

1 A UHPLC method for the simultaneous analysis of biogenic amines, amino acids and  
2 ammonium ions in beer

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31 Running title: UHPLC detection of amino compounds in beer  
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35 ABSTRACT

36

37 This paper reports a novel UHPLC method for simultaneously quantifying nine biogenic  
38 amines, 21 amino acids, and ammonium ions, in beer. Precision values of standard curves  
39 slopes were lower than 3.4% and recovery was between 85% and 106%, indicating the absence  
40 of matrix effect. Linear calibration curves were obtained for analyte concentrations between two  
41 and four orders of magnitude ( $R^2 > 0.996$ ). Repeatability tests returned mean variations of 3.2%  
42 and 0.5% for beer and a standard solution, respectively. Sensitivity ranged between 0.03 mg/L  
43 and 0.63 mg/L for the biogenic amines, and 0.05 mg/L and 5.19 mg/L for other compounds.  
44 Original data on the habitual presence of ethanolamine in beers are presented. The method  
45 allows for more samples to be assayed per unit time, it uses less solvent than other techniques  
46 and therefore reduces costs and the associated waste. It could be a valuable tool for monitoring  
47 the safety and quality of beers.

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51 *Keywords:* biogenic amines, amino acid, UHPLC, DEEMM, beer

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54 Chemical compounds studied in this article

55 Diethylethoxymethylenemalonate (PubChem CID: 6871); Ethanolamine (PubChem CID: 700);

56 Agmatine (PubChem CID: 199); Histamine (PubChem CID: 774); Tyramine (PubChem CID:

57 5610); Ethylamine (PubChem CID: 6341); Putrescine (PubChem CID: 1045); Cadaverine

58 (PubChem CID: 273); Tryptamine (PubChem CID: 1150);  $\beta$ -phenylethylamine (PubChem CID:

59 1001).

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62

## 63 1. Introduction

64 Beer is one of the most consumed of all fermented beverages. Its nutritional value, aroma  
65 and flavour depend greatly on the proteolytic events that the raw materials (mainly barley and  
66 hops) undergo during malting and brewing, resulting in each beer having a particular amino acid  
67 composition (Gorinstein et al., 1999; Bokulich & Bamforth, 2013). The amino acid content of a  
68 beer also reveals whether wheat adjuncts were present during brewing (Dale, Young & Brewer,  
69 1989).

70 Certain amino acids can be decarboxylated by microbial enzymes, producing amino-  
71 containing compounds known as biogenic amines (BA) (reviewed in Kalac & Krizek, 2003).  
72 For instance, the decarboxylation of histidine renders histamine, while tyrosine, ornithine, lysine  
73 and phenylalanine can be decarboxylated to produce tyramine, putrescine, cadaverine and  $\beta$ -  
74 phenylethylamine, respectively (Lonvaud-Funel, 2001; Kalac & Krizek, 2003; Spano et al.,  
75 2010; Linares, Martin, Ladero, Alvarez & Fernandez, 2011). High concentrations of BAs in  
76 food are considered a biological hazard by international regulatory organizations (European  
77 Food Safety Authority [EFSA], 2011; Food and Drug Administration of the United States of  
78 America, 2011; Food & Agriculture Organization of the United Nations, 2014). Indeed, the  
79 ingestion of large quantities of BAs can cause toxicological reactions leading to neurological  
80 problems, headaches, hypo- or hypertension, nausea, heart palpitations and kidney poisoning  
81 etc., with symptoms particularly severe in persons with suboptimal BA-detoxifying amine  
82 oxidase capacity (Shalaby, 1996; Caston, Eaton, Gheorghui & Ware, 2002; Ladero, Calles-  
83 Enríquez, Fernandez & Alvarez, 2010; EFSA, 2011). In addition, tyramine and histamine have  
84 recently been shown to exert considerable cytotoxic effects *in vitro* (Linares, del Rio, Redruello,  
85 Ladero, Fernandez, Martin & Alvarez, 2016). An extra concern regarding the consumption of  
86 alcoholic beverages centres around a potential synergistic effect between ethanol/acetaldehyde  
87 and some BAs causing the inhibition of detoxifying amino oxidases (Maynard & Schenker,  
88 1962).

89 The type and concentration of BAs in beer are affected largely by the raw materials and  
90 brewing techniques employed in the production process, plus the hygiene conditions maintained

91 (Halász, Baráth & Holzapfel, 1999; Kalac & Krížek, 2003). Different concentrations of  
92 histamine, tyramine, putrescine, cadaverine,  $\beta$ -phenylethylamine and tryptamine have been  
93 reported in different types of beer (Zee, Simard & Desmarais, 1981; Izquierdo-Pulido, Albalá-  
94 Hurtado, Mariné-Font & Vidal-Carou, 1996; Kalac, Hlavatá & Krížek, 1997; Halász et al.,  
95 1999; Slomkowska & Ambroziak, 2002; Bunka et al., 2012; Aflaki, Ghoulipour, Saemian &  
96 Sheibani, 2014). However, the presence of ethanolamine and ethylamine, which are known to  
97 appear in other alcoholic beverages (including wine; Galgano, Caruso, & Favati, (2009)), has  
98 been little studied in beer.

99 The availability of rapid and validated methods for detecting BAs in foods is essential if their  
100 concentrations are to be minimised (Kalac & Krížek, 2003; EFSA, 2011; Spano et al., 2010;  
101 Alvarez & Moreno-Arribas, 2014). Currently, high-performance liquid chromatography (HPLC)  
102 is the only reliable technique for monitoring BA concentrations in foods and beverages (EFSA,  
103 2011). The use of chromatographic columns with particles under 2  $\mu\text{m}$  in diameter (so-called  
104 ultra-HPLC [UHPLC]) guarantees shorter elution times, greater sensitivity and improved peak  
105 resolution.

