

1 **Improvement of the protein quality of wheat bread through faba bean sourdough**  
2 **addition**

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20 **Abstract**

21 The effects of the substitution of wheat flour with faba bean flour and faba bean sourdough on the  
22 properties of composite bread were investigated. Bread was prepared by replacing wheat flour with  
23 30% of faba bean flour, native or after sourdough fermentation. The addition of faba bean flour  
24 influenced the structure of the breads, causing a slight decrease of volume and higher hardness  
25 compared to wheat bread. However, when fermented faba bean flour was added, the crumb porosity of  
26 the bread was not affected. The addition of 30% of faba bean flour increased wheat bread protein  
27 content from 11.6 up to 16.5 % of dry matter. The addition of native faba bean flour did not affect the  
28 *in vitro* protein digestibility, resulting similar to wheat bread (64%). On the contrary, faba bean  
29 sourdough bread showed higher protein digestibility (73%). Generally, the addition of native faba bean  
30 flour caused an improvement of the nutritional indexes of the composite bread, further enhanced when  
31 fermentation was carried out. The free amino acid profile, protein chemical score, and biological value  
32 index were the highest in faba bean sourdough bread. In addition, the predicted glycemic index was the  
33 lowest in faba bean sourdough bread.

34 **Keywords:** faba bean, sourdough, wheat bread

35 **Abbreviations:** BV, Biological Value; CS, Chemical Score; EAAI, Essential Amino Acid Index; FAA,  
36 Free Amino Acids; FSB, Faba bean Sourdough Bread; GI, Glycemic Index; HI, Hydrolysis Index;  
37 IVPD, *in vitro* Protein Digestibility; NFB, Native Faba bean Bread; NI, Nutritional Index; OPA, o-  
38 phtaldialdehyde; PER, Protein Efficiency Ratio; RH, Relative Humidity; TPA, Texture Profile  
39 Analysis; TTA, Total Titratable Acidity; WCB, Wheat Control Bread; WSE, Water/salt-soluble  
40 extracts.

## 41 **1. Introduction**

42 Grain legumes have been intensely studied in recent years due to their richness in protein, fibres,  
43 minerals and other bioactive compounds, with the aim to develop novel foods with improved  
44 nutritional profile (Angioloni & Collar, 2012; Vaz Patto *et al.*, 2015). Particularly, the fortification of  
45 cereals with legume flour has been recognized as a good strategy to complement cereal-based food  
46 nutritional quality, setting new technological and marketing possibilities for staples like bread, bakery  
47 products, and pasta (Angioloni & Collar, 2012).

48 With its high protein content (about 30%), protein quality, and other health benefits, faba bean has been  
49 widely used as food and feed in many parts of the world (Crépon *et al.*, 2009). The nutritional and  
50 agronomic properties of faba bean make this legume a good alternative to other protein-rich sources of  
51 animal origin. Considering the good economical, ecological and nutritional properties, the use of  
52 legumes and faba bean should be promoted more among food industry and consumers.

53 Notwithstanding the positive impact on nutrition, the use of legume flours as ingredients in food  
54 manufacturing is not so straightforward. For instance, the presence of anti-nutritional factors such as  
55 trypsin inhibitors, phytic acid, raffinose family oligosaccharides, tannins, and glucopyranosides in faba  
56 beans, are a recognized cause of problems (Youssef & Bushuk, 1986). For this reason, pre-processing  
57 treatments of faba bean flour have been developed, obtaining a reduction of the anti-nutrients  
58 concentration (as reviewed by Multari, Stewart, & Russel, 2015). Particularly, fermentation with lactic  
59 acid bacteria has been shown as a simple, low cost and successful biotechnology to achieve a  
60 nutritionally enhanced ingredient (Coda *et al.*, 2015; Rizzello *et al.*, 2016).

61 The use of faba bean flour in breadmaking has been previously reported in literature (Angioloni &  
62 Collar, 2012; Morad, Leung, Hsu, & Finney, 1980; Youssef & Bushuk, 1986), however, still very little  
63 is known about the use of faba bean sourdough. On the contrary, legume-based sourdough has been

64 used before for bread fortification obtaining an overall improvement of the nutritional quality of the  
65 bread (Chinma *et al.*, 2016; Coda, Rizzello, & Gobbetti, 2010; Rizzello, Calasso, Campanella, De  
66 Angelis, & Gobbetti, 2014).

