

1 **Health benefits of ancient grains. Comparison among bread made with ancient,**
2 **heritage and modern grain flours in human cultured cells**

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Abbreviations: AGE: advanced glycation end products; Ar: arginase; βCE: β-carotene equivalents; BSA: bovine serum albumin; CH: Choteau; cNOS: constitutive nitric oxide synthase; Ctrl: control; DCFH-DA: dichloro-dihydro-fluorescein diacetate; DMEM: Dulbecco's modified Eagle's medium; DPBS: Dulbecco's phosphate-buffered saline; ECACC: European Collection of Authenticated Cell Cultures; EDTA: ethylenediaminetetraacetic acid; eNOS: endothelial nitric oxide synthase; FBS: fetal bovine serum; FO: Fortuna-USA; GAE: gallic acid equivalent; HSD: honestly significant difference; IL-1β: interleukin-1β; IL-8: interleukin-8; IL-10: interleukin-10; iNOS: inducible nitric oxide synthase; JU: Judy; KA: KAMUT® khorasan wheat; LPS: lipopolysaccharides; MA: Marquis; MRP: Maillard reaction products; MTT: 3-(4,5-dimethyldiazol-2-yl)-2,5-diphenyltetrazolium bromide; NaS: sodium salicylate; NF-κB: nuclear factor κ-light-chain-enhancer of activated B cells; nNOS: neuronal nitric oxide synthase; NO: nitric oxide; NOS: nitric oxide synthase; NSAID: nonsteroidal anti-inflammatory drugs; RE: Redwin; RNS: reactive nitrogen species; ROS: reactive oxygen species; SP: Spelt; TAC: total antioxidant capacity; TCC: total carotenoid content; TE: Trolox equivalents; TNF-α: tumor necrosis factor α; TPC: total phenolic content; TU: Turkey Red.

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25 **ABSTRACT**

26 Nowadays the higher nutritional value of whole grains compared to refined grains is
27 recognized. In the last decade, there has been a renewed interest in the ancient wheat
28 varieties for producing high-value food products with enhanced health benefits.
29 This study compared two ancient grains, two heritage grains, and four modern grains grown
30 in the same agronomic conditions considering not only their chemical characteristics, but
31 also their biological effects. Whole grain flours were obtained and used to make bread.
32 Bread was *in vitro* digested, the digesta were supplemented to HepG2 cells, and the
33 biological effects of supplementation were evaluated. In addition, cells previously
34 supplemented with the different digested bread types were then exposed to inflammatory
35 agents to evidence possible protective effects of the pre-treatments. Despite the
36 impossibility to discriminate bread made with different grains based on their chemical
37 composition, results herein reported evidence that their supplementation to cultured cells
38 exerts different effects, confirming the potential health benefits of ancient grains. This
39 research represents an advancement for the evaluation of the apparent positive effects of
40 ancient grains and the formulation of cereal-based products with added nutritional value.

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42 **Key words:** ancient wheat; heritage wheat; modern wheat; KAMUT® khorasan wheat;
43 spelt; cultured cells; antioxidants; inflammation.

44 **1. Introduction**

45 Food products derived from cereal grains constitute a major part of the daily diet, and

46 wheat is the most important crop for humans (Shewry, 2009). Today most of the wheat

47 species grown are hybrids which have been created from ancient wheat over the last 100 to

48 150 years. Although these “modern” wheat varieties have positive properties in terms of

49 yield compared with the original ancient wheat, little attention has been given to their

50 nutritional value because wheat quality has traditionally been judged on the basis of its

51 technological functionality (Adom, Sorrells, & Liu, 2003; Serpen, Gökmen, Karagöz, &

52 Köksel, 2008). In the last decade, there has been a renewed interest in the ancient varieties

53 for producing high-value food products with enhanced health benefits (Bordoni, Danesi, Di

54 Nunzio, Taccari, & Valli, 2017; Dinu, Whittaker, Pagliai, Benedettelli, & Sofi, 2018).

55 These beneficial properties are ascribed to higher levels of proteins, lipids (mostly

56 unsaturated fatty acids), soluble fibers, minerals, vitamins and phytochemicals (Dinelli et

57 al., 2007; Hidalgo & Brandolini, 2014; Piergiovanni, Rizzi, Pannacciulli, & Gatta, 1997;

58 Vrćek et al., 2014). They are chiefly concentrated in the outer layers of grains (Adom,

59 Sorrells, & Liu, 2005; Landberg, Kamal-Eldin, Salmenkallio-Marttila, Rouau, & Åman,

60 2008), which could explain the reduction of the risk of developing many diseases that is

61 associated with higher whole grain consumption (Poutanen et al., 2008; Thorup, Gregersen,

62 & Jeppesen, 2014). Nowadays, the higher nutritional value of whole grains than refined

63 grains is recognized (Slavin, 2003), while the nutritional dominance of ancient *vs* modern

64 grains is still controversial. In the literature, the most of the *in vitro* and animal studies

65 aimed to demonstrate the health benefit of ancient grains have been performed using
66 extracts/lysates (Leoncini et al., 2012; Lucchesi et al., 2014; Whent et al., 2012) or discrete
67 compounds derived from ancient wheat (Masisi et al., 2015). This represents a limitation
68 since it is conceivable that the potential health benefit of ancient grains is not related to
69 single compounds, but to their overall nutritional composition (Slavin, Jacobs, & Marquart,
70 2001). Furthermore, the use of extracts is far from reproducing the physiological situation,
71 since grains undergo extensive treatment to produce foods, and foods must be digested
72 before exerting any action into the body.