106 The simultaneous analysis of amino acids and BAs is difficult given their different structures  
107 and the absence of a specific chromophore; a pre- or post-column derivatization step is therefore  
108 usually required. Among the derivatizing reagents used for the simultaneous analysis of these  
109 compounds in food matrices diethyl ethoxymethylenemalonate (DEEMM) has many  
110 advantages: its coupling with primary and secondary amino compounds, the good stability of  
111 the aminoenone derivatives produced, simplicity of use, and the absence of post-reaction by-  
112 products (Alaiz, Navarro, Girón & Vioque, 1992; Gómez-Alonso, Hermosín-Gutiérrez &  
113 García-Romero, 2007; Redruello, Ladero, Cuesta, Alvarez-Buylla, Martin, Fernandez &  
114 Alvarez, 2013; Wang, Ye, Zhu, Wu & Duan, 2014). Further, it is the official derivatizing agent  
115 of the *Organisation International du Vin* (OIV, 2014).

116 A DEEMM derivatization procedure coupled to UHPLC-photodiode array detection (DAD)  
117 has been reported reliable for the simultaneous analysis of amino acids and BAs in cheeses and  
118 red wines (Redruello et al., 2013; Wang et al., 2014). However, no reports exist on the use of

119 this technique for analysing beers. The present work reports the development and validation of a  
120 UHPLC-based method for the simultaneous analysis of the aminoenone derivatives of the BAs,  
121 amino acids and ammonium ions present in beer.

122

## 123 **2. Materials and Methods**

### 124 *2.1. Reagents and beer samples*

125 HPLC-grade acetonitrile and sodium hydroxide were purchased from VWR (Barcelona,  
126 Spain), methanol and hydrochloric acid from Merck (Darmstadt, Germany), boric acid from  
127 USB (Cleveland, OH, USA), and ammonium acetate, sodium azide, DEEMM, L-2-aminoadipic  
128 acid (internal standard), amino acids, BAs and ammonium chloride from Sigma-Aldrich  
129 (Madrid, Spain). All solutions were made with Milli-Q water. Eleven beers (lager or ale) made  
130 by different European brewers and produced using different techniques, were chosen for  
131 analysis. Four of them (two lager and two ale) were used during the matrix effect analysis (see  
132 2.4.1 section for samples description). All samples were purchased in retail stores in Spain.

133

### 134 *2.2. Derivatization reaction*

135 Containers of beer were left open for 2 h at room temperature to remove their carbon dioxide  
136 content. Samples of the de-carbonated beers were then centrifuged at 8000 g for 5 min to  
137 eliminate any particulate matter. DEEMM derivatization reactions were performed as described  
138 in Redruello et al. (2013), using 100 µl samples (or of standard solution when constructing  
139 calibration curves). When necessary, samples were diluted with 0.1 N HCl. After derivatization,  
140 samples were filtered through 0.22 µm polytetrafluoroethylene (PTFE) membranes (VWR) into  
141 conical vials (VWR) prior to injection into the UHPLC system.

142

### 143 *2.3. Equipment and chromatographic conditions*

144 The chromatographic column and the UHPLC equipment used were those described in  
145 Redruello et al. (2013). The mobile phase consisted of 25 mM acetate buffer plus 0.02% sodium  
146 azide (eluent A; pH 6.7), methanol 100% (eluent B) and acetonitrile 100% (eluent C). Samples

147 (1 µl) were applied to the column and eluted at a flow rate of 0.45 mL/min according to the  
148 ternary gradient shown in Table 1. The column was then returned to the initial conditions within  
149 1 min, and allowed to equilibrate for 4.5 min before the next injection. Data were acquired and  
150 analysed using Empower 2 software (Waters). The target compounds were identified by their  
151 retention times compared to standards, and quantified using the internal standard method.

152

## 153 *2.4. Method validation*

### 154 *2.4.1. Evaluation of matrix effect*

155 The precision value (RSD, relative standard deviation) of standard curves slopes in five  
156 different lots of a biofluid was used to evaluate the existence of matrix effect (Matuszewski,  
157 2006). This value should not exceed 4% for the method to be considered free from matrix effect  
158 (Matuszewski, 2006). Additionally, the RSD of the peak areas measured at all the spiked  
159 concentrations in the five lots of biofluids should not exceed 10-15% (Matuszewski, 2006). We  
160 used as five different biofluids four beer samples of different matrix complexity (an alcohol-free  
161 french lager, an artisan spanish lager, and two abbey-style dark belgian ale beers) and a 0.1 N  
162 HCl solution acting as solvent matrix. Mixtures of analytes at five different concentrations (15,  
163 30, 60, 120 and 240 µM) were added (spiked) to each of the five matrices. The calibration  
164 curves obtained for each analyte in the five matrices were then calculated and their slopes  
165 compared. The RSD of the standard curves slopes as well as the RSD of the peak areas  
166 measured at all spiked concentration were then calculated.

167 Recovery of each analyte was calculated from the calibration data obtained as described  
168 above as  $[(\text{area measured in the spiked sample}) - (\text{area measured in the non-spiked sample}) / (\text{area}$   
169  $\text{measured in the solvent 0.1 N HCl solution})] \times 100$ . Total recovery for each analyte was the  
170 average of the individual recoveries calculated from all the spiked concentrations and all the  
171 matrices.