67 In this work faba bean flour, native or fermented with lactic acid bacteria, was added to wheat bread at  
68 a high percentage (30%), aiming at the improvement of the protein content and quality. Together with  
69 the reduction of anti-nutritional factors, sourdough technology can be used to modify the protein  
70 quality of a vegetable food matrix, due to the effects of acidification on the activation of endogenous  
71 proteolytic enzymes, and to the proteolytic activity of the microorganisms (Ganzle *et al.*, 2008). The  
72 technological and nutritional characteristics of wheat bread enriched with faba bean sourdough were  
73 compared to wheat bread containing native faba bean and to common wheat bread in order to assess the  
74 effects imputable to faba bean addition and its fermentation.

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## 76 **2. Materials and Methods**

### 77 **2.1 Material and microorganism**

78 Faba bean (*Vicia faba* major, harvest year 2014) flours, obtained from stone-milling of the dehulled  
79 seeds, was purchased from CerealVeneta (San Martino di Lupari, PD, Italy). The flour had the  
80 following chemical composition: moisture content of  $9.45 \pm 0.72$ g/100g; carbohydrates  $51.2 \pm$   
81  $2.1$ g/100g of dry matter (d.m.); protein  $35.7 \pm 1.2$ g/100g of d.m; lipids were  $1.63 \pm 0.25$ g/100g of d.m;  
82 dietary fibers and ash were  $7.23 \pm 0.75$ g/100g and  $3.87 \pm 0.12$ g/100g of d.m., respectively. Wheat flour  
83 purchased from Fazer (Fazer Mills, Lahti, Finland) had the following composition: moisture,  $14 \pm$   
84  $1$ g/100g; protein,  $14 \pm 2$ g/100g of d.m.; fat, 1.7g/100g of d.m.; ash, 0.6g/100g  $\pm 0.05$  of. d.m.; and total  
85 carbohydrates, 65g/100g of d.m.

86 *Pediococcus pentosaceus* I02, previously isolated from faba bean flour (Coda *et al.*, 2017) was used as  
87 starter for sourdough fermentation. The strain was routinely propagated at 30°C in MRS broth (Oxoid,  
88 Basingstoke, Hampshire, England).

89

## 90 **2.2 Sourdough fermentation**

91 Prior fermentation, *P. pentosaceus* I02, was cultivated at 30°C until the late exponential phase of  
92 growth was reached (ca. 12 h). Cells were harvested by centrifugation (10,000 x g, 10 min, 4°C),  
93 washed twice in 50 mmol/L sterile potassium phosphate buffer (pH 7.0) and re-suspended in the tap  
94 water used for dough preparation. Faba bean flour and tap water were mixed to obtaining a dough with  
95 a yield (DY, dough weight x 100/flour weight) of 250, corresponding to 40 and 60% wt/wt flour and  
96 water, respectively. The cells of the lactic acid bacterium were inoculated at an initial cell density of ca.  
97 log 6.0 cfu/g of dough. The faba bean dough was fermented at 20°C for 24 h and used as ingredient for  
98 bread making as described in 2.4. The pH value of faba bean dough was determined by a pH meter  
99 with a food penetration probe (Hanna Instruments). Total titratable acidity (TTA) was determined on  
100 10 g of dough with the official AACC method (AACC, 2003). Presumptive lactic acid bacteria were  
101 enumerated using MRS agar medium (Oxoid, Basingstoke, Hampshire, United Kingdom)  
102 supplemented with cycloheximide (0.1 g liter). Plates were incubated at 30°C for 48 h, under  
103 anaerobiosis (AnaeroGen and AnaeroJar, Oxoid).

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## 105 **2.3 Chemical characterization**

106 Water/salt-soluble extracts (WSE) of the uncooked doughs were prepared according to Weiss,  
107 Vogemeier, & Görg (1993) and used to analyze organic acids, ethanol, peptides, and free amino acids  
108 (FAA). Organic acids were determined by High Performance Liquid Chromatography (HPLC), using  
109 an ÄKTA Purifier system (GE Healthcare, UK) equipped with an Aminex HPX-87H column (ion

110 exclusion, Biorad, Richmond, CA), and an UV detector operating at 210 nm. Elution was at 60°C, with  
111 a flow rate of 0.6 ml/min, using H<sub>2</sub>SO<sub>4</sub> 10 mmol/L as mobile phase (Coda, Rizzello, Trani, & Gobbetti,  
112 2011).