73 In addition, genetically-determined compositional differences existing among ancient and
74 modern grains and varieties of the same species (Carvalho, Curto, & Guido, 2015; Righetti
75 et al., 2016; Ziegler et al., 2015) are also affected by environmental factors (Danesi, Valli,
76 Elementi, & D'Antuono, 2014; Menga, Fares, Troccoli, Cattivelli, & Baiano, 2010).

77 Recently, Shewry (2017) highlighted that the most of studies comparing ancient and
78 modern grains do not consider the interactions between genotype and environment, this
79 hindering any comparison between ancient and modern grains.

80 In the attempt to further compare ancient and modern grain, we considered two ancient, two
81 heritage, and four modern grains cultivated in the same location and growing season, using
82 the same agronomic techniques. Whole grain flours were obtained from grains and bread
83 was prepared using the same processing. The different bread types were characterized and
84 compared, then they were *in vitro* digested and the ultra-filtered digesta were supplemented
85 to HepG2 cells. To evidence whether the supplementation could exert a protective effect

86 toward a following inflammatory stimulus, in some experiments cells were pre-treated with
87 the supplemented media and then submitted to an exogenous inflammatory stress. The
88 effects of the supplementation were investigated by measuring cell viability, reactive
89 oxygen species (ROS) and nitric oxide (NO) production, the expression of inducible nitric
90 oxide synthase (iNOS) protein, and the secretion of a pro-inflammatory (IL-8) and an anti-
91 inflammatory (IL-10) interleukin.

92 **2. Material and Methods**

93 **2.1. Material**

94 HepG2 cells were obtained from the European Collection of Authenticated Cell Cultures
95 (ECACC; Salisbury, UK). Dulbecco's modified Eagle's medium (DMEM) and Dulbecco's
96 phosphate-buffered saline (DPBS) were from Lonza (Basel, Switzerland). All other
97 chemicals were from Sigma-Aldrich Co. (St. Louis, MO, USA). All chemicals and solvents
98 were of the highest analytical grade. Ingredients for bread formulation, except flour, were
99 purchased at a local market.

100 **2.2. Grains**

101 Two ancient grains (KAMUT® khorasan wheat, KA; Spelt, SP), two heritage grains
102 (Marquis, MA; Turkey Red, TU), and four modern grains (Choteau, CH; Fortuna-USA,
103 FO; Judy, JU; Redwin, RE) were considered. Details about the different wheat varieties are
104 from the Genetic Resources Information System for Wheat and Triticale website (GRIS,
105 2016). To minimize differences due to agronomic and environmental factors, all grains
106 were organically cultivated in the same location and growing season. The eight wheat

107 varieties were planted after two years of green manure, one year of peas, one year of
108 buckwheat. They were planted in May 2014 and harvested in August 2014.
109 Kernels were separated from the husk using a plot combine which was completely cleaned
110 out between plots. The threshed grain was further cleaned from residues using sieves with
111 different pores diameter. To obtain flour, cleaned grains were then milled with a small
112 milling system (Molino Davide 4V, Novital; Lonate Pozzolo, Italy). After every grinding,
113 each part of the milling system was carefully cleaned in order to avoid contamination, and
114 flours were packed under vacuum and stored at 4°C.

115 **2.3. Bread preparation**

116 All bread types were made according to the same recipe (**Table 1**), limiting as much as
117 possible the amount of other ingredients besides flour. A small-scale bread-maker (Pane
118 Express, Ariete; Campi Bisenzio, Italy) was used to standardize the dough mixing and the
119 baking steps; the same program (number 3) in the machine was set for all the preparations.
120 Once baked, bread was cooled at room temperature, cut into pieces and stored at -20°C
121 until analysis.

122 **2.4. Bread nutritional composition and color analysis**

123 Bread moisture, total nitrogen, carbohydrates, lipids, fibers, and ash were evaluated
124 according to Baldini et al. (1996). Selenium concentration was determined by inductively
125 coupled plasma-atomic emission spectrometry (Navarro-Blasco & Alvarez-Galindo, 2004).
126 To evaluate the total antioxidant capacity (TAC) and the total phenolic content (TPC), 1 g
127 of each bread was extracted according to Danesi et al. (2013) with a final volume of 6 mL

128 ethanol/water (70:30) acidified with 0.1% HCl. TAC was measured using the method of Re
129 et al. (1999) and expressed as micromoles of Trolox equivalents (TE) per gram of bread.
130 TPC was determined using Folin-Ciocalteu method, adapted to a 96-well plate assay
131 according to Dicko et al. (2002). Results were expressed as mg gallic acid equivalent
132 (GAE) per gram of bread.
133 The total carotenoid content (TCC) was determined using the method described by Valli et
134 al. (2016) with some modifications. Briefly, 1 g of bread was mixed with 4 mL of hexane-
135 acetone (50:50, v/v), shaken 20 min at 40°C, vortexed at high speed, sonicated, vortexed
136 again, and centrifuged at 120 g for 3 min. The absorbance of the supernatants was measured
137 at 450 nm and compared to the concentration–response curve of a β-carotene standard.
138 Results were expressed as micrograms of β-carotene equivalents (βCE) per gram of bread.
139 The CIE system color profile of the eight bread samples was measured by a reflectance
140 colorimeter (CR-400, Minolta; Milan, Italy) using illuminant source C (The International
141 Commission on Illumination, 1978). Measurements were randomly taken at different
142 locations in the bread samples. Results were expressed as values of the three-color
143 components: L* the lightness (that ranges from 0 black to 100 white), a* the redness (that
144 ranges from green associated with negative values to red associated with positive values)
145 and b* the yellowness (that ranges from blue associated with negative values to yellow
146 associated with positive values). The colorimeter was calibrated using a standard white
147 ceramic tile.
148 **2.5. In vitro digestion**

