1, 28.77% for XW2 and 55.65% for XW3, respectively, indicating  
369 that  $\alpha$ -amylase had the most significant effect on XW3, and this difference may be  
370 related to the genotype of different pea varieties. The light transmittance has been  
371 shown to be influenced by the amylose content, starch granule size and the ratio of  
372 amylose to amylopectin (Zhang et al., 2019). Wang, Tang, Fu, Huang and Zhang (2016)  
373 have concluded that the reduction in light transmittance of starch during retrogradation  
374 is due to the association of starch with each other through hydrogen bonds. In this study,

375 the lower value of the light transmittance of pea starch could be attributed to its lower  
376 amylose content and lower distribution of A-granules (Table 1). Therefore, the modified  
377 pea starch was not suitable for foods with high light transmittance requirements like  
378 cold skin, cold noodles and crystal shrimp dumplings. In addition, we speculated that  
379 the molecules of pea starch in this study were rearranged and amylose was reassembled  
380 to form crystals after  $\alpha$ -amylase hydrolysis, thus resulting in the reduction of the light  
381 transmittance.

### 382 *3.8 Absorption capacities of water and oil*

383 The absorption capacities of water and oil of the native and enzymatically  
384 modified pea starch were shown in Fig. S 2. The water absorption capacity of the native  
385 pea starch ranged from 1.82 to 1.85 g/g, whereas that of the enzymatically modified  
386 starch was increased by 8.90% for XW1, 12.64% for XW2 and 12.97% for XW3,  
387 respectively. As for the oil absorption capacity, all the values significantly increased  
388 with the increase of enzyme hydrolysis time, and that of XW1, XW2 and XW3 after 16  
389 h enzyme hydrolysis was increased by 10.70%, 10.16% and 22.40%, respectively. Song  
390 et al. (2020) have found that both the water-absorption capacity and oil-absorption  
391 capacity of corn starch were obviously increased with increasing enzyme hydrolysis  
392 time, which was similar to the findings of our study. It has been reported that the  
393 increased water absorption capacity of starch was related to the small starch granule  
394 size, which could explain the finding that there was more B-granules of pea starch after  
395 *Bacillus*-produced  $\alpha$ -amylase hydrolysis. These results showed that the water  
396 absorption capacity and oil absorption capacity of the native pea starch could be

397 significantly affected by  $\alpha$ -amylase hydrolysis, which was mainly due to the formation  
398 of a large number of pores and destruction of the amorphous region, making the  
399 granules expand more freely. The differences in the water absorption capacity and oil  
400 absorption capacity of pea starch might be related to the genotypes among three  
401 varieties.

### 402 *3.9 Pasting properties*

403 The pasting profiles of the native and enzymatically modified pea starch were  
404 presented in Fig. 3, and the corresponding parameters were summarized in Table 3. All  
405 starch samples showed a single peak curve, while there was significant variation  
406 between different pea varieties. Peak viscosity can reflect the swelling degree of starch  
407 granules (Gao et al., 2016). After enzyme hydrolysis, the PV significantly decreased  
408 and ranged from 90.00 to 3879.00 cP (XW1), from 362.00 to 3585.67 cP (XW2) and  
409 from 1635.00 to 2265.00 cP (XW3), respectively, which was consistent with the results  
410 on corn starch (Zhao et al., 2018). The finding of this study indicated that  $\alpha$ -amylase  
411 hydrolysis can change the swelling degree of pea starch granules, thereby influencing  
412 the granule size and reducing the PV. The obvious decrease in the PV could be related  
413 to the hydrolysis of starch molecules, since small molecules provide lower viscosity  
414 than large molecules (Benavent-Gil & Rosell, 2017). As observed in 3.2, the A-granule  
415 distribution of pea starch significantly decreased with the time of enzymatic hydrolysis,  
416 which could be used to explain the decrease in the PV. Similar result was found in the  
417 TV, and the TV values of XW1, XW2 and XW3 were reduced by 99.65%, 99.42% and  
418 92.51%, respectively, after 16 h of enzymatic hydrolysis compared with the native