### 172 *2.4.2. Linearity, repeatability and sensitivity*

173 Linearity, repeatability and sensitivity were validated according to Taverniers, de Loose &  
174 van Bockstaele (2004). Linearity was tested by regression analysis from three independent

175 calibration curves that contained all the analytes (a mixture of amino acids, BAs and ammonium  
176 chloride) dissolved in 0.1 N HCl as solvent matrix and that ranged from 0.0007 mM to 1.5 mM.  
177 All the calibration mixtures included a fixed concentration (0.07 mM) of the internal standard  
178 (IS). Calibration curves were calculated by plotting analyte peak area/IS peak area ratio against  
179 the known concentrations of the analyte.

180 Intra-day repeatability (same analyst, apparatus and reagents) was assessed by injecting a  
181 mixture containing all the analytes six times during the same chromatographic run. Inter-day  
182 repeatability (same analyst and apparatus but different reagents) was assessed by injecting  
183 individual samples of a standard mixture over eight days.

184 LOD and LOQ were calculated for each analyte as three times and 10 times the  
185 baseline/noise ratio respectively. The 10 blank replicates used contained 0.1 N HCl instead of  
186 the sample. The lowest concentration in the linear range was deemed to represent the LOQ.

187

### 188 **3. Results and Discussion**

#### 189 *3.1. Optimisation of the UHPLC separation step*

190 Ethanolamine and ethylamine co-eluted with other amino compounds present in the beer  
191 matrix: ethanolamine co-eluted with ammonium ions and tyrosine, while ethylamine co-eluted  
192 with lysine. Modification of the pH of the ammonium acetate buffer did not improve the  
193 separation achieved due to the very similar pKa values of the alpha ammonium ions of  
194 ethanolamine (pKa 9.40) and tyrosine (pKa 9.11), and that of regular ammonium ions (pKa  
195 9.26). Fine tuning of the solvent proportions (aqueous buffer/acetonitrile/methanol) providing  
196 the ternary gradient was required until the profile described in section 2.4 was reached. The  
197 final ternary gradient allowed the separation of the 21 amino acids, 9 BAs and ammonium ions  
198 searched for within a 14 min elution time (Fig. 1A). The amino-compounds were identified in a  
199 beer sample by comparison of their retention times against those recorded for the standard  
200 mixture. No interfering peaks were observed (Fig. 1B).

201 The chromatographic run time was between 4 and 6 times faster than reported for previous  
202 HPLC methods designed to simultaneously analyse amino acids and BAs in beer (Gómez-

203 Alonso et al. 2007; Hu et al., 2014). The achieved runtime highlights the proposed method as  
204 one of the fastest liquid chromatography approaches for simultaneous amino acids, BAs and  
205 ammonium ions analysis so far (the fastest UHPLC method was reported by Fiechter, Sivec &  
206 Mayer in 2013 for acid-curd cheeses analysis). This would be an advantage for research and  
207 company laboratories that deem speed an asset. Shorter analysis times also signify the use of  
208 less solvent, reducing costs and the associated waste (and thus the environmental impact of the  
209 method). The method might help also to rapidly evaluate technological aspects such as the  
210 influence of substrate availability on amino acid metabolism and BA synthesis during brewing.  
211 Also, questions regarding the influence of bacteria and yeasts on BA accumulation in beers, or  
212 even the selection/application of degrading bacteria to eliminate BAs could be rapidly  
213 answered. Many of these factors are being studied in the production process of wines (Ortega-  
214 Heras et al., 2014; Tristezza et al., 2013; Capozzi et al., 2011; Arena et al., 2011; Landete,  
215 Arena, Pardo, Manca de Nadra & Ferrer, 2008).

216

### 217 *3.2. Method validation*

#### 218 *3.2.1. Absence of matrix effect*

219 We have calculated the RSD from five standard curve slopes constructed after spiking four  
220 beers of different complexity plus a 0.1 N HCl solution as solvent matrix with five different  
221 analytes' concentration. All the slopes RSD values were  $\leq 3.4\%$  (Table 2); none of them  
222 exceeded the cut-off RSD value (4%) to consider a bioanalytical method free from a matrix  
223 effect (Matuszewski, 2006). Moreover, the RSD of the peak areas measured at all the spiked  
224 concentrations and in the five matrices did not exceed 10 % in any case (Table 2). These high  
225 precision values support the absence of matrix effect and the reliability of the present method to  
226 quantify 31 aminoenone derivatives in beer samples, under the experimental conditions  
227 employed. In a previous study involving beers and wines, no matrix effect was reported for any  
228 of the aminoenones analysed therein (Gomez-Alonso et al., 2007). However, other authors have  
229 reported a matrix effect for the aminoenones of proline and ethanolamine in wine in the early



230 stages of fermentation (Wang et al., 2014). This effect was attributed to the presence of glucose  
231 concentrations of >50.0 g/L.

232 Table 2 also shows the total recovery of each analyte, after computing the recoveries  
233 obtained in the five matrices and the five spiked concentrations of analyte. Recovery values  
234 (from 85 % the lowest to 106 % the highest) are within the acceptable limits for the  
235 concentrations added (Taverniers et al., 2004), indicating the accuracy of the proposed method.  
236 The individual recoveries from each of the spiked concentrations can be found in Redruello,  
237 Ladero, del Rio, Fernandez, Martin & Alvarez (2016).

238

### 239 *3.2.2. Linearity, repeatability and sensitivity of the method*

240 Calibration curves were then constructed in 0.1 N HCl as solvent matrix solution. The  
241 linearity of the results was verified by analysing the variance of the regression. An  $R^2$  value of  
242 >0.995 was returned for all the calibration curves (Table 3). The concentration range was linear  
243 between two and four orders of magnitude, depending on the analyte.

