



## Physicochemical changes of oat seeds during germination

Binqiang Tian<sup>a</sup>, Bijun Xie<sup>a,\*</sup>, John Shi<sup>b</sup>, Jia Wu<sup>a,c</sup>, Yan Cai<sup>a</sup>, Tuoming Xu<sup>a</sup>, Sophia Xue<sup>b</sup>, Qianchun Deng<sup>a,d</sup>

<sup>a</sup> College of Food Science and Technology, Huazhong Agricultural University, Wuhan 430070, China

<sup>b</sup> Guelph Food Research Center, Agriculture and Agri-Food Canada, 93 Stone Road West, Guelph, Ontario, N1G 5C9 Canada

<sup>c</sup> College of Bioscience and Biotechnology, Fuzhou University, Fuzhou 350108, China

<sup>d</sup> Institute of Oil Crop, Chinese Academy of Agricultural Sciences, Wuhan 430062, China

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### ABSTRACT

The physicochemical properties of native and germinated oat seeds cultivated in China and their correlations were investigated. The growth curve during germination of oat seeds was described. The malt yield was 84% at the end of malting. The losses by removing of shoots and rootlets were the major cause of the total dry matter losses in the last 24 h of germination. With total starch enzymes activities increasing continuously, the starch content decreased considerably from 60% to 20%, and the reducing and soluble sugars contents increased. Oat seed kernel protein increased slightly, but the lysine content increased almost 30% at the end of germination. The phytic acid content declined from 0.35% to 0.11% during germination. There is a significant correlation among compositions including starch, protein, free and reducing sugars, free amino acid, and phytic acid. A close correlation also was found between the colour of malt flour dried at 50 °C and the length of shoots and rootlets. The results suggest that oats grown in China are a good food material and that germination can improve their nutritional properties.

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### 1. Introduction

Oats are the fifth largest cereal crop in the world. China, as one of the cradle lands for oats, produces about 700 thousand tons per year (FAO, 2005). However, the oat consumption in China is very low so far. Besides consumer's habits, one critical aspect is a lack of detailed information on the dietary advantages of oats grown in China.

Many studies carried out in the world have shown that oats are an all-value cereal with high quality protein and fatty acids (Peterson, 2002; Zarkadas, Hulan, & Proudfoot, 1982; Zhou, Holmes, Glennie, & Ronards, 1998). Unlike other cereal proteins, oat seed protein has poor solubility at neutral and slightly acidic pH (Ma, 1983). The properties of oat protein concentrate and isolate have been improved through modification by chemical and exogenous enzymes (Guan, Yao, Chen, Shan, & Zhang, 2006; Ma & Khanzada, 1987; Ma & Wood, 1987), but these methods are high cost, require complex treatments and often result in bitterness in the final product. In recent years, Oats have attracted research and commercial attention mainly due to their high contents of  $\beta$ -glucan and phenolic compounds with high antioxidant activities

(Gray et al., 2000; Liu, Zubik, Collins, Marko, & Meydari, 2004; Malkki, Myllymaki, Teinila, & Koponen, 2004; Peterson, Emmons, & Hinns, 2001).

The process of cereal seed germination has been used for centuries for the purpose of softening the kernel structure, improving its nutritional value, and reducing anti-nutritional effects. In fact, the germination process is also one of methods used to improve the functionality of oat seed protein (Kaukovirta-Norja, Wilhemson, & Poutanen, 2004). During germination, oat seed proteins were degraded to increase the soluble protein content (Wu, 1983), and the oat protein properties were improved without any chemical modifications being required. After germination and subsequent drying, oat malts can be used as good replacements for barley malt in the brewing industry, and also can be used as ingredients in some convenience foods (Taylor, Humphrey, and Smith, 1998). The chemical composition of malted oat seeds depends on the conditions and the level of germination (Wilhemson et al., 2001), and its sensory profile depends on the processing parameters of subsequent drying such as drying speed and temperature profile (Heiniö, Oksman-Caldentey, Latva-Kala, Lehtinen, and Poutanen, 2001), as well as drying methods. Therefore, the level of germination and drying will affect oat product quality and commercial utilization.