419 starch. High breakdown viscosity indicates that the starch is less resistant to shear forces  
420 during heating (Kong, Zhu, Sui, & Bao, 2015). In this study, the BD of the pea starch  
421 treated with Bacillus-produced  $\alpha$ -amylase was lower than that of native starch, which  
422 might be due to the weakened structure of granule caused by the mechanical forces of  
423  $\alpha$ -amylase hydrolysis. This finding indicated that enzymatic hydrolysis could enhance  
424 the resistance of pea starch to heating, which may be related to the fact that enzymatic  
425 hydrolysis preferentially occurs in the amorphous region as observed in 3.6. Similar  
426 result has been proved that  $\alpha$ -amylase hydrolyzed corn starch granules with lower BD  
427 compared with the native starch (Dura, Blaszcak, & Rosell, 2014), while there was a  
428 slight increase of the BD on popcorn starch studied by Song et al. (2020), which was  
429 not consistent with our results, and the difference might be due to the various reactions  
430 of different starch sources to  $\alpha$ -amylase hydrolysis. With the increase of  $\alpha$ -amylase  
431 hydrolysis time, the FV also significantly reduced and ranged from 11.00 to 5554.67 cP,  
432 and obvious difference could be obtained among three pea varieties. Setback viscosity  
433 can reflect the retrogradation tendency of starch paste, the higher setback viscosity, the  
434 higher ability to retrograde (Zhu et al., 2017). When enzyme hydrolysis time reached to  
435 16 h, the SB of pea starch was reduced by 99.93%, 99.82% and 98.48%, corresponding  
436 to XW1, XW2 and XW3, respectively. The low setback value at high enzyme  
437 hydrolysis time indicated that it was difficult for pea starch to retrograde after  $\alpha$ -  
438 amylase hydrolysis. Pasting temperature refers to the temperature when the starch paste  
439 begins to rise (Zhu et al., 2017). Li, Li and Guo, (2020) have concluded that wheat  
440 starch possessed higher pasting temperature at higher enzyme hydrolysis time, while a

441 significant decrease was observed on pea starch as enzyme hydrolysis time increased,  
442 indicating that it was hard for the enzymatically modified pea starch to swell. The  
443 difference in pasting behaviors might be due to the variations in granule size distribution,  
444 amylose content and branch-chain length distribution of amylopectin (Yang et al., 2019).

### 445 *3.10 Thermal properties*

446 The DSC analysis was used to determine the gelatinization properties of the native  
447 and enzymatically modified pea starch. The thermograms were presented in Fig. 2 C  
448 and the thermal parameters were shown in Table 3. All starch samples displayed a single  
449 peak in the DSC thermogram, which was consistent with the XRD analysis, indicating  
450 that  $\alpha$ -amylase hydrolysis cannot change the crystalline structure of pea starch, which  
451 confirmed the conclusion that  $\alpha$ -amylase hydrolysis mainly occurred in the amorphous  
452 region of the native pea starch. The melting temperatures of starch crystals, including  
453 onset temperature, peak temperature and conclusion temperature, are indirectly  
454 controlled by the amorphous region around starch granules (Kalin, Plyushchev, Fedotov,  
455 Sevryukov, & Gol'tsev, 2002). In this study, the  $T_o$  was in the range of 55.33-58.42°C,  
456 the  $T_p$  ranged from 63.29 to 67.27°C, and the  $T_c$  ranged from 71.20 to 76.01°C. In  
457 addition, significant difference was observed among three pea varieties, XW3 showed  
458 higher gelatinization temperatures than XW1 and XW2, which might be due to the  
459 genotypes of different pea varieties. After  $\alpha$ -amylase hydrolysis, it was shown that pea  
460 starch had higher values of the  $T_o$ ,  $T_p$  and  $T_c$ , indicating that the gelatinization process  
461 was delayed when treated with  $\alpha$ -amylase, which was similar to the findings of corn  
462 starch (Zhao et al., 2018). With increasing enzyme hydrolysis time, the gelatinization