244 Table 3 shows also the repeatability and sensitivity of the proposed method. The variation in  
245 analyte retention time within the chromatographic column was <0.23% in intra-day tests  
246 (repeatability) and <0.27% in inter-day tests (reproducibility). The variability of the peak area  
247 for the analytes was between 0.06% and 1.66% in intra-day analysis, and between 0.33% and  
248 1.58% in inter-day runs. These results indicate an acceptable repeatability and reproducibility of  
249 the method (Taverniers et al., 2004).

250 Proline returned the highest LOQ of all the amino acids (5.19 mg/L), while serine returned  
251 the lowest (0.05 mg/L). For the BAs, the LOQ ranged between 0.03 mg/L for putrescine and  
252 0.63 mg/L for ethylamine. Ammonium ions returned an LOQ of 0.49 mg/L. The LOD was  
253 below 0.13 mg/L for ethylamine, tyramine and histamine and  $\leq$ 0.10 mg/L for ethanolamine,  
254 agmatine, putrescine, tryptamine, cadaverine and phenylethylamine. The LOD range for the  
255 amino acids and ammonium ions was between 1.04 mg/L for proline and 0.01 mg/L for serine.  
256 Overall, the sensitivity results agree well with those provided by other UHPLC methods for  
257 determining amino compounds in different foods (Latorre-Moratalla, Bosch-Fuste, Lavizzari,

258 Bover-Cid, Veciana-Nogues & Vidal-Carou, 2009; Mayer, Fiechter & Fischer, 2010; Redruello  
259 et al., 2013; Wang et al., 2014) and even with that reported using quantitative nuclear magnetic  
260 resonance (NMR) technique (Chatzimitakos, Exarchou, Ordoudi, Fiamegos & Stalikas, 2016).  
261 Some analytical methods that employ mass detectors can reach sensitivities between 10 and  
262 1000 times higher than those of HPLC-derived techniques (Daniel, Dos Santos, Vidal & do  
263 Lago, 2015). However, HPLC-derived methods are amply sensitive to quantify the toxic  
264 concentrations of BA (EFSA, 2011).

265

### 266 *3.3. Analysis of aminoenone derivatives in beer samples*

267 Under optimized experimental conditions, the method was used to determine the  
268 aminoenone derivatives of amino acids, ammonium ions and BAs in different beer samples.  
269 Wide variation was detected in the amino acid and BA concentrations of the different beers  
270 (Table 4).

#### 271 *3.3.1. Amino acid content*

272 The amino acid content of a beer determines its aroma and flavour. It depends directly on the  
273 proteolytic events that take place during the transformation of the raw materials (barley, hops  
274 and other cereals such as wheat or corn) during brewing (Gorinstein et al., 1999). Between the  
275 initial and final stages of beer-making, the protein content decreases while the content of some  
276 amino acids increase concomitantly (Gorinstein et al., 1999). The assimilation of the released  
277 amino acids by microorganisms, mainly yeasts, during fermentation influences their final  
278 concentrations in the beer (Jones & Pierce, 1964). In the present work, the most abundant amino  
279 acid was always proline, with concentrations ranging from 238 to 688 mg/L (mean 421.33  
280 mg/L). These findings are consistent with those of previous work (Gomez-Alonso et al., 2007).  
281 Proline is also the most abundant amino acid in other fermented beverages, such as red wines,  
282 although its concentration is some 4-6 times higher than in beers (Gomez-Alonso et al., 2007;  
283 Kutlán & Molnár-Perl, 2003). A possible explanation for the abundance of proline in beer is its  
284 poor assimilation by the yeasts present (Jones & Pierce, 1964). The next most abundant amino  
285 acids detected were  $\gamma$ -aminobutyric acid (GABA) (mean concentration 57.79 mg/L), alanine

286 (49.21 mg/L), tyrosine (40.98 mg/L), phenylalanine (37.68 mg/L) and arginine (29.57 mg/L).  
287 The mean concentrations of the remaining amino acids did not exceed 25 mg/L. The least  
288 abundant amino acid was glutamine, the concentration of which never exceeded 3.5 mg/L,  
289 followed by ornithine (mean concentration 2.62 mg/L), threonine (2.98 mg/L) and methionine  
290 (4.73 mg/L). The few reports that exist regarding the amino acid content of beers generally  
291 corroborate this concentration distribution (Gomez-Alonso et al., 2007; Hu et al., 2014; Jones &  
292 Pierce, 1964; Dale et al., 1989). The only exception is GABA; some of these studies report it as  
293 one of the most abundant amino acid, while others report it to be among the least abundant. This  
294 might be explained by the analytical techniques employed. For instance, in those studies in  
295 which DEEMM was the derivatizing agent (Gomez-Alonso et al., 2007; this work), GABA was  
296 among the most abundant amino acids. However, where o-phthalaldehyde- $\beta$ -mercaptoethanol  
297 was used to derivatize the sample, only trace amounts of GABA were detected (Hu et al., 2014).

298 The amino acids and BAs profile of a beer has also been recently used to discriminate  
299 between homofermentative and heterofermentative beer spoilage LAB (Geissler, Behr, von  
300 Kamp & Vogel, 2016).