149 Bread samples were digested according to the standardized method of Minekus et al.
150 (2014). The digestion process was performed on 50 g of experimental bread or 50 g of
151 water (blank digestion) for 240 min (120 min of gastric digestion and 120 min of intestinal
152 digestion) at 37°C. During the process, several consecutive enzymatic treatments took place
153 by addition of simulated saliva (containing 75 U/ml α -amylase), simulated gastric juice
154 (containing 2000 U/mL pepsin) at acid pH, and simulated pancreatic juice (containing 10
155 mM bile and 100 U/mL pancreatin) at neutral pH.

156 The digested solutions were centrifuged at 50,000 g for 15 min, and the supernatants
157 filtered with 0.2 μ m membranes. To separate compounds which size is small enough to be
158 potentially absorbable through the intestinal mucosa, an aliquot was sequentially ultra-
159 filtered with Amicon Ultra at 3 kDa of molecular weight cut-off (Millipore; Billerica, MA,
160 USA) (<3kDa, bio-accessible fraction). Ultra-filtered solutions derived from two different
161 digestions of the same bread were mixed and frozen at -20°C until experiments. TAC and
162 TPC of the different bread digesta were determined as described above.

163 **2.6. HepG2 cells culture and supplementation**

164 HepG2 cells were maintained at 37°C, 95% air, 5% CO₂ in DMEM supplemented with
165 10% (v/v) fetal bovine serum (FBS), 100 U/mL penicillin and 100 mg/mL streptomycin.
166 Once a week, cells were split 1:20 into a new 75 cm² flask, and the medium was refreshed
167 (Di Nunzio et al., 2017). Cells were seeded in 12-well plates at the concentration of 8×10^5
168 cells/mL. Cell counting was carried out using the TC20TM Automated Cell Counter (Bio-
169 Rad Laboratories; Hercules, CA, USA). After 24 h (75-80% confluence) cells were

170 incubated with DMEM without phenol red containing 100 U/mL penicillin, 100 µg/mL
171 streptomycin, 1 mg/mL BSA, 2 mM glutamine, and the <3kDa digested bread solutions at
172 the concentration of 100 µL/mL. In preliminary experiments, scalar concentration of bread
173 digesta were tested for cytotoxicity by the MTT assay (data not shown), and the 100 µL/mL
174 concentration was the highest one having no toxic effect. Some cells were supplemented
175 with 4 mM sodium salicylate (NaS) to compare the effect of digested bread to the effect of
176 a well-known anti-inflammatory agent. NaS was supplemented to cell at a concentration
177 that can be found in human plasma after therapeutic administration of the drug (Insel,
178 1996). To avoid interference due to the vehicle, some cells received a corresponding
179 amount of a solution obtained from the “blank” digestion that is an *in vitro* digestion
180 performed without food. Preliminary experiments were performed to check possible
181 differences in terms of cell viability and cytokine secretion between cells receiving the
182 “blank” digesta and cells receiving a corresponding amount of sterile water. No significant
183 differences were observed (data not shown), so cells receiving the “blank” digesta were
184 used as control (Ctrl).
185 After 24 hours (basal condition) media were removed, cells scraped-off and maintained at -
186 20°C until analyses.
187 In some experiments, 24 h after supplementation media were removed and cells were
188 incubated for two additional hours with new DMEM containing the inflammatory agent
189 lipopolysaccharides (LPS, 100 ng/mL), interleukin-1 β (IL-1 β , 10 ng/mL), and tumor
190 necrosis factor α (TNF- α , 10 ng/mL) (Hamidi et al., 2012). After additional 2 hours

191 (inflamed condition) media were removed, cells scraped-off and maintained at -20°C until
192 analyses. The experimental design is reported in **Figure 1**.

193 **2.7. Cell viability**

194 Cell viability was measured using the 3-(4,5-dimethyliazol-2-yl)-2,5-diphenyltetrazolium
195 bromide (MTT) colorimetric assay, according to Di Nunzio et al. (2013). Briefly, cells were
196 washed twice with warm DPBS, then MTT dissolved in RPMI-1640 medium (final
197 concentration 0.5 mg/mL) was added to cells. After 1 h at 37°C, medium was completely
198 removed, 1-propanol was added to dissolve the formazan product, and the absorbance
199 measured against a propanol blank at 560 nm using a multiplate reader (Tecan Infinite
200 M200; Tecan, Männedorf, Switzerland). Results are expressed as percentage of the value
201 obtained in pair-matched Ctrl cells.