The aim of this study was to describe the growth curve of oat malt, to determine the nutrient and anti-nutrient contents of germinated oat seeds from the Northwest of China, and to discover

Abbreviations: LS, length of shoot; LR, length of rootlet; FAA, free amino acid; RS, reducing sugar; FS, free sugar; TPC, total phenolic content; PA, phytic acid.

\* Corresponding author. Tel.: +86 27 87283201; fax: +86 27 87282966.

E-mail address: [bijunxie@sina.com](mailto:bijunxie@sina.com) (B. Xie).

any correlations between colour parameters of the malted oat flour and the length of the shoots and rootlets generated and the relations among major compositions during the germination process.

## 2. Materials and methods

### 2.1. Materials

Oat seeds, cultivar *Avena nuda* L., were harvested from Shaanxi Province, the Northwest of China in 2006. After removing small and broken kernels, oat seeds were collected and stored at  $-20^{\circ}\text{C}$  until further processing. The germination activity of the oat seeds was tested to exceed 99%. Amino acid standards were purchased from Sigma–Aldrich Company (USA). All chemicals used in the present study were analytical grade reagents.

### 2.2. Malting procedures

The malting procedure was based on [Beta's method \(1995\)](#) with some modifications. Oat seed surfaces were sterilized by soaking in 2.0% aqueous sodium hypochlorite for 15 min at room temperature, and then rinsed with tap water for at least 20 min. Before germination, the oat seeds were soaked in distilled water at  $16^{\circ}\text{C}$  in the dark for 24 h. After rinsing with distilled water, the steeped oat seeds were spread on wet cellulose pads and left to sprout at  $16^{\circ}\text{C}$  in a dark incubator for 0, 24, 48, 72, 96, 124, or 144 h, respectively.

The collected oat seeds were divided into two groups, the first group was used for malt characterization, and the other was dried to constant weight in a  $50^{\circ}\text{C}$  oven for 24 h. The rootlets and shoots on the grains were manually separated from the kernels. The raw oat seeds and the polished malts were ground to pass through an 80 mesh sieve and stored at  $-20^{\circ}\text{C}$  prior to further chemical composition analyses.

### 2.3. Malt characterization methods

Thirty malting oat seeds were traced by ruler for determination of the length of their rootlets and shoots every 24 h.

The raw weight of triplicate samples (100 seeds each) was weighed accurately, and they were steeped and germinated as the above mentioned method. Then they were transferred into a hot-air-drying oven at  $105^{\circ}\text{C}$  for determination of dry matter weight, and the malt yield was calculated as: % malt yield = (weight of dry malt/weight of dry raw grain)  $\times$  100. After that, the rootlet and shoot were carefully polished off and accurately weighed again. The difference between the dry matter weight of the raw oat seeds and the germinated or steeped oat seeds was considered as losses of dry matter.

Dry matter losses during malting were attributed to two factors: losses by respiration and losses by rootlets and shoots removal ([Novellie, 1962](#)).

### 2.4. Determination of protein content and amino acid analysis

Total nitrogen was determined by the micro-Kjeldahl method. The nitrogen to protein conversion factor of 6.25 was used to calculate protein content.

Free amino acids were analyzed by the following procedures: 100 mg homogenous dry oat seed powder was extracted with 5 ml of 10% (w/v) acetic acid solution for 1 h at room temperature; After centrifugation at 10,000g for 10 min, 1 ml of supernatant was diluted with 200 mM sodium acetate buffer (pH 5.4) to a final volume of 50 ml. The solution was analyzed for free amino acids by the Ninhydrin Colorimetric method ([Wang, 1998](#)). The absorbance

of the solution was measured at 580 nm using a spectrophotometer (755B, Shanghai Precision & Scientific Co. Ltd., China). The amino nitrogen content was calculated according to the standard curve using L-Leucine as a standard.

To determine the amino acid profile the samples were hydrolyzed with 6 M HCl for 24 h at  $110^{\circ}\text{C}$  in a sealed tube. The amino acid composition of hydrolyzate was determined with an automatic amino acid analyzer (Agilent 1100, USA) ([Brinegar and Peterson, 1982](#)). Tryptophan was not determined.