301

### 302 3.3.2. BA content

303 Ethanolamine (mean concentration 8.37 mg/L; range: 4.40-12.95 mg/L), putrescine (2.84  
304 mg/L; 1.59-4.05 mg/L) and cadaverine (0.69 mg/L; detected but not quantified-0.92 mg/L) were  
305 found in all the samples. Agmatine (4.46 mg/L; 0.00-12.50 mg/L) and ethylamine (0.50 mg/L;  
306 0.00-1.35 mg/L) were recorded for eight of the 11 beer types. Histamine and  $\beta$ -  
307 phenylethylamine were found in one sample only (and in trace amounts); tryptamine was  
308 detected in no sample. Tyramine was found in 10 of the 11 beers. Its concentration was,  
309 however, the most variable (relative standard deviation 258%); the majority of samples  
310 contained less than 1 mg/L of tyramine, but one contained around 10 mg/L and another around  
311 60 mg/L. Other authors report similar findings for beers of different geographical origin, and  
312 propose this might be explained by the presence of lactic acid bacteria during fermentation  
313 (Izquierdo-Pulido et al., 1996; Kalac & Krizek, 2003). Tyramine has traditionally been

314 considered responsible for the post-beer-consumption hypertension crises observed in patients  
315 with depression and treated with monoamine oxidase inhibitors (Shulman, Taylor, Walker &  
316 Gardner, 1997).

317 Histamine and cadaverine may also appear in beer due to the metabolism of contaminating  
318 LAB (Kalac & Krícek, 2003). Indeed, the histamine content of beer has been proposed a good  
319 indicator of brewing hygiene (Halász et al., 1999). In the present work, no histamine was  
320 quantified in any sample, and the cadaverine concentration never exceeded 0.92 mg/L. This  
321 would appear to indicate that proper hygiene conditions were followed during the production of  
322 all the analysed beers.

323 Putrescine and agmatine are constituents of natural beer, originating in the malt (Kalac &  
324 Krícek, 2003). The mean concentrations of agmatine and putrescine recorded in the present  
325 work never exceeded 5.0 mg/L and 3.0 mg/L respectively; these values are similar to, or lower  
326 than, those reported in the literature (Zee et al., 1981; Izquierdo-Pulido et al., 1996; Kalac et al.,  
327 1997; Slomkowska & Ambroziak, 2002; Aflaki et al., 2014).

328 No tryptamine was found in any of the samples analysed in the present work. Only a few  
329 reports exist regarding the content of this BA in beers, and in general it has been found at  
330 concentrations of <2 mg/L (Izquierdo-Pulido et al., 1996; Aflaki et al., 2014).

331 Ethanolamine and ethylamine are BAs usually present in grapes and consequently found in  
332 wines (reviewed in Galgano, Caruso & Favati, 2009). Until now, however, only one paper has  
333 reported the presence of ethylamine in beer (Zotou, Loukou, Soufleros & Stratis, 2003), and to  
334 the best of our knowledge the literature contains no report of ethanolamine in this beverage. In  
335 the present work, the mean ethylamine concentration was 0.5 mg/L; the highest concentration  
336 was 1.22 mg/L, quite similar to that recorded (1 mg/L) in the only other reported work to  
337 analyse ethylamine in beer (Zotou et al., 2003). The mean ethanolamine concentration was  
338 however among the highest for all the BAs analysed. The origin of ethylamine and  
339 ethanolamine in beer remains unclear, although their regular presence in the samples examined  
340 in the present work, which came from different countries and were produced following different  
341 brewing methods, suggests they are a common constituent of beer.

342 In agreement with previous reports on the total BA concentration of beers (Kalac & Kricek,  
343 2003; Loret, Deloyer & Dandrifosse, 2005), values of 7.03-78.90 mg/L (mean 23.66 mg/L)  
344 were recorded in the present work. Thus, most of the analyzed samples represented no health  
345 hazard. However, the beer with the highest content of tyramine (58.30 mg/L) might have posed  
346 a risk, especially to persons with a suboptimal BA-detoxifying system.

347

#### 348 **4. Conclusion**

349 The analytical approach presented here is applied for the first time in beer. DEEMM  
350 derivatization followed by UHPLC separation provides a reliable means of simultaneously  
351 determining the amino acid, BA and ammonium ion concentrations of beers. Amino acid  
352 analysis can be used to ensure beer quality, and to detect counterfeit beers. BA determination is  
353 also important in ensuring the safety of drinks and fermented foods.

354 In total, the technique separated nine BAs (histamine, tyramine, putrescine, cadaverine,  $\beta$ -  
355 phenylethylamine, ethanolamine, ethylamine, tryptamine and agmatine), 21 amino acids, and  
356 ammonium ions, in under 14 min of elution time. Not only does the proposed method allow for  
357 more samples to be assayed per unit time, it uses less solvent than other techniques and  
358 therefore reduces costs and the associated waste. Its high resolution, precision (repeatability and  
359 reproducibility), accuracy, and sensitivity (limit of detection [LOD] and limit of quantification  
360 [LOQ]) suggest it could be a very valuable tool for ensuring the food safety of beers.

361

#### 362 **Acknowledgements**

363 This work was performed with the financial support of the Spanish Ministry of Economy and  
364 Competitiveness (AGL2013-45431-R), and via the GRUPIN14-137 project (the latter is co-  
365 financed by the Plan for Science, Technology and Innovation of the Principality of Asturias  
366 2014-2017 and European Regional Development Funds). The authors thank Adrian Burton for  
367 language and editing assistance.

368

369 **Conflict of interest.** The authors declare that no conflict of interest exist.