202 **2.8. ROS intracellular concentration**

203 Intracellular ROS concentration was monitored spectrofluorometrically as described in
204 detail by Valli et al. (2012). Briefly, dichloro-dihydro-fluorescein diacetate (DCFH-DA, 2
205 mM) in absolute ethanol was kept in the dark at -20°C until use. Ethanol final concentration
206 in the media was 1%, which has been already reported as not toxic (Wang et al., 2015). In
207 basal condition, 10 µL DCFH-DA/mL medium were added to HepG2 cells 30 min before
208 supplementation with digested bread. In inflamed condition, DCFH-DA at the same
209 concentration was added 30 min prior to the inflammatory stimulus. After 24 or 2 h
210 respectively, cells were washed twice with cold DPBS, lysed with 500 µL of cold Nonidet
211 P-40 (0.25% in DPBS), incubated on ice with shaking for 30 min and centrifuged at 14,000

212 *g* for 15 min. DCF fluorescence intensity was detected in supernatants ($\lambda_{\text{ex}}=485$ nm,
213 $\lambda_{\text{em}}=535$ nm) using an Infinite F200 microplate reader (Tecan; Männedorf, Switzerland),
214 normalized for protein content in the sample, and expressed as percent of value in Ctrl cells.

215 **2.9. Nitric oxide (NO) production**

216 NO production was assessed measuring the final products of NO metabolism, nitrite and
217 nitrate, in the cell media. The Nitrite/Nitrate Fluorometric Assay Kit (Cayman Chemical;
218 Ann Arbor, Michigan, USA) was used following the manufacturer's instruction. No
219 determination is based on a two-step reaction. In the first one, nitrates in the sample are
220 converted to nitrites by nitrate reductase. Then, 2,3-diaminonaphthalene and NaOH are
221 added to allow conversion of nitrites into a fluorescent product, 1(H)-naphthotriazole,
222 which is detected fluorimetrically ($\lambda_{\text{ex}} = 360$ nm, $\lambda_{\text{em}} = 430$ nm) and is proportional to NO_2^-
223 concentration.

224 Results were normalized for protein content in the well, and are expressed as nanomoles
225 NO/mL medium/mg protein.

226 **2.10. Cytokines secretion in the cell media**

227 The level of the pro-inflammatory IL-8 and the anti-inflammatory IL-10 was estimated in
228 cell media in basal condition and after cell treatment with the inflammatory agents by
229 AlphaLISA assay kits (Perkin Elmer Inc.; Waltham, MA, USA) using 96-microwell plates
230 (96 1/2 AreaPlate from Perkin Elmer Inc.) and an EnSpire™ plate reader (Perkin Elmer
231 Inc.), and following the manufacturer's instructions (Bielefeld-Sevigny, 2009). In the
232 AlphaLISA assay, a biotinylated anti-analyte antibody binds to the streptavidin-coated

233 donor beads while another anti-analyte antibody is conjugated to AlphaLISA acceptor
234 beads. In the presence of the analyte, the beads come into close proximity. The excitation of
235 the donor beads provokes the release of singlet oxygen molecules that triggers a cascade of
236 energy transfer in the acceptor beads, resulting in a sharp peak of light emission at 615 nm.

237 Results were normalized for protein content in the well, and are expressed in pg/mg protein.

238 **2.11. iNOS protein expression**

239 Whole cell lysate from HepG2 cell was obtained using 0.25% Nonidet P40 plus protease

240 inhibitor cocktail (1 mM AEBSF, 800 nM aprotinin, 50 µM bestatin, 15 µM E64, 20 µM

241 leupeptin, 10 µM pepstatin A, and 5 mM EDTA) (Life Technologies Inc.; Camarillo, CA,

242 USA). Proteins in cell lysate (40 µg) were analyzed on 10% Mini-PROTEAN TGX Stain-

243 Free™ Gels (Bio-Rad Laboratories; Hercules, CA, USA), which are able to produce, after

244 UV-induction, a stable, quantitative, and western blotting compatible protein fluorescent

245 signal due to the reaction of the trihalocompound incorporated into gel formulations with

246 the tryptophan residues contained in proteins (Kazmin, Edwards, Turner, Larson, &

247 Starkey, 2002).

248 After electrophoresis (200 mV for 30 min), gel proteins were activated by UV exposure for

249 5 min, transferred onto a nitrocellulose membrane using a trans-blot turbo system (Bio-Rad

250 Laboratories); protein fluorescence was acquired using a ChemiDoc™ MP Imaging System

251 (Bio-Rad Laboratories) with the Image Lab software (version 5.2.1). Proteins were then

252 probed at room temperature for 60 min with the specific rabbit primary antibody anti-iNOS

253 (1:1,000) (Life Technologies Inc.; Camarillo, CA, USA). After further washing, the

254 membrane was incubated with HRP-conjugated goat anti-rabbit IgG for 60 min (1:20,000)
255 (Life Technologies Inc.; Camarillo, CA, USA). Final detection was performed with an
256 enhanced chemiluminescence (ECL Prime) Western Blotting detection kit (GE Healthcare;
257 Buckinghamshire, UK), and the images were acquired using the ChemiDoc™ MP Imaging
258 System. Densitometry differences were analyzed with the Image Lab software and
259 normalized for total fluorescent protein signal intensity.

260 **2.12. Protein content**

261 Cells were washed with cold DPBS, lysed with 500 µL of cold Nonidet P-40 (0.25% in
262 DPBS), incubated on ice with shaking for 30 min and centrifuged at 14,000 g for 15 min.
263 Supernatants were collected and stored at -20°C until protein determination. Protein content
264 was determined according to Bradford (1976) using bovine serum albumin (BSA) as
265 standard.

266 **2.13. Statistical analysis**

267 All data were analyzed for statistical significance by one-way ANOVA, followed by
268 Dunnett's test or Tukey's honestly significant difference (HSD) test.