463 temperatures of pea starch significantly increased, which indicated that the linear  
464 dextrin produced during enzymatic hydrolysis of starch granules could be rearranged  
465 into thermally stable crystalline structure. Higher gelatinization temperatures mean that  
466 starches require higher cooking temperatures and longer cooking time. The results of  
467 this study indicated that the cooking temperature and time of pea starch-based foods  
468 were enhanced by  $\alpha$ -amylase and heating during hydrolysis. The differences of  
469 gelatinization temperatures at different enzyme hydrolysis time might be related to the  
470 granule size distribution of starch, amylose content, and fine structure of amylopectin  
471 (Park, Ibáez, Fang, & Shoemaker, 2007). Gelatinization enthalpy ( $\Delta H$ ) reflects the  
472 quantity of crystallinity of the starch and is used to measure the loss of the double helical  
473 structure and crystalline structure of the starch (Hoover & Ratnayake, 2002). In this  
474 study, significant increases were obtained in the  $\Delta H$  of pea starch with increasing  
475 enzymatic hydrolysis time, ranging from 6.33 to 8.27 J/g for XW1, from 6.78 to 8.09  
476 J/g for XW2 and from 7.66 to 8.17 J/g for XW3, respectively. The high value of the  $\Delta H$   
477 on pea starch was attributed to the high relative crystallinity degree and low amylose  
478 content after enzyme hydrolysis (Zhu et al., 2016), which was consistent with the results  
479 of the XRD analysis and amylose content as shown in Table 1. These results indicated  
480 that the interactions between the double helix structures of pea starch hydrolyzed by  
481 *Bacillus*-produced  $\alpha$ -amylase may be more extensive through hydrogen bonding to  
482 form crystalline regions.

### 483 *3.11 Rheological properties*

484 The rheological properties of the native and enzymatically modified pea starch

485 were shown in Fig. 4. When the shear rate was about  $90 \text{ s}^{-1}$ , the shear viscosity of pea  
486 starch rapidly decreased and then tended to be stable with the increase of shear rate (Fig.  
487 4 A, B and C). Compared with the native pea starch, the shear viscosity of enzymatically  
488 modified pea starch was lower and significantly decreased with increasing  $\alpha$ -amylase  
489 incubation time. The phenomenon of increased shear rate and reduced shear viscosity  
490 indicated that pea starch can be regarded as a shear-thinning system, which was in  
491 accordance with the quinoa starch studied by Jiang et al. (2020). In addition, significant  
492 difference could be found between the wrinkled and smooth pea, and the shear-thinning  
493 phenomenon of XW3 was more obvious but lower than XW1 and XW2, which may be  
494 due to the differences in amylose content as reported in 3.1.

495 At present, frequency scanning method has been widely used to further understand  
496 the dynamic rheological behavior of starch. The storage modulus ( $G'$ ) and loss modulus  
497 ( $G''$ ) represent the solid-like and liquid-like properties of starch gels, respectively (Yuan,  
498 Sang, Wang, & Cui, 2018). In this study, the  $G'$  and  $G''$  of all starch samples stably  
499 increased at first and then rapidly increased to the maximum value with the increase of  
500 angular frequency, and there was no crossing both the  $G'$  and  $G''$ . After the  $\alpha$ -amylase  
501 hydrolysis, the  $G'$  and  $G''$  of all samples significantly decreased with the minimum  
502 value at 16 h, while the values of the  $G'$  and  $G''$  of the enzymatically modified pea starch  
503 were significantly lower than those of the native pea starch. In addition, the  $G'$  was  
504 significantly higher than the corresponding  $G''$  at different enzymatic time within the  
505 frequency scanning range (Fig. 4 D-F). These results indicated that the gel strength of  
506 pea starch could be weakened when treated by  $\alpha$ -amylase, and the gel strength of the

507 native pea starch was higher than the enzymatically modified starch. It has been found  
508 that the rheological behaviors of starch depend on the interactions between the amylose  
509 chains and the swelling granules (Li et al., 2017). In this study, the amylose content and  
510 A-granule distribution of pea starch gradually decreased with increasing  $\alpha$ -amylase  
511 incubation time, resulting in lower values of the  $G'$  and  $G''$ .