### 2.5. Determination of starch, free and reducing sugar contents, and amylase activity

To determine the starch, free and reducing sugar contents, the dry sample (200 mg) was repeatedly extracted four times with 20 ml 80% ethanol at room temperature and centrifuged at 10,000g for 20 min, the supernatant were collected and evaporated at  $50^{\circ}\text{C}$  on vacuum, the residue was dissolved to 20 ml distilled water with 0.5 g poly(vinylpyrrolidone), then the mixture was centrifuged at 10,000g for 10 min. The supernatant was made up to a known volume and was assayed for total free sugars and reducing sugars by the phenol–sulphuric acid method ([Taylor, 1995](#)) and the dinitrosalicylic acid method ([Ghose, 1987](#)), respectively. The alcohol-insoluble residue was dissolved with 52% perchloric acid. The sugar content of the filtered perchloric acid extract was estimated by the phenol–sulphuric acid method ([Taylor, 1995](#)), and multiplied by 0.9 to the approximate the starch content.

To assay amylase activity, 1 g sample was extracted using 25 ml citrate buffer (0.1 M, pH 5.6) at the room temperature for 20 min, and then the slurry was centrifuged at 3000g for 10 min. The extraction was repeated three times. The supernatant was collected and made up to 100 ml with citrate buffer for enzymes assay. The total activity of enzymes solution was assayed directly at  $40^{\circ}\text{C}$  by 1% starch solution. Alpha amylase activity was also measured by 1% starch solution except that beta amylase of enzymes solution was inactivated at  $70^{\circ}\text{C}$  water bath for 15 min ([Taylor, 1993](#)) and then cooled to  $40^{\circ}\text{C}$ . The ability of degrading soluble starch and produce 1 mg maltose per minute was defined as one unit of amylase activity. The difference between total and alpha amylase activity was regarded as beta amylase activity ([Wang, 2006](#)).

### 2.6. Evaluation of phytic acid in oats

The phytic acid contents of the samples were determined by the method of [Miller, Youngs, and Oplinger \(1980\)](#).

### 2.7. Determination of total phenolic compounds

Total phenols were extracted from 0.2 g samples with 25 ml of 1% HCl in methanol for 2 h at room temperature according [Yu's \(2004\)](#) method with some modifications. The methanol was evaporated on vacuum at  $50^{\circ}\text{C}$ , and the residue was dissolved with distilled water and centrifuged at 10,000g for 10 min. The supernatant was used for determination of total phenolic compounds. According to the procedure of [Folin–Ciocalteu's method \(Swain & Hillis, 1959\)](#) with some modifications, 12 ml  $\text{dH}_2\text{O}$ , 1.0 ml of Folin–Ciocalteu's reagent and 3.0 ml of 20% sodium carbonate solution were mixed with 0.2 ml of extract (diluting if necessary), and the final volume was made up to 20 ml with distilled water. The reaction mixture was vortexed for 10 s, and stood at room temperature for 30 min, the absorbance was measured at 765 nm using a spectrophotometer (755B, Shanghai Precision & Scientific Co. Ltd., China). According to the standard curve which was obtained with gallic acid, the phenol content of the sample was detected. The

total amount of phenolic compounds is expressed in mg gallic acid equivalent per one gram dry weight of oat seed flour.

### 2.8. Colour analysis

Sample slice ( $\varnothing 15 \times 5$  mm) was made manually using a tablet pressing machine under 27 MPa pressure. The oat flour colour was measured using the CIE (Commission Internationale de l'Eclairage, 1976)  $L^*$ ,  $a^*$ , and  $b^*$  colour system.  $L^*$  is rightness,  $a^*$  is redness, and  $b^*$  is yellowness. In addition, the total colour difference ( $\Delta E$ ) of oat seed flour caused by germination and drying at 50 °C for 24 h was calculated as following equation:

$$\Delta E = \sqrt{(L_{sample}^* - L_{ref}^*)^2 + (a_{sample}^* - a_{ref}^*)^2 + (b_{sample}^* - b_{ref}^*)^2}$$

The raw oat seed flour was used as a reference (called "ref"). Colour measurements were performed in triplicate with a colourimeter (Hunter Lab Ultrascan XE Version 2.4 Software).