113 To evaluate the degree of proteolysis of the uncooked doughs, the concentration of peptides and free  
114 amino acids was determined on the WSE. The concentration of peptides was determined by the *o*-  
115 phthaldialdehyde (OPA) method as described by Church, Swaisgood, Porter, & Catignani (1983). Free  
116 amino acids were analyzed by a Biochrom30 series Amino Acid Analyzer (Biochrom Ltd, Cambridge  
117 Science Park, UK) with a Na-cation exchange column (20 cm x 0.46 cm internal diameter as reported  
118 in Rizzello, Nionelli, Coda, De Angelis, & Gobbetti (2010a).

119

## 120 **2.4 Bread making**

121 Three breads were prepared: wheat control bread (WCB), native faba bean bread (NFB) and faba bean  
122 sourdough bread (FSB). In faba bean containing bread, wheat flour was replaced with 30% of faba  
123 bean flour. The formulas used for bread making are reported in Table 1.

124 Breads were prepared by mixing ingredients for 3 min slow + 4 min fast with a Diosna spiral mixer (SP  
125 12 F, Dierks & Söhne, Osnabrück, Germany). After a floor time of 15 min at 26°C and 75% RH, the  
126 doughs were divided into 250 g loaves and modelled manually. The loaves were proofed in pans (45  
127 min, 35°C, 75 RH%) and baked at 200°C, with 15 s of steam. Breads were cooled for 2 h before further  
128 analyses.

129

## 130 **2.5 Structural and image analysis of bread**

131 Loaf volume was determined using the rapeseed displacement method as in AACC (2003). Specific  
132 loaf volume was calculated dividing the loaf volume by the corresponding loaf weight (AACC 2003).

133 Bread structure was evaluated by Texture profile analysis (TPA) by using a TPA analyzer (Stable

134 Micro Systems, UK). Breads (6 parallel samples) were sliced into 25-mm thick slices and cut with  
135 round mould on the centre of bread. TPA were performed by using a 35-mm diameter probe SMS P/36,  
136 5-kg load cell, 40% penetration depth, at a compression rate of 5 mm/s and a 30-s gap between  
137 compressions. Pre-test and test speed were 1.7 mm/s and post-test speed was 10 mm/s. Hardness values  
138 were expressed as g.

139 The crumb grain of breads was evaluated after 24 h of storage using image analysis technology. Images  
140 of the sliced breads were captured using an Image Scanner (Amersham Pharmacia Biotech, Uppsala,  
141 Sweden). Images were scanned full-scale at 300 dots per inch and analyzed in gray scale (0–255).  
142 Image analysis was performed using the UTHSCSA ImageTool program (Version 2.0, University of  
143 Texas Health Science Centre, San Antonio, Texas, available by anonymous FTP from  
144 maxrad6.uthscsa.edu). A threshold method was used for differentiating gas cells and non-cells  
145 (Crowley, Grau, & Arendt, 2000). Analysis was carried out on two sub-images of 500×500 pixels (field  
146 of view) selected from within the bread slice. Two slices were analyzed per treatment. The crumb cell  
147 features recovered were: number, area, perimeter, and gas cell to total area ratio.

148

## 149 **2.6 Nutritional characterization**

150 **Energy value was calculated as reported by USDA method (IOM, 2002).** The *in vitro* protein  
151 digestibility (IVPD) of breads was determined by the method of Akeson & Stahmann (1964)  
152 modified by Rizzello, Nionelli, Coda, Di Cagno, & Gobbetti (2010b). The IVPD was expressed as  
153 the percentage of the total protein, which was solubilized after enzyme hydrolysis. The supernatant,  
154 which contained the digested protein, was freeze-dried and used for further analysis. The modified  
155 method of AOAC (2005) was used to determine the total amino acid profile. The digested protein  
156 fraction, which derived from 1 g of sample, was added to 5.7 mol/L HCl (1 mL/10 mg of proteins),  
157 under a nitrogen steam and incubated at 110°C for 24 h. Hydrolysis was carried out under anaerobic