370

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560 **Figure caption**

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562 **Fig. 1.** Chromatograms of a 0.15 mM standard solution (A) and a beer sample (B) showing the  
563 aminoenone derivatives of amino acids, ammonium ions and biogenic amines at 280 nm. Peak  
564 assignments: 1, aspartic acid; 2, glutamic acid; 3, asparagine; 4, serine; 5, glutamine; 6,  
565 histidine; 7, glycine; 8, threonine; 9, arginine; 10, GABA; 11, alanine; 12, proline; 13,  
566 ammonium ion; 14, ethanolamine; 15, tyrosine; 16, agmatine; 17, histamine; 18, valine; 19,  
567 methionine; 20, tryptophan; 21, isoleucine; 22, leucine; 23, phenylalanine; 24, ornithine; 25,  
568 lysine; 26, ethylamine; 27, tyramine; 28, putrescine; 29, tryptamine; 30, cadaverine; 31,  $\beta$ -  
569 phenylethylamine. IS, internal standard.

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**Table 1**

Ternary elution gradient for UHPLC determination of aminoenone derivatives of 31 amino compounds.

Time (min)	0.00	1.20	1.90	2.00	6.52	7.53	7.82	9.20	10.00	13.50	14.00	14.50	16.50
% eluent A	90.0	92.0	92.0	90.0	90.0	83.0	83.0	71.0	75.0	40.0	18.0	-	-
% eluent B	2.0	1.6	1.6	2.0	2.0	3.4	3.4	5.8	-	-	-	20.0	20.0
% eluent C	8.0	6.4	6.4	8.0	8.0	13.6	13.6	23.2	25.0	60.0	82.0	80.0	80.0

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**Table 2**

Precision (relative standard deviation, RSD) and accuracy (recovery) of the UHPLC method for the determination of amino compounds. BAs are highlighted in grey colour.

Compound	Slopes RSD (%) <sup>a</sup>	Peak area total RSD (%) <sup>b</sup>	Total recovery (%) <sup>c</sup>
Aspartic acid	1.60	3.99	96.77
Glutamic acid	1.15	3.24	97.46
Asparagine	0.59	5.85	100.70
Serine	1.34	3.58	102.44
Glutamine	1.48	6.89	101.98
Histidine	2.44	5.69	99.23
Glycine	1.35	3.83	98.96
Threonine	1.05	6.85	100.56
Arginine	1.67	9.17	99.32
GABA	1.53	5.44	100.01
Alanine	2.37	5.00	105.75
Proline	3.40	4.28	95.98
Ammonium ion	2.55	4.43	85.00
Ethanolamine	2.63	4.01	99.89
Tyrosine	3.15	4.82	102.81
Agmatine	0.86	9.69	97.87
Histamine	2.49	4.39	102.51
Valine	0.96	4.88	99.59
Methionine	3.13	6.02	87.12
Tryptophan	2.18	2.73	99.10
Isoleucine	1.11	3.52	101.79
Leucine	1.10	5.67	100.62
Phenylalanine	1.06	5.12	99.36
Ornithine	0.61	2.59	101.78
Lysine	1.03	4.16	101.32
Ethylamine	0.84	2.75	98.99
Tyramine	0.94	3.20	103.43
Putrescine	1.85	3.59	102.74
Tryptamine	2.64	4.05	100.58
Cadaverine	1.50	3.78	105.90
Phenylethylamine	1.56	4.00	103.96

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<sup>a</sup> Precision value of slopes of standard curves constructed in five different matrices

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<sup>b</sup> Precision value of the peak areas of each compound taking into account all the spiked concentrations and all the matrices used

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<sup>c</sup> Recovery value of each compound taking into account all the spiked concentrations and all the matrices used

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**Table 3** Repeatability, linearity (calibration) and sensitivity of the UHPLC method for the determination of amino compounds (data derived from standards). The results for biogenic amines are highlighted in grey.

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Compound	Precision (%)				Calibration		Sensitivity		
	Intra-day <sup>a</sup>		Inter-day <sup>b</sup>		R <sup>2</sup>	Linear range <sup>c</sup> (mg/L)	LOQ <sup>d</sup>	LOD <sup>e</sup>	
	Rt	area	Rt	area			μM	mg/L	μM
Aspartic acid	0.10	0.70	0.12	0.78	0.999	1.20 – 199.65	9.00	0.24	1.80
Glutamic acid	0.15	0.71	0.20	0.94	0.999	0.99 - 220.70	6.70	0.20	1.34
Asparagine	0.23	0.31	0.27	0.70	0.999	0.21 - 198.18	1.60	0.04	0.32
Serine	0.18	0.49	0.22	0.88	0.999	0.05 - 157.64	0.50	0.01	0.10
Glutamine	0.15	0.42	0.17	1.24	0.999	0.95 - 219.21	6.50	0.19	1.30
Histidine	0.13	0.32	0.16	0.80	0.999	0.25 - 232.73	1.60	0.05	0.32
Glycine	0.10	0.41	0.12	0.39	0.999	0.41 - 112.61	5.40	0.08	1.08
Threonine	0.11	0.51	0.14	0.58	0.999	0.35 - 178.68	2.90	0.07	0.58
Arginine	0.13	0.45	0.16	0.82	0.999	0.30 - 261.30	1.70	0.06	0.34
GABA	0.15	0.70	0.18	1.04	0.999	0.20 - 154.68	1.90	0.04	0.38
Alanine	0.20	0.61	0.21	1.02	0.998	0.50 - 133.64	5.60	0.10	1.12
Proline	0.07	0.27	0.08	0.48	0.996	5.19 - 575.65	45.10	1.04	9.02
Ammonium ion	0.05	0.27	0.06	1.25	0.998	0.49 - 27.08	27.40	0.10	5.48
Ethanolamine	0.04	0.38	0.05	1.58	1.000	0.23 - 91.62	3.70	0.05	0.74
Tyrosine	0.04	0.50	0.04	1.01	0.998	0.72 - 271.79	4.00	0.14	0.80
Agmatine	0.03	0.44	0.03	0.83	0.999	0.31 - 195.29	2.40	0.06	0.48
Histamine	0.03	0.41	0.03	0.47	0.999	0.58 - 166.73	5.20	0.12	1.04
Valine	0.02	0.43	0.02	0.43	0.996	1.15 - 175.73	9.80	0.23	1.96
Methionine	0.02	0.43	0.02	0.73	0.999	0.36 - 223.82	2.40	0.07	0.48
Tryptophan	0.03	0.52	0.03	0.71	0.999	1.04 - 306.35	5.10	0.21	1.02
Isoleucine	0.02	0.43	0.03	0.73	0.999	0.45 - 196.77	3.40	0.09	0.68
Leucine	0.02	0.59	0.02	1.20	0.999	0.26 - 196.77	2.00	0.05	0.40
Phenylalanine	0.02	0.69	0.02	1.16	0.999	0.13 - 247.79	0.80	0.03	0.16
Ornithine	0.02	0.45	0.02	0.81	0.999	0.61 - 198.24	4.60	0.12	0.92
Lysine	0.02	1.18	0.02	1.57	0.999	1.61 - 219.29	11.00	0.32	2.20
Ethylamine	0.02	1.66	0.02	1.45	0.998	0.63 - 67.62	14.00	0.13	2.80
Tyramine	0.02	0.16	0.02	0.72	0.999	0.62 - 205.77	4.50	0.12	0.90
Putrescine	0.01	0.09	0.01	1.03	0.999	0.03 - 132.23	0.30	0.01	0.06
Tryptamine	0.01	0.06	0.01	0.33	0.998	0.50 - 240.33	3.10	0.10	0.62
Cadaverine	0.01	0.42	0.01	0.83	0.999	0.50 - 153.27	4.90	0.10	0.98
Phenylethylamine	0.01	0.90	0.01	0.88	0.999	0.33 - 181.77	2.70	0.07	0.54