### 2.9. Statistical analysis

The colour determination was repeated for 10 times and other analyses were carried out in triplicate. All results were reported as means  $\pm$  standard deviation. The data were subjected to correlation analysis to identify relationships among physicochemical properties using SPSS software (version 16.0, The Predictive Analytics Company, Chicago, USA).

## 3. Results and discussion

### 3.1. Effects of germination on dry weight and length of oat seeds

Fig. 1 shows the changes in length and dry weight of oat shoots and roots during the germination process. Although oat rootlets were always longer than the shoots during the malting period, the dry weight percentage of oat rootlets was lower than that of the shoots. It was observed that the total rootlet and shoot dry weight increased to above 35% after germination for 144 h, the dry weight percentage of the oat kernel correspondingly decreased to about 64% (Fig. 1).

The malt yield and dry matter losses of oat seeds during germination at 16 °C in the dark are showed in Fig. 2. About 84% of the malts yields were obtained after germination for 144 h, in agree-

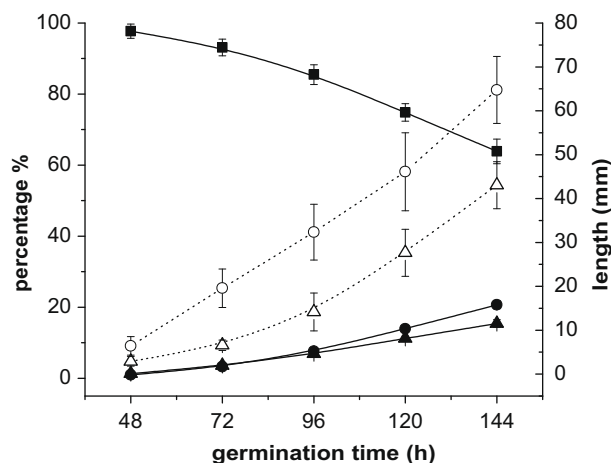


Fig. 1. Changes of dry weight of malt kernel, shoot and rootlet and length changes of shoot and rootlet during oat germination. The data were reported as means  $\pm$  standard deviation. ■, weight of kernel; ●, weight of shoot; ▲, weight of rootlet; ○, length of rootlet; △, length of shoot.

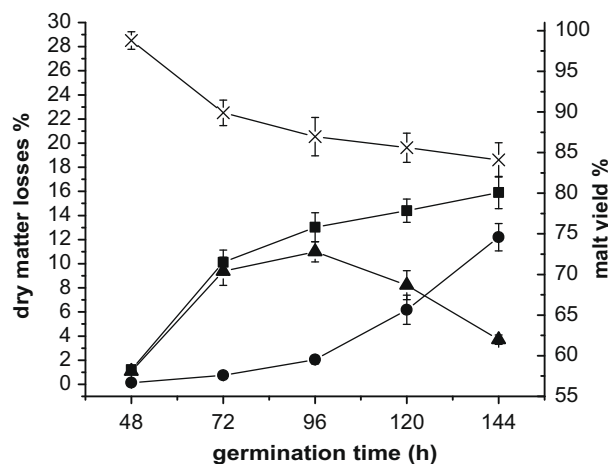


Fig. 2. Dry matter losses and malt yield of Shaanxi oat grains during germination. The data were reported as means  $\pm$  standard deviation. ×, malt yield; ■, total dry matter losses; ●, losses for removed root and shoot; ▲, respiration losses.

ment with the results of Wu (1983). The dry matter losses increased with the increase of germination, and reached about 15.9% at 144 h. The fastest respiration losses rate appeared from 48 to 72 h, and the respiration losses increased from 1.1% to 9.4%. Although the respiration losses continuously increased from 72 to 96 h, the increase rate was lower than the previous 24 h. After 96 h germination, the dry matter losses due to respiration significantly decreased. During the last 48 h of germination, the respiration losses accounted for 57% of dry matter losses, which was similar to that of sorghum (61%) germinated at 28 °C for 5 days (Beta, Rooney, & Waniska, 1995). These results suggested that in the first half course of germination, life activity of malting oats was very vigorous, but metabolism of storage materials mainly presented energy release instead of establishing new organs. On the contrary, in the second half course of germination, the dry matter losses by removal of rootlets and shoots became more and more important and up to 12.2% at 144 h.