158 conditions to prevent the oxidative degradation of amino acids. After freeze-drying, the hydrolyzate  
159 was re-suspended (20 mg/mL) in sodium citrate buffer, pH 2.2, and filtered through a Millex-HA  
160 0.22 µm pore size filter (Millipore Co.). Amino acids were analyzed by a Biochrom 30 series Amino  
161 Acid Analyzer as described above. Since the above procedure of hydrolysis does not allow the  
162 determination of tryptophan, it was estimated by the method of Pinter-Szakács & Molnán-Perl  
163 (1990). Chemical Score (CS) estimates the amount of protein required to provide the minimal  
164 essential amino acids (EAA) pattern, which is present in the reference protein (hen's egg). It was  
165 calculated using the equation of Block & Mitchel (1946). The sequence of limiting essential amino  
166 acids corresponds to the list of EAA, having the lowest chemical score Block & Mitchel (1946). The  
167 protein score indicates the chemical score of the most limiting EAA present in the test protein Block  
168 & Mitchel (1946). Essential Amino Acid Index (EAAI) estimates the quality of the test protein,  
169 using its EAA content as the criterion. EAAI was calculated according to the equation (1):

$$170 \quad EAAI = \sqrt{\frac{(EAA_1*100)(EAA_2*100)(...)(EAA_n*100)[sample]}{(EAA_1*100)(EAA_2*100)(...)(EAA_n*100)[reference]}} \quad (1)$$

171 The Biological Value (BV) indicates the utilizable fraction of the test protein. BV was calculated using  
172 the equation of Oser (1959) (2):

$$173 \quad BV = ([1.09*EAAI]-11.70) \quad (2)$$

174 The Protein Efficiency Ratio (PER) estimates the protein nutritional quality based on the amino acid  
175 profile after hydrolysis. PER was determined using the equation (3) developed by Ihekoronye (1981):

$$176 \quad PER = -0.468 + (0.454*[Leucine]) - (0.105*[Tyrosine]) \quad (3)$$

177 The Nutritional Index (NI) normalizes the qualitative and quantitative variations of the test protein  
178 compared to its nutritional status. NI was calculated using the equation (4) of Crisan & Sands (1978),  
179 which considers all the factors with an equal importance:

$$180 \quad NI = (EAA*Protein (\%)/100) \quad (4)$$



181

## 182 **2.6 Starch hydrolysis index and predicted glycemic index**

183 The analysis of starch hydrolysis was carried out on breads with a procedure mimicking the *in vivo*  
184 digestion of starch (De Angelis *et al.*, 2009). Portion of bread, containing 1 g of starch, were given in  
185 randomized order to 10 healthy volunteers (aged 21-45 years), who rinsed their mouths with tap water  
186 and chewed the samples for 15 s. The samples were then expectorated and subjected to a multi-step  
187 enzymatic digestion, according to the protocol previously proposed by De Angelis *et al.*, 2009. The  
188 glucose content of the dialysates obtained from digested samples was measured with D-Fructose and  
189 D-Glucose kit (Megazyme International Ireland Ltd., Bray Business Park, Bray, Co. Wicklow, Ireland).  
190 The degree of starch digestion was expressed as percentage of potentially available starch hydrolyzed  
191 at different times (30, 60, 90, 120 and 180 min). A non-linear model (De Angelis *et al.*, 2009) was  
192 applied to determine the kinetics of starch hydrolysis, using the software Statistica 8.0. Wheat flour  
193 bread was used as the control to estimate the hydrolysis index (HI = 100). The predicted glycemic  
194 index (GI) was calculated using the equation (5) with wheat bread as the reference (GI wheat bread =  
195 100):

$$196 \text{ GI} = 0.549 \cdot \text{HI} + 39.71 \quad (5)$$

197

## 198 **2.7 Statistical analyses**

199 The results of the microbiological, chemical and bread properties analyses are presented as an average  
200 of two parallel measurements (two repetitions). The statistical difference was measured with one-way  
201 analysis of variance (ANOVA). The effect of treatments was measured with Tukey's test with  
202 significance level of  $P < 0.05$  (Statistica for Windows).

