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Food Chemistry

Food Chemistry 105 (2007) 317–324

www.elsevier.com/locate/foodchem

Analytical, Nutritional and Clinical Methods

Analysis of free amino acids in cereal products

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Received 30 August 2006; received in revised form 20 October 2006; accepted 20 November 2006

Abstract

Free amino acids were extracted from cereal products using 50% ethanol to prevent solubilization of polysaccharides and other viscous polymers and to avoid starch gelatinization. The extracts were analyzed by GC after ion-exchange solid phase extraction and chloroformate derivatization using Ez-Faast technology (Phenomenex). Free amino acids in cereal products could be analyzed within 1 h of extraction and determination, with good separation between peaks and repeatable retention times. Relative correction factor for each amino acid was established. The matrix did not affect the results and the method was repeatable for most of the amino acids (coefficient of variation was in the order of 10%). Different fractions and products of wheat, rye, oats and barely were analyzed. The bran contained more free amino acids than did the other analysed fractions of cereals. Fermentation seemed to consume free asparagine and aspartic acid and to use or release other amino acids.

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Keywords: Free amino acids analysis; Cereal fractions; Cereal products; Fermentation; Baking; Gas chromatography

1. Introduction

Cereals and cereal products contain variable amounts of free amino acids, depending largely on the species, cultivar and growing conditions [\(Abdel-Aal & Hucl, 2002\)](#page-7-0). Amino acids serve as important substrates for dough microorganisms and are important from the sensory point of view as they contribute to bread flavour [\(Benedito De Barber, Pri](#page-7-0)[eto, & Collar, 1989; Collar, Mascarods, & Benedito De](#page-7-0) [Barber, 1992\)](#page-7-0). Free amino acids in raw materials of heattreated foods take part in the Maillard reaction, which is important for cereal food quality. Recently, acrylamide was proven to be formed by a reaction between free Asn and reducing sugars [\(Mottram, Wedzicha, & Dodson,](#page-7-0) [2002; Stadler et al., 2002; Taeymans et al., 2004](#page-7-0)). In a recent study, it was shown that whole grain wheat flour contained 0.5 g/kg of Asn, while whole grain rye contained 1.1 g/kg (Fredriksson, Tallving, Rosen, $\&$ Åman, 2004). The study also showed that sifted fractions of the flours

contained the least amount of Asn, which was mainly concentrated in the germ and the bran.

Free amino acids can be analyzed by both liquid and gas chromatography. Some of the liquid chromatography methods, e.g. the standard method using the amino acid analyzer, have drawbacks, such as the lengthy cleanup and preparation steps. Gas chromatography is also used after derivatization of both functional groups in the amino acid to suitable volatile derivatives [\(Davies, 2002; Molnar-Perl, 2000](#page-7-0)). For this purpose, Husêk (1998) recommended derivatization of amino acids with propyl chloroformate (Husêk, 1998; Husêk [& Sweeley, 1991\)](#page-7-0). Phenomenex ([Phenomenex, 2001](#page-7-0)) released an analytical kit based on this method for analysing a range of free amino acids in physiological fluids. This method involves a simple solid phase extraction (SPE) step, followed by a rapid derivatization reaction and analysis by gas chromatography (GC) with internal standard ([Farkas](#page-7-0) [& Toulouee, 2003](#page-7-0)). This method has recently been applied to the analysis of amino acids in potato, wheat and rye products but no validation of the method for these type of matrixes has been reported [\(Elmore, Koutsidis, Dodson,](#page-7-0) [Mottram, & Wedzicha, 2005a](#page-7-0)).

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^{0308-8146/\$ -} see front matter © 2006 Elsevier Ltd. All rights reserved. doi:10.1016/j.foodchem.2006.11.044

The aim of this study was to develop an extraction procedure for cereal products that gives stable extracts that can readily be used at the SPE step. The Phenomenex method was tested for validity with respect to repeatability and recovery of standards added to different cereal matrices. The method was used to analyze the free amino acid contents in cereals and cereal products and to test the effect of fermentation on free amino acid content.

2. Materials and methods

2.1. Cereal materials

Flour samples of rye bran, sifted rye flour, whole grain wheat, wheat bran, sifted wheat flour, low fibre oat flour, oat bran and oat grouts were supplied by Lantmännen (Stockholm, Sweden) and whole grain rye was from Wasabröd AB (Filipstad, Sweden). Soft wheat bread was baked from sifted wheat flour using dry yeast (Saccharomyces cerevisiae) Kronjäst original (Jästbolaget AB, Sweden) according to the recipe described by Surdyk, Rosén, Andersson, and Aman (2004) and dough from the same baking batches was also used in the analysis. Whole grain rye crisp bread was baked using the same yeast according to the recipe described by [Mustafa, Andersson, Rosen,](#page-7-0) Kamal-Eldin, and \AA man (2005).