### 3.2. Effects of germination on the changes in protein and amino acid

The protein concentration of oat seeds slowly increased from 18.98% to 22.02% due to the germination process (Table 1). The increase of these proteins might be attributed to the dry weight losses through respiration during malting. Thus, the germinated oat seeds on a unit weight basis would contain more seeds and therefore more nitrogen than the ungerminated material. The results are in agreement with Dalby and Tsai (1976). Free amino acid contents increased continuously after steeped and reached 0.37%

Table 1  
Chemical changes (% dry basis) of Shaanxi oat grain during germination.<sup>a</sup>

Samples	Protein	Starch	Free sugar	TPC <sup>b</sup>	PA <sup>c</sup>
Raw	18.98 $\pm$ 0.19	59.80 $\pm$ 3.05	5.23 $\pm$ 0.39	0.20 $\pm$ 0.01	0.35 $\pm$ 0.02
Steeped	19.76 $\pm$ 0.11	56.00 $\pm$ 2.09	4.06 $\pm$ 0.28	0.19 $\pm$ 0.01	0.32 $\pm$ 0.01
Germination					
24 h	20.73 $\pm$ 0.11	52.89 $\pm$ 0.54	4.95 $\pm$ 0.02	0.25 $\pm$ 0.03	0.28 $\pm$ 0.03
48 h	21.05 $\pm$ 0.17	48.89 $\pm$ 1.48	7.94 $\pm$ 0.59	0.27 $\pm$ 0.03	0.26 $\pm$ 0.01
72 h	21.29 $\pm$ 0.08	37.46 $\pm$ 0.55	9.73 $\pm$ 0.41	0.42 $\pm$ 0.11	0.24 $\pm$ 0.02
96 h	21.72 $\pm$ 0.13	33.55 $\pm$ 0.64	20.64 $\pm$ 0.83	0.71 $\pm$ 0.08	0.17 $\pm$ 0.01
120 h	21.84 $\pm$ 0.11	22.46 $\pm$ 2.71	25.84 $\pm$ 0.37	0.90 $\pm$ 0.15	0.16 $\pm$ 0.03
144 h	22.02 $\pm$ 0.33	20.87 $\pm$ 0.48	28.11 $\pm$ 1.88	0.91 $\pm$ 0.13	0.11 $\pm$ 0.01

<sup>a</sup> The data were reported as means  $\pm$  standard deviation,  $n = 3$ .

<sup>b</sup> TPC – total polyphenol content (gallic acid equivalent).

<sup>c</sup> PA – phytic acid content.

by the end of germination, which was almost 10-fold as compared with the raw oats (Table 2). The reason is that the proteins in the raw oat seeds were degraded and converted into a soluble state after germination. It was a remarkable fact that free amino acids content decreased during steeping, mostly during the initial germination stage. The speed of utilizing the amino acid to synthesize the bioenzymes was faster than the proteins were being degraded into amino acids.

Table 4 shows the amino acid profile of the germinated and raw oat seeds. The threonine content of the germinated oat seeds increased after 72 h and subsequently increased 30% until 144 h. The change of valine was similar with threonine except the amplitude was smaller. The contents of isoleucine presented continuously increasing since germinated for 24 h, and reached 2-fold of raw oats at the end. The lysine content of germinated oats was always higher than that of raw oats, and the highest one was 1.22 g/100 g dry weight when germinated for 144 h. Hamad and Fields (1979) reported an increase in available lysine in germinated oat seeds based on *Terahymena pyriformis* W. assay. Dalby and Tsai (1976) found an increase in lysine content expressed as percent of dry weight of oat seeds during germination. Wu (1983) observed increases in lysine content of more than 10%.