203

## 204 **3. Results and discussion**

### 205 **3.1 Sourdough and bread dough properties**

206 *P. pentosaceus* was the most represented species isolated during faba bean flour fermentation and thus was  
207 selected as autochthonous starter for fermentation (Coda *et al.*, 2017). In particular, the starter was inoculated  
208 at the initial cell density of  $5.9 \pm 0.03$  log cfu/g. After fermentation, lactic acid bacteria cell density  
209 increased of ca. 3.3 log cycles, reaching a value of  $9.3 \pm 0.1$  log cfu/g of sourdough. The pH and TTA  
210 values of the faba bean flour dough before fermentation were 6.2 and 3.3 mL of NaOH 1 N,  
211 respectively. In the sourdough, pH decreased to 5.3, while TTA increased to  $8.6 \pm 0.5$  mL of NaOH 1  
212 N. The results obtained can be related to an efficient growth of the lactic acid bacteria, as compared  
213 with previous faba bean fermentation process (Coda *et al.*, 2015), and to a mild acidification, achieved  
214 by the low fermentation temperature (20° C). These conditions were selected in order to avoid a  
215 potential negative impact of strong acidity on the technological quality of sourdough, as previously  
216 shown for other food matrices (Coda *et al.*, 2014; Katina *et al.*, 2005).

217 The chemical composition of the doughs before baking is reported in Table 2. Due to the fermentation,  
218 the amount of lactic acid in the dough containing 30% of faba bean sourdough, reached 25 mmol/kg of  
219 dough, while acetic acid amount was similar for both the doughs containing faba bean flour. Ethanol in  
220 the bread doughs before cooking was mostly the result of the baker's yeast activity and its content was  
221 the highest in NFB dough. Peptides and free amino acid concentration clearly distinguished the three  
222 doughs (Table 2). Generally, the simple addition of faba bean flour caused an increase of the peptides  
223 and free amino acids, markedly when fermentation was carried out. The dough containing 30% of faba  
224 bean sourdough was in fact characterized by a content of peptides ca. 15 and 30% higher than NFB and  
225 WCB, respectively (Table 2). Similarly, the total free amino acid amount of FSB dough reached 2007  
226 mg/kg of dough, corresponding to an increase of ca. 20 and 80% in comparison with NFB and WCB  
227 doughs (Table 2).

228 The effects of fermentation on protein modification also reflected on the single amino acids profile  
229 (Fig. 1). The concentration of almost all the essential amino acids increased in FSB dough compared to  
230 NFB and WCB doughs, and particularly Thr, Val, Phe, and Lys, which reached concentrations from 3  
231 up to 8 times higher than the value in WCB dough, corresponding to 55, 98, 75, and 81 mg/kg  
232 respectively. Additionally, the content of  $\gamma$ -Aminobutyric acid (GABA) increased in both NFB and  
233 FSB doughs to values of 89 and 315 mg/kg of dough. GABA is the major inhibitory neurotransmitter  
234 of the central nervous system and has several physiological functions with positive effects (Coda *et al.*,  
235 2010). It has been shown that daily intake of 10 mg of GABA (contained in fermented milk) for 12  
236 weeks decreased blood pressure by 17.4 Hg in hypertensive human patients (Inoue *et al.*, 2003).  
237 Therefore, in theory, the consumption of 50 g of bread made with 30% of faba bean sourdough,  
238 containing ca 15 mg of GABA could potentially have a beneficial effect on the diet.

239 The extent of the protein degradation together with the proportion of sourdough in the bread are  
240 important parameters to consider, since they will impact on the final bread properties. Generally, a  
241 moderate proteolysis does not cause adverse effects on texture and volume and beneficially improves  
242 bread flavor (Thiele, Gänzle, & Vogel, 2002).

243

### 244 **3.2 Structure of faba bean enriched breads**

245 The pH values of the three breads ranged from  $5.50 \pm 0.03$  to  $4.92 \pm 0.02$ , while TTA values ranged  
246 from  $2.6 \pm 0.2$  to  $7.4 \pm 0.1$ , with lower pH and higher TTA value belonging to FSB. Faba bean flour  
247 sourdough addition slightly but significantly decreased the specific volume of bread as compared to  
248 WCB and NFB (Table 3). The high percentage of faba bean flour substitution induced an effect on the  
249 textural properties of bread (Table 3). Compared to WCB, hardness was ca. 30 and 50% higher in NFB  
250 and FSB, respectively. Cohesiveness, springiness and resilience decreased significantly in faba bean

251 flour enriched breads, independently of fermentation, and no significant differences were found  
252 between native or fermented faba bean flour additions for these parameters. On the contrary, chewiness  
253 of WCB and FSB was comparable, whereas it had a lower value for NFB (Table 3). In these  
254 conditions, the high replacement of wheat flour with faba bean markedly affected the texture of bread  
255 due to a decrease in gluten content, and weakening of the gluten network.