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<sup>a</sup> RSD (relative standard deviation) of peak retention time (Rt), and peak area, based on six runs of a standard mixture (187 μM) in one day

<sup>b</sup> RSD of peak Rt, and peak area, based on eight runs of a standard mixture (187 μM) over eight independent days.

<sup>c</sup> Concentration range between the limit of quantification and the upper linear limit.

<sup>d</sup> Limit of quantification : signal/noise ratio = 10.

<sup>e</sup> Limit of detection: signal/noise ratio = 3.



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706**Table 4**  
Biogenic amines, amino acids and ammonium ions in different samples of beer (mg/L). Results for biogenic amines are highlighted in grey.

Analytes	Brewing style	Lager	Lager	Lager	Lager	Lager	Lager	Lager	Lager	Ale	Ale	Ale	Mean ± SD	RSD <sup>a</sup>
	Colour country	Pale Spain	Pale Spain	Pale Spain	Pale Spain	Pale Spain	Pale Portugal	Dark Spain	Dark Spain	Pale Belgium	Dark Belgium	Dark Belgium		
Aspartic acid		10.65	11.31	22.89	10.65	6.66	15.17	31.81	27.42	11.18	41.26	11.45	18.22 ± 11.06	60.69
Glutamic acid		8.39	13.09	20.75	6.03	2.80	14.27	38.25	23.10	13.09	41.78	7.95	17.23 ± 12.78	74.17
Asparagine		3.17	4.49	22.46	3.17	1.06	4.49	7.27	10.70	2.77	10.31	3.17	6.64 ± 6.10	91.83
Serine		2.21	3.26	16.50	2.63	1.05	3.05	5.57	13.98	4.52	7.36	3.15	5.75 ± 5.02	87.28
Glutamine		0.73 <sup>b</sup>	3.22	1.90	nd	nd	0.29 <sup>b</sup>	0.88 <sup>b</sup>	nd	nd	1.75	nd	0.81 ± 1.06	130.63
Histidine		14.27	32.43	19.86	20.01	14.89	18.15	34.75	37.39	26.07	40.03	9.31	24.29 ± 10.42	42.92
Glycine		12.69	29.88	13.51	13.36	8.48	14.56	36.33	27.40	27.78	38.89	13.51	21.49 ± 10.75	50.03
Threonine		0.83	0.23 <sup>b</sup>	14.53	0.48	0.12 <sup>b</sup>	0.48	1.55	8.81	0.71	4.53	0.48	2.98 ± 4.65	156.13
Arginine		15.16	36.76	34.49	14.28	3.83	18.64	60.97	20.03	38.50	76.65	5.92	29.57 ± 22.87	77.36
GABA		54.24	76.62	27.22	68.68	48.36	42.38	55.99	51.35	80.95	64.76	65.17	57.79 ± 15.59	26.97
Alanine		26.73	67.71	31.98	27.97	10.96	37.42	114.57	67.00	72.52	60.58	23.88	49.21 ± 30.17	61.30
Proline		511.29	608.69	237.63	335.60	349.88	279.31	688.02	366.46	325.93	562.53	369.34	421.33 ± 146.78	34.84
Ammonium ion		9.55	2.92	8.50	9.39	2.96	5.58	31.46	18.14	15.38	3.21	2.92	10.00 ± 8.80	87.96