### 3.3. Effects of germination on the changes of reducing and free sugar, starch and amylase

Dinitrosalicylic acid can react with the reducing materials especially reducing phenolic compounds in oat seeds and produce dark red products. Before and after removal of phenolic compounds, the error in sugar concentration was more than 50%. The highest level of phenolic compound reduction in our study was up to 0.91% (Table 1). Therefore, poly(vinylpyrrolidone) was added after

**Table 4**

Changes of amino acid compositions of Shaanxi oat during germination.<sup>a</sup>

Amino acid	Samples			
	Raw	Germinated		
		24 h	72 h	144 h
Aspartic acid	0.55 ± 0.02	0.37 ± 0.01	0.36 ± 0.01	0.86 ± 0.02
Glutamic acid	3.36 ± 0.06	2.87 ± 0.05	2.86 ± 0.06	2.64 ± 0.03
Serine	0.76 ± 0.03	0.74 ± 0.02	0.77 ± 0.03	0.73 ± 0.02
Glycine	0.56 ± 0.03	0.45 ± 0.02	0.39 ± 0.02	0.40 ± 0.02
Histadine	0.51 ± 0.02	0.56 ± 0.02	0.72 ± 0.03	0.92 ± 0.03
Arginine	0.68 ± 0.01	0.66 ± 0.01	0.49 ± 0.01	0.77 ± 0.01
Threonine	0.52 ± 0.03	0.49 ± 0.03	0.57 ± 0.02	0.70 ± 0.02
Alanine	1.03 ± 0.04	1.00 ± 0.03	1.18 ± 0.02	0.84 ± 0.03
Proline	1.16 ± 0.06	1.30 ± 0.05	1.33 ± 0.04	1.13 ± 0.04
Tyrosine	0.34 ± 0.01	0.31 ± 0.01	0.37 ± 0.01	0.47 ± 0.01
Valine	0.53 ± 0.02	0.40 ± 0.01	0.61 ± 0.02	0.65 ± 0.01
Methionine	0.14 ± 0.01	0.11 ± 0.02	0.07 ± 0.01	0.20 ± 0.01
Cystine	0.09 ± 0.01	0.09 ± 0.01	0.04 ± 0.00	0.30 ± 0.02
Isoleucine	0.38 ± 0.01	0.38 ± 0.02	0.59 ± 0.01	0.78 ± 0.01
Leucine	1.07 ± 0.02	0.71 ± 0.01	1.15 ± 0.02	1.44 ± 0.01
Phenylalanine	1.17 ± 0.03	0.99 ± 0.03	0.67 ± 0.01	1.48 ± 0.03
Lysine	0.90 ± 0.02	1.15 ± 0.03	1.02 ± 0.03	1.22 ± 0.03

<sup>a</sup> All values are expressed as gram per 100 g dry weight, the data were reported as means ± standard deviation, *n* = 3.

extracting the sugars to remove phenolic components when determining the content of reducing and free sugars.

According to Wood's study (1991), starch is the main chemical compound in oat seeds, about 60% of the dry weight. Table 1 showed that the oat starch content decreased significantly from 60% to nearly 20%. A decrease in the starch content was observed after 24 h germination, compared with raw oat seeds, but a greater reduction in starch content was observed after 48 h (Table 1). It could be explained that total amylase activity increased rapidly

**Table 2**

Colour parameters  $L^*$  (brightness),  $a^*$  (redness),  $b^*$  (yellowness), Total colour difference ( $\Delta E$ ), and levels of reducing sugars and free amino acids of flour of raw and germinated oats.<sup>a</sup>

Sample	$L^*$ ( <i>n</i> = 10)	$a^*$ ( <i>n</i> = 10)	$b^*$ ( <i>n</i> = 10)	$\Delta E$ ( <i>n</i> = 10)	FAA% ( <i>n</i> = 3)	Reducing sugar% ( <i>n</i> = 3)
Raw	80.01 ± 0.11	2.11 ± 0.10	9.15 ± 0.11		0.03 ± 0.01	1.11 ± 0.08
Steeped	78.07 ± 0.04	2.70 ± 0.03	9.64 ± 0.06	2.09 ± 0.16	0.01 ± 0.00	1.07 ± 0.12
<i>Germinated</i>						
24 h	80.36 ± 0.02	2.37 ± 0.02	9.76 ± 0.04	0.76 ± 0.04	0.12 ± 0.03	1.28 ± 0.05
48 h	75.84 ± 0.04	3.45 ± 0.03	14.32 ± 0.03	6.77 ± 0.17	0.16 ± 0.04	1.02 ± 0.02
72 h	72.23 ± 0.02	4.26 ± 0.03	13.72 ± 0.05	9.27 ± 0.19	0.30 ± 0.00	2.91 ± 0.08
96 h	62.04 ± 0.02	7.15 ± 0.02	20.82 ± 0.09	22.01 ± 0.18	0.36 ± 0.01	10.98 ± 0.12
120 h	62.23 ± 0.03	7.76 ± 0.04	21.86 ± 0.07	22.57 ± 0.19	0.36 ± 0.01	11.49 ± 0.14
144 h	54.77 ± 1.04	8.80 ± 0.16	21.75 ± 0.11	29.94 ± 0.15	0.37 ± 0.02	14.47 ± 0.37

<sup>a</sup> The data were reported as means ± standard deviation, *n* = sample number.