256 The crumb grain of the breads was determined by image analysis technology. Digital images were pre-  
257 processed to detect crumb cell total area by a binary conversion (black/white pixels) (Table 3 and Fig.  
258 2). The gas cell-total area (corresponding to the black pixel ratio) of the breads containing faba bean  
259 were lower than WCB, however, fermentation improved the porosity of the bread, in comparison with  
260 the addition of native faba bean. Crumb cell detection of bread slice portions showed that no significant  
261 difference in the mean area of gas cells could be observed between WCB and FSB, having values of  
262 48.53 and 41.44 pixels, respectively. In general, WCB showed rounder and more uniform crumb cells  
263 while more uneven crumb cells distribution was found for NFB and FSB (Fig. 2).

264 The incorporation of high amount of legumes has been successfully obtained in biscuits, cake, and  
265 pasta (Gómez, Oliete, Rosell, Pando, & Fernández, 2008; Rizzello *et al.*, 2017). On the contrary, it has  
266 been challenging in bread making, thus limiting the addition of legumes below 15% of wheat flour  
267 (Angioloni & Collar, 2012; Gómez *et al.*, 2008; Jayasena, Leung, Nasar-Abbas, Palta, & Berger, 2008;  
268 Rizzello *et al.*, 2014). Comparably to the results of this study, the addition of legume flour was  
269 previously shown to increase crumb firmness (Angioloni & Collar, 2012; Yamsaengsung,  
270 Schoenlechner, & Berghofer, 2010). A similar behavior was observed when fermented cowpea flour  
271 was used at 20% for wheat bread making, leading to high dough resistance (Hallén, İbanoğlu, &  
272 Ainsworth, 2004). However, in the presence of fermented faba bean flour, the bread porosity was less  
273 affected, resulting in higher mean area of gas cells. This phenomenon could be attributed to the

274 intrinsic structure of faba bean starch and protein and to their modification occurring during  
275 fermentation, as consequence of the activity of flour enzymes and microorganisms. More in depth  
276 analysis of crumb structure is although required in order to clarify the impact of faba bean addition on  
277 the physical structure of bread.

278

### 279 **3.3 Nutritional properties of the breads**

280 The characterization of the nutritional properties of breads was mostly focused on the protein  
281 component, to assess the impact of native and fermented faba bean flour on its quality. Based on  
282 calculation, the sole addition of 30% on flour weight (f.w.) of faba bean flour increased wheat bread  
283 protein content from 11.6 up to 16.5 % of dry matter. **This ratio was chosen to obtain a “high protein  
284 bread”. According to EC regulation, in order to receive the “high protein claim”, 20% of the energy  
285 value of food must be provided by protein. In this study, the “protein dependent” energy value of faba  
286 bean bread was 24% of the total value of bread, calculated according to USDA method (IOM 2002).**

287 For the determination of the protein quality indexes, the digestible protein fraction was used. The  
288 addition of native faba bean flour did not affect the IVPD of NFB compared to WCB (Table 4). On the  
289 contrary, when faba bean flour was fermented, the IVPD value reached 74%, showing an increase of  
290 ca. 13%, compared to the other breads. The IVPD gives information on the stability of protein  
291 hydrolysates, and on how they withstand to digestive processes. The increase of IVPD in FSB can be  
292 attributed to the proteolysis occurring during fermentation, as already reported for other cereal-legume  
293 processing (Chinma *et al.*, 2016; Rizzello *et al.*, 2014) and protein-rich sources (Arte *et al.*, 2015).  
294 Protein quality is one of the most important attribute for defining the nutritional characteristics of a  
295 food matrix. The protein digestibility value in combination with amino acid composition therefore  
296 gives a better prediction of the nutritive value.

297 It was previously observed that the total protein content analysis should hide the effect of the  
298 proteolysis degree, which results otherwise in similar values for samples that are instead characterized  
299 by different bioavailability and nutritional features of the protein (Rizzello *et al.*, 2014). Based on CS,  
300 the sequence of limiting amino acids for all the bread samples were found to be Lys, Thr, and Met  
301 (Table 4). Nevertheless, compared to WCB (CS of 19, 33, and 40% for Lys, Thr, and Met,  
302 respectively), the addition of native faba bean flour caused significant ( $P<0.05$ ) increase of the CS in  
303 NFB (34, 55, and 45% for Lys, Thr, and Met, respectively), and particularly after fermentation, leading  
304 to the highest CS of FSB for almost all the EAA (data not shown).