Ethanolamine		7.02	11.73	4.40	9.04	6.54	5.31	7.64	9.22	8.49	12.95	9.77	8.37 ± 2.57	30.73
Tyrosine		49.65	84.98	31.71	31.16	4.53	12.14	6.70	65.41	66.68	84.43	13.41	40.98 ± 30.72	74.95
Agmatine		7.03	12.11	nd	nd	nd	0.13 <sup>b</sup>	8.46	0.13 <sup>b</sup>	0.39	12.50	8.33	4.46 ± 5.24	117.41
Histamine		nd	nd	nd	nd	nd	nd	nd	nd	0.33 <sup>b</sup>	nd	nd	nd	-
Valine		13.36	28.70	15.46	7.73	1.64	7.61	41.82	30.58	27.06	24.13	3.05	18.29 ± 13.01	71.13
Methionine		2.83	5.67	8.80	3.88	3.73	4.33	8.65	5.22	3.28	3.88	1.79	4.73 ± 2.24	47.26
Tryptophan		17.36	28.39	16.34	6.13	11.85	11.85	23.89	25.32	21.24	19.61	8.99	17.36 ± 7.11	40.98
Isoleucine		3.94	13.91	17.05	3.67	1.18	5.12	32.80	18.23	10.10	13.12	2.36	11.04 ± 9.42	85.28
Leucine		5.38	24.27	34.11	5.64	2.10	8.53	40.53	42.90	20.46	31.75	4.46	20.01 ± 15.54	77.66
Phenylalanine		29.90	62.28	32.21	15.86	2.97	16.85	83.92	55.50	49.89	59.47	5.62	37.68 ± 26.30	69.80
Ornithine		1.72	2.38	0.53 <sup>a</sup>	2.11	1.45	2.78	4.63	6.61	2.11	2.64	1.85	2.62 ± 1.66	63.50
Lysine		1.75	3.36	21.49	3.22	0.88 <sup>b</sup>	5.85	9.36	7.46	3.22	24.56	2.34	7.59 ± 8.06	106.26
Ethylamine		0.31 <sup>b</sup>	nd	0.49 <sup>b</sup>	0.54 <sup>b</sup>	0.40 <sup>b</sup>	0.49 <sup>b</sup>	nd	1.22	0.68	nd	1.35	0.50 ± 0.45	90.92
Tyramine		0.96	0.96	0.14 <sup>b</sup>	0.55 <sup>b</sup>	0.96	10.15	<b>58.30</b>	nd	0.82	0.55 <sup>b</sup>	0.55 <sup>b</sup>	6.72 ± 17.35	258.08
Putrescine		2.29	3.44	1.59	3.35	2.29	1.85	3.53	4.05	2.38	3.88	2.64	2.84 ± 0.84	29.50
Tryptamine		nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	-
Cadaverine		0.61	0.82	0.41 <sup>b</sup>	0.82	0.61	0.51	0.61	0.92	0.61	0.82	0.82	0.69 ± 0.16	23.12
Phenylethylamine		nd	nd	nd	nd	nd	nd	0.36	nd	nd	nd	nd	0.03 ± 0.11	331.66
BA total content		18.24	29.05	7.03	14.30	10.81	18.56	78.90	15.54	13.71	30.69	23.47	23.66 ± 19.70	<del>87.45</del>
Amino acids total content		786.23	1141.62	641.43	582.28	478.56	523.26	1328.27	910.87	808.07	1214.00	557.18	815.62 ± 298.07	36.55
Analytes total content		814.02	1173.59	656.96	605.96	492.33	547.40	1438.63	944.56	837.15	1247.91	583.57	849.28 ± 317.37	<del>374.6</del>

747

a, relative standard deviation for the samples analysed (as a percentage); b, value between the LOD and LOQ.

748 FIGURE 1

749

750 A

751

752 Standard mixture

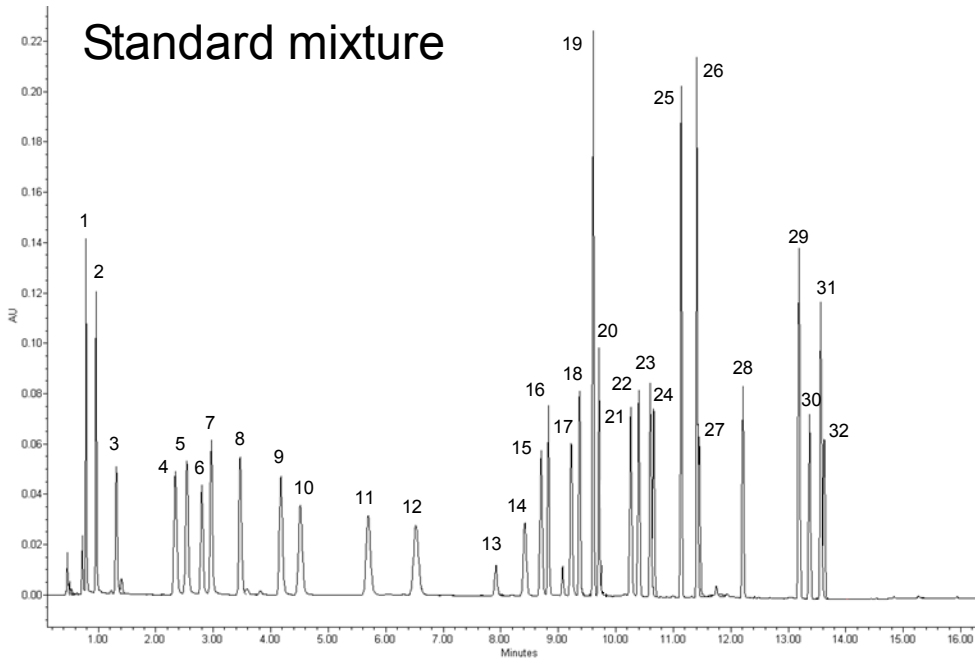
753

754

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B

Beer