**Table 3**

Correlation analysis between physicochemical properties of raw and germinated Shaanxi oat.<sup>a</sup>

	LS	LR	$L^*$	$a^*$	$b^*$	Protein	PA	FAA	Starch	FS
LR	0.958**									
$L^*$	-0.743**	-0.828**								
$a^*$	0.787**	0.855**	-0.993**							
$b^*$	0.803**	0.878**	-0.956**	0.977**						
Protein	0.082	0.108	0.043	0.091	0.200					
PA	-0.083	0.001	-0.174	-0.006	-0.155	-0.851**				
FAA	0.049	0.049	0.169	0.022	0.162	0.890**	-0.938**			
Starch	-0.133	-0.048	-0.168	-0.017	-0.150	-0.851**	0.975**	-0.941**		
FS	0.089	0.014	0.172	0.005	0.128	0.679**	-0.944**	0.881**	-0.925**	
RS	0.048	-0.002	0.183	-0.006	0.122	0.645**	-0.933**	0.846**	-0.903**	0.983**

LS – length of shoot; LR – length of rootlet; FAA – free amino acid; FS – free sugar; RS – reducing sugar; TPC – total polyphenol content using gallic acid as a standard; PA – phytic acid content.

<sup>a</sup> Pearson correlation coefficients.

in this period and reached to six times as much as that in raw oat seeds. The  $\alpha$ -amylase activity reached to the level of 80 mg/g min, which was twenty times as much as the initial raw stage (Fig. 3). Although change multiple of activity was lower, the absolute activity of  $\beta$ -amylase was always higher than  $\alpha$ -amylase during the total period of germination. It fluctuated during germination with a climax of 228.9 mg/g min at 96 h, which was more than 4-fold of raw oats.

Most starch is undergoes modification during malting, as it is converted to maltose and other sugars. The free sugar contents increased about 3–4-folds during malting (Table 1), except sugars content of soaked seeds was lower than raw grains. The presence of fermentable sugars in the malt is important for its utilization in the brewing industry.

The starch and free sugar contents of oats steeped and oats germinated for 24 h were both lower than raw seeds (Table 1). The reason is that in germinating seeds anoxia occurs after imbibition and before rupture of the seed coat (Aldasoro & Nicolas, 1980), and maybe in this period the speed of consumption of free sugars that degraded from starch in anaerobic metabolism was faster than subsequent aerobic metabolism.

#### 3.4. Effects of germination on the changes of phytate and total phenolic content

The phytate content was determined to be 0.35% in native Shaanxi oat seeds. The results differ from those of Miller and coworkers study results (1980). Miller et al. (1980) considered that the effects of environment and cultivar on oat phytic acid concentrations were not significant, but their deduction was rooted in the detection of only four oat cultivars. The phytate content decreased from 0.35% to 0.11% during germination. The decrease is attributed to an increase in phytase activity as germination progressed (Larsson & Sandberg, 1992). The phytate contents could be reduced 15–35% during even a short 3 day germination process (Kaukovirta-Norja, Wilhemson, and Poutanen, 2004).