269 **3. Results**

270 **3.1. Bread nutritional composition**

271 The nutritional composition of the different flours is presented in **Table 2**. Bread made with
272 MA, CH and FO grains had the highest content of total nitrogen, and bread made with MA
273 and FO grains the lowest content of available carbohydrates. Water, lipids, ash, energy, and
274 selenium content were similar among the different samples.

275 The bread color profile is reported in **Table 3**. The highest L* was detected in SP and JU
276 samples, followed by TU. The ancient MA showed the highest a*, while KA the lowest.
277 The highest b*value was detected in KA.
278 TAC, TPC, and TCC were species-specific, with no clear discrimination between ancient,
279 heritage and modern grains (**Figure 2**). Overall, SP showed the highest TAC, TPC, and
280 TCC. A significant positive correlation was observed between bread TAC and TPC
281 (Pearson correlation coefficient: $r^2=0.87$; $p<0.001$), while no correlation was detected
282 between bread TAC and TCC.

283 **3.2. Digested bread**

284 Digestion causes the release of compounds from the food matrix. Consequently, after *in*
285 *vitro* digestion, both TAC and TPC were higher in the digesta than in the corresponding
286 bread. Both parameters were similar in all digesta of all bread types, except in modern RE
287 bread which showed significantly lower TAC (**Figure 3**). In the digesta, a significant
288 positive correlation was observed between TAC and TPC (Pearson correlation coefficient
289 $r^2=0.57$; $p<0.05$).
290 TCC in the digested fraction was below the detection limit, probably due to the low
291 bioaccessibility of these molecules, as previously reported by other authors (Corte-Real,
292 Richling, Hoffmann, & Bohn, 2014; Estévez-Santiago, Olmedilla-Alonso, & Fernández-
293 Jalao, 2016).

294 **3.3. Effects on cultured cells – basal condition**

295 To evaluate the effect of bread digesta in basal condition, all markers were evaluated after
296 24 h supplementation. To avoid misleading results, cytotoxicity screening should be
297 considered mandatory before performing *in vitro* studies (Di Nunzio et al., 2017).
298 Accordingly, we used the MTT method to exclude any cytotoxic effect of the supplemented
299 digesta. Supplementation with bread digesta did not decrease cell viability, which appeared
300 higher in cells exposed to ancient grains than in controls. In contrast, NaS caused a
301 significant decrease in cell viability (**Figure 4A**).
302 Compared to controls, supplementation with all bread digesta except MA and FO, and with
303 NaS decreased ROS intracellular concentration (**Figure 4B**).
304 NO secretion in the cell media increased in cells supplemented with KA and TU (ancient
305 and heritage grain, respectively) and CH (modern grain), and mainly in NaS supplemented
306 cells (**Figure 4C**).
307 Compared to controls, secretion of pro-inflammatory IL-8 was significantly higher in 3 out
308 of 4 groups of cells supplemented with modern grain bread, and in cells supplemented with
309 NaS. On the contrary, IL-8 secretion was significantly lower in KA supplemented cells than
310 in controls (**Figure 5A**). In all cells, IL-10 secretion was very low, below the detection
311 limit.
312 No differences in iNOS protein expression were detected in supplemented cells compared
313 to control ones except in FO supplemented cells that evidenced a lower expression (**Figure**
314 **5B**).
315 **3.4. Effects on cultured cells – inflamed condition**

316 To evidence a possible protective effect exerted by the different bread digesta on a
317 following inflammatory stimulus, after 24 h supplementation media were changed, and
318 cells received fresh, not supplemented medium containing the inflammatory agents. All
319 markers were evaluated after 2 h inflammation.

320 In inflamed cells, no significant differences in cell viability were detected between control
321 and cells supplemented with bread digesta, and the detrimental effect of NaS was still
322 present (**Figure 6A**). Compared to control cells, ROS concentration was significantly
323 increased in all cells supplemented with bread made with modern grains, except CH ones
324 (**Figure 6B**). NO production was not influenced by the different supplementation except JU
325 and NaS, which caused a significant increase of NO concentration in the media (**Figure**
326 **6C**).
327 The pro-inflammatory stimulus greatly increased IL-8 production in all cells compared to
328 their basal counterparts. Compared to the control cells, IL-8 production was significantly
329 higher in NaS and modern grain supplemented cells except CH ones, while no differences
330 were detected among controls and cells supplemented with ancient and heritage grains
331 (**Figure 7A**). Even in inflamed condition, IL-10 secretion was below the detection limit.
332 No changes in iNOS protein expression were detected in supplemented cells compared to
333 controls (**Figure 7B**).
334 **4. Discussion**
335 To point out differences among the different grains, bread made with the corresponding
336 flours was characterized in term of nutritional composition, color profile, TAC, TPC, and

337 TCC. Analyses evidenced a substantial similarity of nutritional profiles and selenium
338 content among bread made with the different wheat varieties. Although these results are in
339 disagreement with a previous report (Gianotti et al., 2011), they are explained by the same
340 agronomic and environmental conditions in which grains were cultivated.

341 Differences among varieties were detected in the bread color profile. The color of plant
342 foods is mainly due to natural classes of pigment as carotenoids and anthocyanins. Several
343 studies have investigated the relationship between color and carotenoids (Fratianni, Irano,
344 Panfili, & Acquistucci, 2005; Hentschel et al., 2002) underlining that the degree of
345 yellowness in wheat grain and its end products is affected by carotenoids degradation
346 during processing (Ficco et al., 2014). Accordingly, in this study, the highest L* values
347 were detected in bread having the highest TCC, namely SP and JU bread.