### 512 *3.12 Correlation analysis*

513 The correlation analysis was used to explore the relationship between the  $\alpha$ -  
514 amylase and physicochemical properties of pea starch (Fig. 5). It was clearly shown  
515 that the amylose content of pea starch after enzyme hydrolysis was positively correlated  
516 with the water absorption capacity and pasting parameters, but negatively correlated  
517 with the branching degree, relative crystallinity, oil absorption capacity and  
518 gelatinization enthalpy. The branching degree of pea starch was positively correlated  
519 with the relative crystallinity and gelatinization enthalpy, but negatively correlated with  
520 the pasting temperature. In addition, there were significant differences between the  
521 three pea varieties. For XW1 and XW2, the amylose content was positively correlated  
522 with the A-chains, but the oil absorption capacity was negatively correlated with the  
523 ratio of 1022/995  $\text{cm}^{-1}$ . However, an opposite change trend was observed on the XW3.  
524 The differences might be related to the variability of genotypes between the wrinkled  
525 and smooth pea. These results suggested that the hydrolysis of  $\alpha$ -amylase had a  
526 significant effect on the structural and physicochemical properties of pea starch and that  
527 different types of pea starch responded differently to  $\alpha$ -amylase.

## 528 **4. Conclusions**

529 In this study, *Bacillus*-produced  $\alpha$ -amylase was applied to modify pea starch  
530 isolated from three varieties to explore the changes in structural, physicochemical and  
531 rheological properties. With increasing enzyme hydrolysis time, the amylose content,  
532 amylopectin chain length distribution and water adsorption capacity significantly  
533 decreased, while branching degree and light transmittance obviously increased.  
534 Moreover, the crystalline structure was not changed but the relative crystallinity  
535 significantly increased after enzyme hydrolysis. Compared with the native pea starch,  
536 the viscosity, pasting temperature, shear viscosity, storage modulus and loss modulus  
537 of enzymatically modified starch all significantly decreased, while significant increases  
538 were found in gelatinization enthalpies. Overall, pea starch modified by *Bacillus*-  
539 produced  $\alpha$ -amylase has a wide range of applications in the food industry, as it can  
540 improve the texture, stability and shelf-life of various food products. The results of this  
541 study could provide valuable information for the enzymatic modification of pea starch  
542 to design novel products with desirable structural and physicochemical properties.

#### 543 **Acknowledgements**

544 This study was financially supported by the National Natural Science Foundation  
545 of China (31671631), Science and Technology Key R & D Program of Shaanxi  
546 Province (2022NY-178), and Minor Grains Industry Technology System of Shaanxi  
547 Province (NYKJ-2021-YL(XN)40).

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## 685 **Figure legends**

686 **Fig. 1** Granule size distribution and chain length distribution of amylopectin of the  
687 native and enzymatically modified pea starch.

688 **Fig. 2** X-ray diffraction patterns, ATR-FTIR spectra and DSC thermograms of the  
689 native and enzymatically modified pea starch.

690 **Fig. 3** RVA curves of the native and enzymatically modified pea starch.

691 **Fig. 4** Diagram of shear viscosity, storage modulus and loss modulus of frequency scan  
692 of the native and enzymatically modified pea starch.

693 **Fig. 5** Correlations analysis of the structural and physicochemical properties of pea

694 starch. Am: amylose content; Bd: branching degree; Rc: relative crystallinity; Lt: light  
695 transmittance; Wa: water absorption capacity; Oa: oil absorption capacity; PV: peak  
696 viscosity; TV: trough viscosity; FV: final viscosity; SB: setback; BD: breakdown; PT:  
697 pasting temperature; To: onset gelatinization temperature; Tp: peak gelatinization  
698 temperature; Tc: conclusion gelatinization temperature;  $\Delta H$ : gelatinization enthalpy.  
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