2.2. Chemicals and reagents

Standard solutions of the amino acids Ala, Asn, Asp, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val, in addition to the eluting and derivatization agents, were all provided in an inclusive kit (EZ-Faast GC-FID for amino acid analysis) purchased from Phenomenex (Torrance, CA, USA). The amino acids Asn, Gly, Val, Ser, Ala, Asp, Trp and Glu, used for spiking, were purchased from Pierce (Amino Acid Standard kit, St Louis, Il, USA). Additionally, Trp (98% by TLC) and the internal standard l-norvaline were purchased from Sigma Chemicals Co. (St Louis, MO, USA). Ethanol was purchased from Solveco Chemicals AB (Stockholm, Sweden).

2.3. Extraction and derivatization

All samples were milled using an ultra centrifuge mill type ZM1 with a 0.5 mm ring sieve (Retsch, Hann, Germany). Fermented dough and soft wheat bread were freeze-dried before milling. Samples were weighed in test tubes with screw caps, 0.2 g for whole grain and bran samples and 0.5 g for sifted flours and breads. Samples were first subjected to alcohol extraction. Ethanol (50% at 50 °C) and internal standard l-norvaline (70 mg/ml water) were added in volumes of 14 and 1 ml, respectively. Samples were mixed in a rotatory mixer at 50° C for 20 min inside an incubator. After mixing, samples were subjected to centrifugation for 20 min at 1350g. An aliquot of $500 \mu l$ of the supernatant was subjected to solid phase extraction (SPE) and derivatization steps using the EZ-Faast technology and kit [\(Phenomenex, 2001\)](#page-7-0).

2.4. Gas chromatography analysis

The derivatized amino acids were analyzed using a GC-FID instrument (Hewlett Packard; HP, 5890 Series II) equipped with an auto-sampler (Avondale, PA, USA). Aliquots of the derivatized amino acids (2 µ) were injected at 1:15 split ratio at 250 °C into a Zebron column $(ZB -$ AAA, 10 m and 0.25 mm in diameter) programmed from 110–320 °C at 32 °C/min. Helium was used as a carrier gas at 60 kPa and nitrogen was used as a make-up gas. The detector temperature was 320° C.

2.5. Calibration

Six different standard solutions with different concentrations of both the free amino acid standards and the internal standard were prepared. Concentrations ranged from 25 to 200 nmol/500 µl. Samples were analyzed in triplicate. Relative correction factors (RCF) were obtained as $(A_{IS} \times C_{aa})/A$ $(A_{aa} \times C_{IS})$ where IS = internal standard, aa = amino acid, $C =$ concentration, $A =$ peak area.

2.6. Analytical method validation

Within a day and day-to-day variations were determined using samples of rye bran, whole grain rye, sifted rye flour, rye crisp bread, wheat bran, sifted wheat flour and wheat bread run in triplicates for three different days. Relative standard deviation, expressed as coefficient of variation (CV), was used as a measure of precision. To check matrix

Table 1

Relative retention times (RRT) and relative correction factor (RCF) for individual amino acids

Amino acid	RRT ^a	$RCFa$ (CV $n = 6$)		
Ala	0.80	1.27(8.8)		
Gly	0.85	1.38(8.2)		
Val	0.94	1.05(7.4)		
Ile	1.04	0.85(7.7)		
Leu	1.06	0.97(7.2)		
Thr	1.16	1.49(12.0)		
Ser	1.18	1.87(11.6)		
Pro	1.22	1.07(7.0)		
Asn	1.26	1.63(11.3)		
Asp	1.50	1.17(10.3)		
Met	1.52	0.94(8.9)		
Glu	1.66	2.23(10.5)		
Phe	1.68	0.62(8.6)		
Gln	1.95	2.79(8.8)		
Lys	2.23	0.72(12.5)		
His	2.32	0.98(23.2)		
Tyr	2.44	0.58(8.7)		
Trp	2.59	0.60(11.8)		

Calibration range is 25–200 nmol/500 µl for individual amino acids.
^a RRT and RCF are relative to internal standard IS (l-norvaline).

Fig. 1. Chromatogram showing the amino acid profiles in sifted wheat and whole grain flour (IS = internal standard:norvaline).

effect on recovery, four different samples (rye bran, sifted rye flour, rye crisp bread and soft wheat bread) and a blank sample were spiked with eight standard amino acids (Asn, Ala, Asp, Glu, Gly, Ser, Trp, Val). The spiking concentration used for each amino acid was an average of the amino acid concentration in the different samples. A blank sample was subjected to the same experimental conditions as the test samples.