305 Overall, EAAI values ranged from 68 to 75.4, showing a slightly higher value for FSB, even though  
306 not significant (Table 4). On the contrary, BV index was highest for FSB (71.8) while no significant  
307 difference was observed between WSB and NFB. EAAI indicates the ratio of essential amino acids of  
308 the sample compared to the reference, while BV estimates the nitrogen potentially retained by human  
309 body after consumption. The PER index, which reflects the capacity of a protein to support the body  
310 weight gain, was not significantly different for the three breads, even though, also in this case, slightly  
311 higher values were found when faba bean flour was added. Within the indexes that are used to evaluate  
312 the nutritional value of foods, NI combines qualitative and quantitative factors and it is considered a  
313 global predictor of the protein quality (Curiel *et al.*, 2014). In the conditions here applied, the value of  
314 NI, varying from 16.9 to 23.6, did not show any significant difference between the breads (Table 4).

315 Starch hydrolysis, determined mimicking the *in vivo* digestion, represents a presumptive measure of the  
316 glycemic index (GI) in healthy subjects (De Angelis *et al.*, 2009). In this analysis, white bread is the  
317 control, corresponding to a HI = 100. The HI value of NFB was 94% and a significantly lower value of  
318 81 % was found for FSB. Consequently, the predicted GI value of NFB and FSB was 91.4 and 84.2%  
319 (Table 4). The lowest value of HI (and predicted GI) of bread containing fermented faba bean flour,  
320 could be attributed to biological acidification, which is one of the main factors that decreases starch

321 hydrolysis rate and HI (De Angelis *et al.*, 2009). Generally, GI depends on the food texture and particle  
322 size, type of starch, degree of starch gelatinization, and physical entrapment of starch molecules within  
323 food, food processing and other ingredients (Petitot, Boyer, Minier, & Micard, 2010). A decrease of  
324 starch digestibility after fermentation was previously observed for faba bean fermented matrices  
325 attributed also to the strict interactions between protein and starch (Coda *et al.*, 2015). Faba bean flour  
326 was shown to have a compact protein structure surrounding the starch granules, suggesting strong  
327 interactions between protein and starch which appeared markedly changed after fermentation (Coda *et*  
328 *al.*, 2015).

329

#### 330 **4. Conclusions**

331 The addition of faba bean sourdough had a positive impact on the nutritional properties of the wheat  
332 bread. Notwithstanding the high level (30%) of faba bean flour substitution, the technological  
333 performance of faba bean sourdough bread was not severely affected, resulting in slightly smaller  
334 volume than the white bread, but with comparable chewiness and porosity. **Although sensory analysis**  
335 **is ongoing to complete the assessment of the impact of native and fermented faba bean on bread**  
336 **attributes, the acceptability of the organoleptic profile of other cereal foods fortified with fermented**  
337 **faba bean flour was already reported (Rizzello *et al.*, 2017).** In comparison with white bread and with  
338 the bread containing native faba bean, the better amino acids profile, higher protein digestibility,  
339 protein biological value, and lower glycemic index of faba bean sourdough bread, indicate the  
340 important role of fermentation technology in the effective modification of protein and nutritional  
341 quality of the legume-wheat bread.