348 According to Dinelli et al. (2011), a high variability of antiradical activity and phenolic
349 content were observed among the investigated bread, and a significant correlation was
350 detected between TAC and TPC, as reported by Adom & Lui (2002). Anyway, it was not
351 possible to discriminate ancient, heritage, and modern grains based on their TAC, TPC and
352 TCC values.

353 Digestion process and pH conditions result in starch hydrolysis, proteolysis and release of
354 phenolics from their conjugation forms as well as cell wall matrices (Li, Koecher, Hansen,
355 & Ferruzzi, 2016; Liyana-Pathirana & Shahidi, 2005; Szawara-Nowak, Bączek, &
356 Zieliński, 2016). Accordingly, bread *in vitro* digestion allowed the release of phenolic
357 substances from the food matrix, and an about 2-fold increase of TAC and TPC was

358 observed in the digesta compared to the corresponding undigested bread. Even in the
359 digested fractions, a significant positive correlation was observed between TAC and TPC,
360 but it was not possible a discrimination of different grains based on these parameters.

361 The chemical characterization of foods is far from being a valid indicator of their
362 nutritional and health value, and biological effects must be considered. Therefore, in the
363 second part of the study we aimed to discriminate grains based on their effects when
364 supplemented as digested bread to cultured liver cells. Hepatic cells were used as model
365 system since they carry a nearly complete complement of xenobiotic metabolizing
366 enzymes, and a subportion of the catalyzed reactions result in accumulation of metabolites
367 that can cause either direct liver injury or indirect liver injury through activation of
368 inflammation (Woolbright & Jaeschke, 2015). Furthermore, oxidative stress is considered
369 as a conjoint pathological mechanism that contributes to initiation and progression of liver
370 injury (Li et al., 2015), and the liver resembles a central organ of cytokine activity
371 (Ramadori & Armbrust, 2001). HepG2 cells persist a large part of cellular functions like
372 those of normal hepatocytes (Dehn, White, Conners, Shipkey, & Cumbo, 2004; Roe,
373 Snawder, Benson, Roberts, & Casciano, 1993).

374 In basal condition, cell viability increased in cells supplemented with KAMUT® khorasan
375 bread and spelt bread, while no effect of bread pre-supplementation was observed in
376 inflamed cells. This allow excluding any effect on cell proliferation, since an increase in
377 cell number during supplementation would affect viability also after inflammation. Since

378 the MTT assay evaluates the activity of mitochondrial dehydrogenase enzyme in living
379 cells, our results seem mainly related to an increased cell vitality than cell number.
380 The about 20% decrease in cell viability observed in NaS supplemented cells compared to
381 controls could be ascribed to the alteration in mitochondrial respiratory function already
382 reported by Raza et al. (2011) in HepG2 cells. Since a similar decrease compared to pair-
383 matched controls was observed also in inflamed condition, NaS effect could be also related
384 to a cell cycle arrest and inhibition of cell proliferation (Raza et al., 2011).
385 The decrease in ROS production observed in almost all supplemented cells in basal
386 condition is suggestive of a protective effect of the supplementation against oxidative
387 stress. In inflamed condition, the protective effect observed in basal condition was not
388 present anymore; on the contrary, the pre-treatment with the bread digesta significantly
389 increased ROS concentration in cells supplemented with 3 out of 4 bread types made with
390 modern grains (FO, RE, and JU), suggesting that the pre-exposure to modern grain digesta
391 enhances the cell response to an inflammatory stimulus.
392 In basal condition, we observed an about 4-fold increase of NO concentration in KA, TU
393 and CH supplemented cells, and a > 30-fold increase in cells exposed to NaS. The
394 inflammatory stimulation increased NO production, that was similar in control and
395 supplemented cells except JU and NaS ones.
396 Oxidative stress in the form of ROS or reactive nitrogen species (RNS) generation or
397 disruption of the redox homeostasis in the cells is involved in cell signaling, self-defense,
398 and apoptosis (Zhang et al., 2016). As a RNS, NO could initiate the oxidative stress.

399 Although RNS act together with ROS to damage cells, ROS generation and NO generation
400 are not always induced in parallel. As example, silibinin has been reported to induce RNS
401 generation without inducing ROS generation (Yu et al., 2012), and Huang et al. (2017)
402 recently confirmed in pituitary GH3 cells that increased NO level can mediate the oxidative
403 stress without any increase in the ROS level. Data herein reported further confirm the
404 uncoupling of ROS and RSN generation.