2.7. Biochrom method

This is a cation-exchange chromatography method that analyzes amino acids using the amino acid analyzer ([Davies, 2002\)](#page-7-0). Samples were extracted using 5-sulphosalicylic acid with norleucine as internal standard. The method involves a post-column derivatization of the amino acids with ninhydrin that produces coloured amino acid derivatives that can be determined spectrophotometerically at 570 and 440 nm.

3. Results and discussion

3.1. General

In this study, we used alcohol extraction, followed by the EZ-Faast method, to analyze the levels of amino acids in cereals and cereal fractions. Amino acids were extracted from the cereal using 50% ethanol at $50\degree\text{C}$ in order to partially inactivate enzymes, and prevent the extraction of polysaccharides and other viscous polymers, in addition to avoiding starch gelatinization. The alcohol extraction gave a stable extract that was readily used for solid phase extraction (SPE) using an ion-exchange sorbent provided in the analysis kit.

The calibration solutions had six different concentrations for each of the amino acid standards and internal standard (l-norvaline). The chromatographic separation of peaks was good, which made the identification of the amino acids easy. All amino acids were separated within

Table 2 Sample weight and recovery of free amino acids (%) after spiking: means \pm SD ($n = 3$)^a

	Sample weight (mg)	Recovery percent							
		Asn	Glv	Val	Ser	Ala	Asp	Trp	Glu
Blank		96 ± 1	$97 + 0$	$112 + 0$	$108 + 0$	$95 + 0$	104 ± 1	75 ± 0	$111 + 1$
Rye bran	200	109 ± 12	96 ± 3	104 ± 1	105 ± 5	$94 + 1$	108 ± 2	77 ± 5	130 ± 133
Sifted rve flour	500	97 ± 4	$91 + 0$	100 ± 1	104 ± 1	94 ± 1	118 ± 3	82 ± 0	182 ± 1
Rye crisp bread	500	89 ± 2	93 ± 1	99 ± 0	98 ± 1	$93 + 3$	105 ± 2	78 ± 2	185 ± 18
Wheat bread	500	89 ± 5	$91 + 1$	98 ± 0	$96 + 4$	94 ± 0	105 ± 1	74 ± 1	178 ± 19

The amount used for spiking was the average content of each of free amino acids in the four samples.

A. Mustafa et al. | Food Chemistry 105 (2007) 317-324 A. Mustafa et al. / Food Chemistry 105 (2007) 317–324

Table 3

8 min of run-time with a good consistency in the retention time ($CV \le 0.2\%$). Relative correction factor (RCF) was calculated for each of the amino acids with reference to the internal standard; the calibration range used was 25–200 nmol/500 ll; standards were run in duplicates ([Table 1](#page-1-0)). The CV for the RCF of the individual amino acids was $\leq 12\%$, except for histidine, which had a higher CV value (ca. 23%), consistent with previous findings ([Elmore, Koutsidis, Dodson, Mottram, & Wedzicha,](#page-7-0) [2005b\)](#page-7-0).

The starting amount of the sample had to be adjusted to the concentration in the products. For whole grain flours and brans, 200 mg were used while, for sifted flour and products, 500 mg were used. The GC chromatograms, for both the raw material and the products, showed good separation and high consistency in the retention time for all the analyzed amino acids [\(Fig. 1](#page-2-0)).

Rye bran, sifted rye flour, rye crisp bread and wheat bread were used to test the recovery of amino acids [\(Table](#page-2-0) [2\)](#page-2-0). Eight amino acids (Asn, Gly, Val, Ser, Ala, Asp, Trp, and Glu) were chosen for the spiking experiment according to their structure and abundance in cereals. Most of the amino acids had a satisfactory recovery in the order of $100 \pm 10\%$, except for Trp and Glu. To further investigate this problem, a sample of sifted rye flour at different weights (100, 300 and 500 mg) was spiked with Glu and Trp. The recovery of Glu was found to increase with the amount of the sample, while Trp showed a low recovery (in the order of 75%), regardless of the sample amount. The blank sample had a recovery in the order of $100 \pm 5\%$ for all amino acids except Trp, which consistently showed about 75% recovery. This method gave satisfactory repeatability within a day and between days. The relative standard deviation was ca. 5% for the major amino acids and ca. 10% for the minor amino acids in cereal fractions.