Phenolic compounds present in oats would contribute to functional and nutritional properties of the grain. The changes of total phenolic content during oats germination are shown in Table 1. More than a 4-fold increase in phenolic compound contents was found in the oat seeds after germination for 120 h, and up to 0.90% in dry weight (Table 1). This could also be attributed to the better extractability of phenolic compounds from the kernel struc-

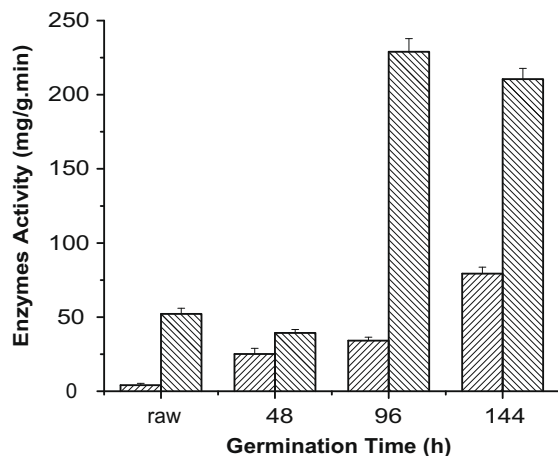


Fig. 3. Changes of amylase activities in Shaanxi oat kernel during germination. The data were reported as means  $\pm$  standard deviation.  $\alpha$ -amylase;  $\beta$ -amylase.

tures after germination. A similar result was observed by Kaukovirta-Norja et al. (2004). Avenanthramides are a group of phenolic compounds with high bioactivities such as anti-inflammatory, antiatherogenic and antioxidants, which exist exclusively in oat seeds (Dimberg, Theander, and Lingnert, 1993). The processes of steeping and germination resulted in increased levels of avenanthramides (Skoglund, 2008).

#### 3.5. Effects of germination on the changes of colour of oat malt flour

Two phenomena were observed when the colours of germinated and dried oats flour were compared with raw oats flour. The first one was that the brightness ( $L^*$ ) of germinated oats decreased except those germinated for 24 h; meanwhile, both of their redness ( $a^*$ ) and yellowness ( $b^*$ ) increased with the increase of germination time (Table 2). The reason is that with germination degree deepening, more starch and protein hydrolysates were formed, and subsequently Maillard reaction between them had happened during drying treatment, resulting in the oats with the deepest degree of germination present the biggest  $\Delta E$  as compared to raw oat seeds. This phenomenon was similar to that which was observed by Lamberts, Brijs, Mohamed, Verhelst, and Delcour (2006) in parboiled rice. The second phenomenon was that the  $\Delta E$  was higher during the soaking period than during the first 24 h germination (Table 2). The major reason is that the pigments are not uniformly distributed in oat seeds. The bran contains much higher levels of yellow and red pigment than does the endosperm. Therefore, the migration of bran pigments into the soaking water and diffusion of bran pigments into the endosperm during soaking and/or heating treatments might impact the brown oat colour.

#### 3.6. Correlation analysis of physicochemical properties of raw and germinated oats

Table 3 presents the relation between physicochemical properties of raw and germinated Shaanxi oats. We observed that reducing and free sugars had the closest relation among compositions, and the correlation coefficient is 0.983. The starch content significantly correlated negatively with two sugars during oats germination. At the same time, the protein content of oats correlated negatively with phytic acid and starch content, and correlated positively with free amino acids, free and reducing sugars. Two conclusions can be gained from those close relations. Firstly, any composition does not change alone, it would affect each other during oat germination. Secondly, the carbohydrates supply main energy for oats growing, meanwhile, proteins are degraded into amino acids that are easy to absorb.

Furthermore, an interesting phenomenon was observed. The brightness of the malted oat flour correlated negatively with the length of the shoot and rootlet, but the yellowness of the flour correlated positively with them (Table 3). This suggests that the length of the malt shoot and root can be considered as the indicators for the colour of oat seeds treated by germination, drying and milling.

## 4. Conclusions

The changes in the physicochemical properties of oat seeds from the Northwest of China during germination using raw grains as controls were investigated. The raw oat seeds have especially low phytic acid concentration compared to other references' results. The experiments demonstrated that the removal of the shoot and rootlet had a great influence on the apparent losses in dry matter of oat seeds after the first five-day's germination, and the colour of malted oat powder deepened after drying. Moreover,

the length of the shoot and rootlet can be considered as the indicators of the development of colour in malted and dried oat seeds. Major nutrients were greatly changed during germination. For example the contents of protein, starch and phytate decreased significantly, the free amino acids, reducing sugars, free sugars and phenolic compounds increased to a larger extent. A significant correlation among them was found. Chinese oat seeds are good sources for beneficial nutrients. Germination processes can improve raw oats nutritional value and digestibility, and make oat seeds into a better food material than the raw grain.

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