405 NO is produced by nitric oxide synthase (NOS), which exists in three isoforms: neuronal
406 (nNOS or NOS-1), inducible (iNOS or NOS-2) and endothelial (eNOS or NOS-3). All of
407 them share similar structures and catalytic modes, but they show different mechanisms
408 regulating their expression and activities (Alderton, Cooper, & Knowles, 2001). The
409 expression of NOS isoforms, including those constitutively expressed, may be triggered by
410 different stimuli and in a tissue-dependent manner. Since in different cell types NaS
411 (Callejas, Casado, Boscá, & Martín-Sanz, 2002) and phenolics (Costa, Francisco, Lopes,
412 Cruz, & Batista, 2012; Vodovotz et al., 2004) have been reported to modulate NOS-2, the
413 expression of NOS-2 protein was evaluated in the different experimental conditions.
414 Unexpectedly, no modifications of NOS-2 protein expression were observed in
415 supplemented cells compared to control ones, neither in basal nor in inflamed condition.
416 The uncoupling of the observed increased in NO production to NOS-2 protein expression
417 could be ascribed to the increased activity of another NOS isoform, NOS-3. In the liver,
418 NO can be synthesized by the activity of any of the NOS isoforms, but the endothelial nitric
419 oxide synthase (NOS-3) is the main source of endogenous NO (Rockey, 1997). NOS-3

420 activity can be regulated (Gonzalez-Rubio et al., 2016), and the use of molecular treatments
421 associated with the increase of NOS-3 expression and activity has shown a beneficial effect
422 for the liver (Biecker et al., 2008). Alternatively, the increased NO availability could be due
423 to a decreased arginase (Ar) activity. Ar competes with NOS for the common substrate, L-
424 arginine. Under normal conditions, NOS metabolizes L-arginine into L-citrulline,
425 producing NO while Ar metabolizes L-arginine into L-ornithine and urea (Yang & Ming,
426 2014). Flavonoids have been reported to inhibit Ar activity in cultured endothelial cells,
427 thus increasing NO production (Schnorr et al., 2008). Further studies are needed to unravel
428 the mechanism at the basis of the observed increase in NO concentration.

429 Cytokines are the major local mediators of intercellular communications required to
430 integrate the stimuli response in immune and inflammatory processes. IL-8 is a pro-
431 inflammatory molecule inducing cytotoxic effects (Makni et al., 2011), whereas IL-10 is a
432 prototypical regulatory cytokine exerting several immune-modulatory effects, and cereals
433 have been shown to stimulate its production in monocytes (Yamazaki, Murray, & Kita,
434 2008). Since HepG2 cells have been reported to produce IL-8 and IL-10 in response to
435 specific stimulation (Valli et al., 2016), these two cytokines were chosen as markers to
436 further evaluate the possible modulation of inflammation by the different bread digesta.
437 Interestingly, in basal condition supplementation with bread made with modern grains
438 except RE increased IL-8 secretion. On the contrary, supplementation with KA reduced IL-
439 8 level. Gliadin, a class of proteins that together with glutenins is the main component of
440 the gluten fraction of the wheat seed, broadly induces cytokine (including IL-8) production

441 in cultured Caco-2 cells (Capozzi et al., 2013) and in peripheral blood mononuclear cells
442 from both patients with celiac disease and healthy controls (Lammers et al., 2011). The
443 concentration of gliadin proteins carrying allergenic epitopes among the total protein
444 pattern can influence the inflammatory response, and KAMUT® khorasan wheat has been
445 showed to have a lower percentage of epitopes than heritage and modern wheat (Valerii et
446 al., 2015). Results herein reported confirm a lower inflammatory potential of KAMUT®
447 khorasan wheat (Carnevali et al., 2014) than other tested grains. A higher concentration of
448 epitopes in gliadin protein of modern grains could also explain the observed additive effect
449 of the inflammatory stimulus and modern bread pre-supplementation on IL-8 secretion.
450 NaS supplementation (basal condition) or pre-supplementation (inflamed condition)
451 increased IL-8 secretion. A similar effect of salicylate in not-inflammatory condition has
452 been reported already in human skin fibroblasts (Ulrich-Merzenich et al., 2017). This could
453 be ascribed to the inability of nonsteroidal anti-inflammatory drugs, including NaS, to
454 interfere with NF-κB (nuclear factor κ-light-chain-enhancer of activated B cells (Callejas et
455 al., 2002), which regulates the production of many pro-inflammatory cytokines, including
456 IL-8 (Roebuck, 1999).

457 **5. Conclusions**

458 Despite the impossibility to discriminate bread made with ancient, heritage or modern
459 grains based on their chemical composition, the effects exerted by their supplementation to
460 cultured cells were different. Different markers were used to evaluate the protective role of
461 bread and, in basal condition, ancient grains ameliorated the most of them. In inflamed

462 condition, the pre-treatment with most of the bread made with modern grains enhanced
463 ROS concentration and IL-8 production.
464 The positive activity of bread made with ancient wheat and the negative activity of bread
465 made with modern wheat could be due not only to compounds naturally present in grains
466 but also to increased browning reaction during baking and toasting processes (Slavin,
467 2003). It has been reported that some Maillard reaction products (MRP), in particular,
468 melanoidins, have beneficial effects as antioxidant (through the activation of the gene
469 expression of superoxide dismutase) and anti-inflammatory factors (de la Cueva, Seiquer,
470 Mesías, Rufián-Henares, & Delgado-Andrade, 2017; Delgado-Andrade, 2014). On the
471 other hand, other compounds generated during baking and toasting such as advanced
472 glycation end products (AGE) and acrylamide, are pro-inflammatory and toxic (Davis,
473 Prasad, Vijayagopal, Juma, & Imrhan, 2016; Zamani, Shaki, AbedianKenari, &
474 Shokrzadeh, 2017), and the final effect depends on the balance between positive and
475 negative molecules. Polyphenols can inhibit acrylamide formation (Liu et al., 2015), and it
476 is conceivable that the use of different flours led to a different production of MRP, AGE
477 and acrylamide, contributing to the different overall effect (Valli et al., 2016). Furthermore,
478 the structure of fiber matrix and the way the phenolic compounds inserted in the cereal
479 matrix strongly affect their physiological function. Studies *in vivo* (Mateo Anson,
480 Havenaar, Bast, & Haenen, 2010) and *in vitro* (Adam et al., 2002) after gastrointestinal
481 digestion displayed low bioavailability of ferulic acid in cereal cell walls, reflecting its
482 association with the fiber fraction through cross-linking with arabinoxylans and lignin.