When comparing the Ez-Faast method with Biochrom, both methods gave comparable results for most of the amino acids. However, some amino acids were better analyzed by one method than the other ([Table 3\)](#page-3-0). For example, Pro, Met and Trp are not reported by the Biochrom method used. On the other hand, Arg is not analyzable by the Ez-Faast method as has been reported in other studies as well [\(Elmore et al., 2005b; Lee & Harnly, 2005\)](#page-7-0) and results for Trp and Glu were unreliable, as discussed earlier. Ez-Faast gives low levels of some amino acids in rye crisp bread, including Asn; however, some of these amino acids were not given by the Biochrom method. On the other hand, His was found at higher concentration using the Biochrom method.

3.2. Amino acid content in cereal fractions and products

The contents of the individual amino acids varied, depending on the type of cereal and its fraction [\(Fig. 2](#page-5-0)). In wheat fractions, Ala, Ser, Asn, Asp and Glu were the major amino acids in the samples. There is a difference in

Fig. 2. Amino acid content in different fractions of (a) wheat, and (b) rye. All levels were obtained by the EZ-Faast method except for those of Glu which were obtained by the Biochrom method.

the amino acid contents of cereal fractions, with bran having the highest concentration while the sifted flour showed the lowest concentration, a consistent pattern seen in all

amino acids. This difference is very clear in wheat, due to the sharp separation that takes place during the milling of wheat but was less apparent in the rye, due to the fact

Fig. 3. Effect of fermentation and baking on wheat amino acid content. All levels were obtained by the EZ-Faast method except for those of Glu which were obtained by the Biochrom method.

Fig. 4. Effect of baking on rye amino acid content. All levels were obtained by the EZ-Faast method except for those of Glu which were obtained by the Biochrom method.

that there is more of the outer parts of the kernel in the sifted fractions. Samples of rye were richer in individual amino acids than were those of wheat, although varietal differences may exist ([Abdel-Aal & Hucl, 2002](#page-7-0)). These results indicate that the rye samples have higher content of free Asn than have wheat samples and that free Asn is concentrated in the outer parts of the kernel. Oats were rich mainly in Ala, Asn, Asp and Glu. The bran was richer in free amino acids than were oat groats and the low fibre oat flour ([Table 3](#page-3-0)).

3.3. Change of amino acid content during fermentation and baking

Fermented dough from sifted wheat flour showed a major decrease in Asn [\(Fig. 3\)](#page-5-0), in agreement with [Fredriks](#page-7-0)[son et al. \(2004\)](#page-7-0). A similar decrease was also observed in Asp. The variation in the amino acid content after fermentation could be explained by yeast metabolism ([Benedito](#page-7-0) [De Barber et al., 1989\)](#page-7-0) and their release by proteases ([Col](#page-7-0)[lar & Matinez, 1993\)](#page-7-0). For example, there was increase mainly in Ala and Ser during wheat bread-making that could partially be due to the fermentation process, a metabolic state that consumes, as well as releases, different amino acids. Rye crisp bread fermentation and baking showed that Asn, and Asp are decreased during breadmaking as well, while Gly, Ser, Pro and Lys showed a smaller increase (Fig. 4).

The alcohol extraction, coupled with the EZ-Faast amino acid analysis kit, was able to extract and determine free amino acids that are found in low concentrations. It gave reproducible results for most of the amino acids (except Arg, Trp, and Glu) in all the different fractions of wheat, rye, oats and barely, and products from wheat and rye. The chromatograms show about 20 free amino acids appearing in around 8 min, with good separation, as well as consistency, in the retention times. Total analysis time is 1 h including the GC run. Spiking to test the effect of matrix gave satisfactory results for most of the amino acids. The most common free amino acids were Ala, Ser, Asn and Asp. Milling fractions that contain the outer part of the kernel are richer in free amino acids than are the sifted fractions. The rye samples showed higher contents of free amino acids than did the wheat samples. Fermentation and baking seem to use-up, as well as release, certain amino acids.

Acknowledgments

We would like to thank Sune Eriksson at AnalyCen AB for the amino acid analysis using the Biochrom method. This study was carried out with financial support from the Islamic Development Bank in Jeddah (Saudi Arabia), Cerealia AB, Wasabröd AB (Sweden), and the European Commission, Priority 5 on Food Quality and Safety (Contract noFOOD-CT-2003-506820 Specific Targeted Project), 'Heat-generated food toxicants – identification, characterisation and risk minimisation'. This publication reflects the authors' views and not necessarily those of the EC. The information in this document is provided as is and no guarantee or warranty is given that the information is fit for any particular purpose. The user thereof uses the information at its sole risk and liability.

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