342

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346

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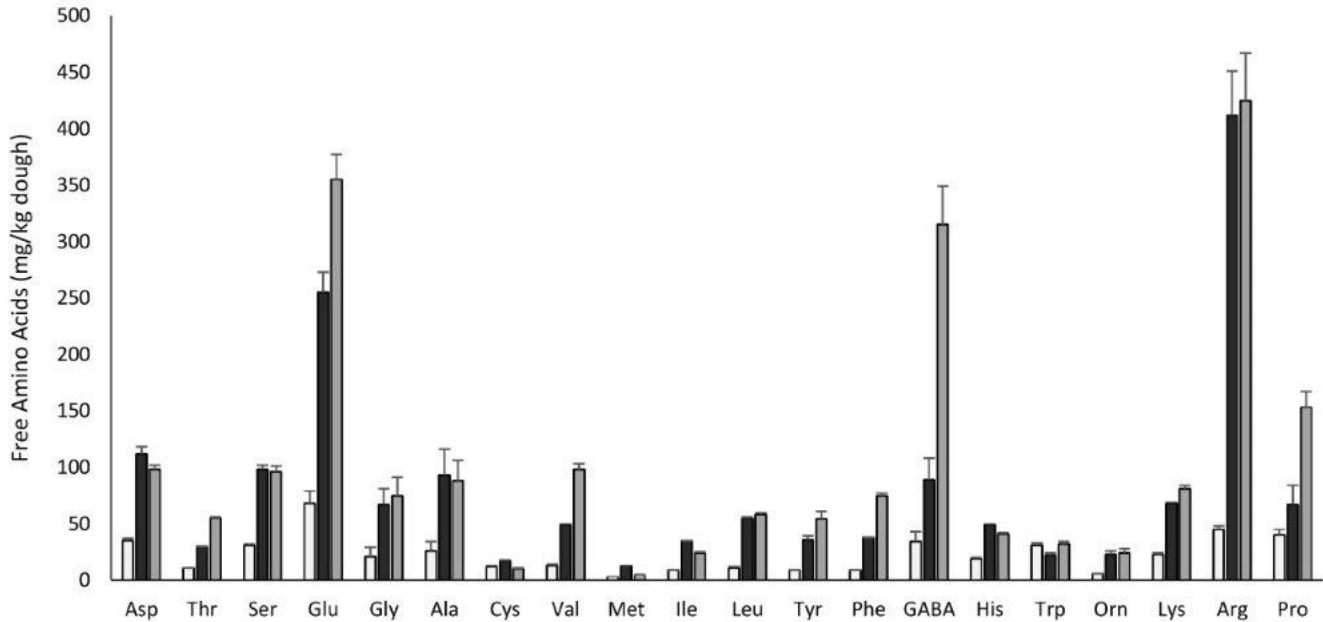
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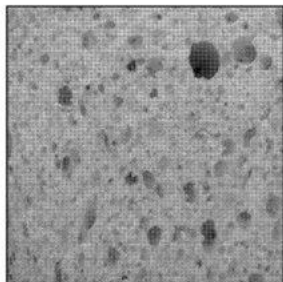
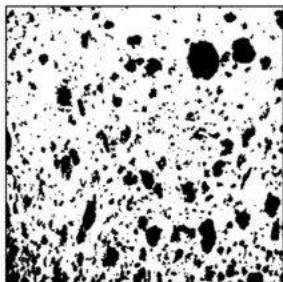
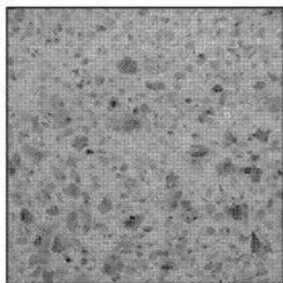
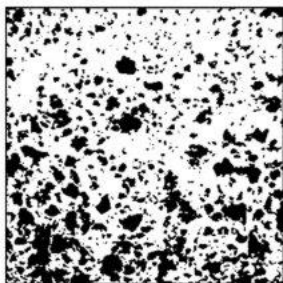
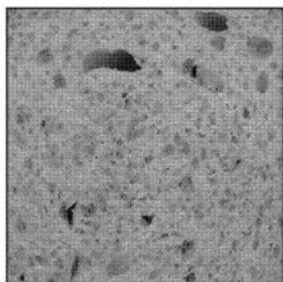
464 **Figure caption**

465 **Figure 1.** Concentration of free amino acids and their derivatives (mg/kg) of the experimental breads:  
466 wheat flour (WCB, □), non-fermented faba (NFB, ■) and faba sourdough (FSB, ■) breads. Data are the  
467 means of three independent analyses. Three-letters amino acid code (IUPAC) is used.

468 **Figure 2.** Representative images of wheat flour (WCB) (panels A and B), non-fermented faba (NFB)  
469 (panels C and D) and faba sourdough (FSB) (panels E and F) breads. Digital images of bread showing  
470 the original gray level images (A, C, and E) and computed binary results from gray level thresholding  
471 at the two-cluster (B, D, and F).

472



**A****B****C****D****E****F**