483 Although this study does not allow to discriminate between protective and detrimental
484 components, this must not be considered as a limitation since the possible synergism among
485 the different molecules and the importance of some aspects related to the food matrix is
486 known (Danesi, Govoni, D'Antuono, & Bordoni, 2016).
487 To the author's knowledge, the present study is the first one comparing ancient, heritage
488 and modern grains grown in the same environment, so leaving out possible bias related to
489 agronomic conditions. Overall, results herein reported confirm the potential health benefits
490 of ancient grains. Although the use of *in vitro* digestion reduced in part the distance from
491 the physiological situation *in vivo*, further investigations are needed to better understand
492 how ancient grains contribute to the maintenance of human health. Until those studies are
493 made, results herein reported highlight that ancient varieties could be useful in improving
494 the nutritional value of cereal products, thereby stimulating producers to use these varieties
495 in their current breeding strategies.

496

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504

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509

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786 **FIGURE LEGENDS**

787

788 **Figure 1. Scheme of experimental design and timeline in (A) basal and (B) inflamed**
789 **condition.**

790

791 **Figure 2. (A) Total antioxidant capacity (TAC), (B) total phenolic content (TPC), and**
792 **(C) total carotenoid content (TCC) of bread made with the different grains.** Data are
793 means \pm SD (n=3). Panel A: Results are expressed as micromoles of Trolox equivalents
794 (TE) per gram of bread. Panel B: Results are expressed as μ moles of mg gallic acid
795 equivalent (GAE) per gram of bread. Panel C: Results are expressed as β -carotene
796 equivalents (β CE) per gram of bread. Statistical analysis was by one-way ANOVA
797 (p<0.001) followed by Tukey's test. Different letters indicate significant differences (at
798 least p<0.05).

799

800 **Figure 3. (A) Total antioxidant capacity (TAC) and (B) total phenolic content (TPC)**
801 **of digested bread made with the different grains. Data are means \pm SD (n=3).** Panel A:
802 Results are expressed as micromoles of Trolox equivalents (TE) per gram of bread. Panel
803 B: Results are expressed as μ moles of mg gallic acid equivalent (GAE) per gram of bread.
804 Statistical analysis was by one-way ANOVA (p<0.001) followed by Tukey's test. Different
805 letters indicate significant differences (at least p<0.05).

806

807 **Figure 4. (A) Cell viability, (B) ROS intracellular concentration, and (C) NO secretion**

808 **in cells in basal condition.** Results are means \pm SD (n=6). Panel A: Results are expressed

809 as percent of value in the control cells (assigned as 100%). Panel B: Results were

810 normalized for protein content in the sample, and are expressed as percent of value in the

811 control cells (assigned as 100%). Panel C: Results are expressed as nmol NO/mL

812 medium/mg protein in the well. Statistical analysis was by one-way ANOVA ($p<0.001$)

813 followed by Dunnett's test: * $p<0.05$ and *** $p<0.001$ vs control cells.

814

815 **Figure 5. (A) Interleukin-8 (IL-8) secretion in the cell media and (B) iNOS protein**

816 **relative expression in cell lysates in basal condition.** Data are means \pm SD (panel A: n=6;

817 panel B: n=4). Panel A: Results are expressed as pg/mL medium/mg protein in the well.

818 Panel B: Results were normalized for total fluorescent protein signal intensity, and are

819 expressed as percent of value in the control cells (assigned as 100%). Statistical analysis

820 was by one-way ANOVA (panel A: $p<0.001$; panel B: $p<0.01$) followed by Dunnett's test:

821 * $p<0.05$ and *** $p<0.001$ vs control cells.

822

823 **Figure 6. (A) Cell viability, (B) ROS intracellular concentration, and (C) NO secretion**

824 **in cells in inflamed condition.** Results are means \pm SD (n=6). Panel A: Results are

825 expressed as percent of value in the control cells (assigned as 100%). Panel B: Results were

826 normalized for protein content in the sample, and are expressed as percent of value in the

827 control cells (assigned as 100%). Panel C: Results are expressed as nmol NO/mL

828 medium/mg protein in the well. Statistical analysis was by one-way ANOVA ($p<0.001$)
829 followed by Dunnett's test: * $p<0.05$, ** $p<0.01$, and *** $p<0.001$ vs control cells.

830

831 **Figure 7. (A) Interleukin-8 (IL-8) secretion in the cell media and (B) iNOS protein**
832 **relative expression in cell lysates in inflamed conditions.** Data are means \pm SD (panel A:
833 n=6; panel B: n=4). Panel A: Results are expressed as pg/mL medium/mg protein in the
834 well. Panel B: Results were normalized for total fluorescent protein signal intensity, and are
835 expressed as percent of value in the control cells (assigned as 100%). Statistical analysis
836 was by one-way ANOVA (panel A: p<0.001; panel B: n.s., not significant) followed by
837 Dunnett's test: * $p<0.05$, and *** $p<0.001$ vs control cells.